This Page Is Inserted by IFW Operations and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents will not correct images, please do not report the images to the Image Problem Mailbox.



WORLD INTELLECTUAL PROPERTY ORGANIZATION International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

WO 96/19495 (51) International Patent Classification 6: (11) International Publication Number: C07K 7/04, 14/025, 14/16, C12N 9/94, 27 June 1996 (27.06.96) (43) International Publication Date: 9/96, 9/98, 9/99

(21) International Application Number:

PCT/US95/16733

(22) International Filing Date:

20 December 1995 (20.12.95)

(30) Priority Data:

360,107 470.896 20 December 1994 (20.12.94) 6 June 1995 (06.06.95)

US

(71) Applicants: DUKE UNIVERSITY [US/US]; Erwin Road, Durham, NC 27706 (US). TRIMERIS INC. [US/US]; 4727 University Drive, Durham, NC 27707-3438 (US).

(72) Inventors: BOLOGNESI, Dani, P.; 17 Harvey Place, Durham, NC 27705 (US). MATTHEWS, Thomas, J.; 5906 Newhall Road, Durham, NC 27713 (US). WILD, Cart, T.; 1702 B Vista Street, Durham, NC 27701 (US). BARNEY, Shawn, O'Lin; 106 Branchway Road, Cary, NC 27502 (US). LAMBERT, Dennis, M.; 101 Centerville Court, Cary, NC 27513 (US). PETTEWAY, Stephen, R., Jr.; 203 Le Gault Drive, Cary, NC 27513 (US). LANGLOIS, Alphonse, J.; 1720 Vista Street, Durham, NC 27701 (US).

(74) Agents: CORUZZI, Laura, A. et al.; Pennie & Edmonds, 1155 Avenue of the Americas, New York, NY 10036 (US).

(81) Designated States: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, LS, MW, SD, SZ, UG).

Published

With international search report.

(54) Title: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

(57) Abstract

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID: 1) peptide corresponding to amino acids 638 to 673 of the HIV-1 LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

		GB	United Kingdom	MR	Mauritania
AT	Austria	GE	Georgia	MW	Malawi
AU	Australia	GN	Guinea	NE	Niger
BB	Barbados	_	Greece	NL	Netherlands
BE	Belgium	GR		NO	Norway
BF	Burkina Faso	HU	Hungary	NZ	New Zealand
BG	Bulgaria	IE	Ireland	PL	Poland
BJ	Benin	IT	Italy	PT	Portugal
BR	Brazil	JP	Japan	RO	Romania
BY	Belanus	KE	Kenya	RU	Russian Federation
CA	Canada	KG	Kyrgystan	SD	Sudan
CF	Central African Republic	KP	Democratic People's Republic	SE	Sweden
CG	Congo		of Korea	SE SI	Slovenia
CH	Switzerland	KR	Republic of Korea		Slovakia
CI	Côte d'Ivoire	KZ	Kazakhstan	SK	
CM	Cameroon	Li	Liechtenstein	SN	Senegal
	China	LK	Sri Lanka	TD	Chad
CN	Czechoslovakia	LU	Luxembourg	TG	Togo
CS		LV	Larvia	TJ	Tajikistan
CZ	Czech Republic	MC	Monaco	TT	Trinidad and Tobago
DE	Germany	MD	Republic of Moldova	UA	Ukraine
DK	Denmark	MG	Madagascar	US	United States of America
ES	Spain	ML	Mali	UZ.	Uzbekistan
Fl	Finland	MN	Mongolia	VN	Viet Nam
FR	France	MIN	taring our		
GA	Gabon				

METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a 5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

The present invention relates, first, to DP178 15 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1_{IAI} transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability, antiviral activity, such as the ability to inhibit HIV 20 transmission to uninfected CD-4+ cells, or an ability to modulate intracellular processes involving coiledcoil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178 25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids 30 558 to 595 of the HIV-1_{LAI} transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion 35 capability, antiviral activity, or the ability to

modulat intracellular processes inv lving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, noncytotoxic inhibitors of HIV-1 transfer to uninfected CD-4 cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

2. BACKGROUND OF THE INVENTION

2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

10

15

Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell death.

2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of each of these types. Infection of human CD-4 Tlymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and

30

10

15

20

replicate via a DNA int rmediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I,-II,-III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

HIV is targeted to CD-4⁺ cells because the CD-4
cell surface protein acts as the cellular receptor for
the HIV-1 virus (Dalgleish, A. et al., 1984, Nature
312:763-767; Klatzmann et al., 1984, Nature 312:767768; Maddon et al., 1986, Cell 47:333-348). Viral
entry into cells is dependent upon gp120 binding the
cellular CD-4⁺ receptor molecules (McDougal, J.S. et
al., 1986, Science 231:382-385; Maddon, P.J. et al.,
1986, Cell 47:333-348) and thus explains HIV's tropism
for CD-4⁺ cells, while gp41 anchors the enveloped
glycoprotein complex in the viral membrane.

35

10

2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991, FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptasetargeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been developed which have been shown to been active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989, Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4⁺ T-cells by some HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,

20

25

recombinant soluble CD-4 clinical trials have pr duced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

Attention is also being given to the development of vaccines for the treatment of HIV infection. 15 HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore, these proteins seem to be the most promising 20 candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system. See for example, Ivanoff, L. et al., U.S. Pat. No. 25 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119.

however, still remain far in the future.

Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

Clinical results concerning these candidate vaccines,

PCT/US95/16733 WO 96/19495

SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate 5 LAI (HIV-1_{LAI}), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1, but found in viruses and/or organisms other than HIV-1,A: Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1_{IAI}, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 30 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1 LAI transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

10

15

20

DP107 peptide sequence present within the gp41 pr tein of HIV-1_{IAI}, but found in viruses and organisms other than HIV-1_{IAI}. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for for example, enveloped viruses, such as retroviruses other than HIV-1_{IAI}, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

15 The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of 20 the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4+ cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory 25 activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides. 30

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-asociated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

35

th peptid s of the invention may be used as modulators of intracellular events inv lving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

10 The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said 15 moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for 20 example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus 25 and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

Embodiments of the invention ar demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4* cell-cell fusion (i.e., syncytial formation) and infection of CD-4* cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

30

10

15

20

3.1. <u>DEFINITIONS</u>

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as follows:

A (alanine) R (arginine) N (asparagine) D (aspartic acid) C (cysteine) 20 Q (glutamine) E (glutamic acid) G (glycine) H (histidine) I (isoleucine) L (leucine) K (lysine) M (methionine) 25 F (phenylalanine) P (proline) S (serine) T (threonine) W (tryptophan) Y (tyrosine)

V (valine)

30

4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV1A1; DP178 homologs derived from HIV-1sp (DP-185; SEQ ID:3), HIV-1_{RF} (SEQ ID:4), and HIV-1_{MN} (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2_{md} (SEQ ID:6) and HIV-2_{NDZ} (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which 10 inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. 15 Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC₅₀ refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

25

30

35

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC₅₀: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

4B: DP-180 (SEQ ID:2) represents a scrambl d c ntrol peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1_{SF2} isolate; Control, refers to the number of syncytial produced in the absence of peptide.

- FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.
- FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1)
 and DP-116 (SEQ ID:9) on CEM cells. Cell
 proliferation data is shown.
- FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM. The proteins are more fully described, below, in Section 8.1.1.
 - FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.
- FIG. 9. Abrogation of DP178 anti-HIV activity. Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41 Δ 178 or M41P Δ 178.
 - FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.
- FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common

f atures of both m dels include (1) the native stat is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally though gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended α-helix. This conformational change positions the fusion peptide for 20 interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

FIG. 20. Search results for HIV-1 (BRU 10 isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (*): PLZIP; Diamonds (*): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program 15 designed to search for such peptide regions). Asterisk (*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and 20 in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations are as in FIG. 20.

25

FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D: Peptides derived from the F1 DP107-like region.

Peptides derived from the FI DP107-11ke reg

Antiviral activity (AV) is represented by the following qualitative symbols:

"-", negative antiviral activity;

"+/-", antiviral activity at greater than
100μg/ml;

"+", antiviral activity at between $50-100\mu g/ml$; "++", antiviral activity at between $20-50\mu g/ml$; "+++", antiviral activity at between $1-20\mu g/ml$; "++++", antiviral activity at $<1\mu g/ml$.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

"-", no helicity;

"+", 25-50% helicity;

30 "++", 50-75% helicity;

 ${\rm IC}_{50}$ refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures

35

25

c ntaining no peptide. IC_{50} values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC₅₀ are as in FIG. 27A-D. IC₅₀ values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3
F1 DP107-like region. Peptide antiviral and CD data.
Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.

27A-D. Purified peptides were used to obtain IC₅₀
values, except where the values are marked by an asterisk (*), in which cases, the IC₅₀ values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3

F1 DP178-like region. Peptide antiviral and CD data.

Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.

27A-D. Purified peptides were used to obtain IC₅₀

values, except where the values are marked by an

asterisk (*), in which cases, the IC₅₀ values were

obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dim rization domain, as defined

25

by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for Pseudomonas aerginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human cfos proto-oncoprotein. Sequence search designations are as in FIG. 20.

35

10

20

FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and IC $_{50}$ are as in FIG. 27A-D. IC $_{50}$ values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

price the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown 20 with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amidoand acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: 25 column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the 30 test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B:

35

10

column to the immediate right of the test peptide name

indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself. IC_{50} is as defined in FIG. 27A-D, and IC $_{50}$ values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC₅₀ was obtained using a crude peptide preparation. 15

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data. IC_{50} as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The

30

length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

5. <u>DETAILED DESCRIPTION OF THE INVENTION</u>

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1_{LAI} transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate

25

intracellular pr cesses involving coil d-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, infra. HIV protein, gp41, DP178 corresponds to a putative α helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced 20 by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. is of interest that mutations in the C-terminal α helix motif of gp41 (i.e., the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is 30 involved in membrane fusion while the C-terminal α helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virusinduced membrane fusion.

On the basis f the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of 10 gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within 15 intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form 20 the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one 25 assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107

peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1_{LAI} isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH2-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)

30

In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below. 10 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH2) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not 15 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or 20 peptide group. Further, "2" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred 25 "X" or "Z" macromolecular group is a peptide group.

30

PCT/US95/16733 WO 96/19495

TABLE I DP178 (SEO ID:1) CARBOXY TRUNCATIONS

X-YTS-Z X-YTSL-Z X-YTSLI-Z X-YTSLIH-Z X-YTSLIHS-Z X-YTSLIHSL-Z X-YTSLIHSLI-Z X-YTSLIHSLIE-Z X-YTSLIHSLIEE-Z X-YTSLIHSLIEES-Z X-YTSLIHSLIEESQ-Z X-YTSLIHSLIEESQN-Z X-YTSLIHSLIEESQNQ-Z X-YTSLIHSLIEESQNQQ-Z X-YTSLIHSLIEESQNQQE-Z X-YTSLIHSLIEESQNQQEK-Z X-YTSLIHSLIEESQNQQEKN-Z X-YTSLIHSLIEESQNQQEKNE-Z X-YTSLIHSLIEESQNQQEKNEQ-Z X-YTSLIHSLIEESQNQQEKNEQE-Z X-YTSLIHSLIEESQNQQEKNEQEL-Z X-YTSLIHSLIEESQNQQEKNEQELL-Z X-YTSLIHSLIEESQNQQEKNEQELLE-Z X-YTSLIHSLIEESQNQQEKNEQELLEL-Z X-YTSLIHSLIEESQNQQEKNEQELLELD-Z X-YTSLIHSLIEESQNQQEKNEQELLELDK-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKW-Z 20 X-YTSLIHSLIEESQNQQEKNEQELLELDKWA-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWAS-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASL-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWN-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limit d to lipid-fatty acid 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE IA DP178 (SEO ID:1) AMINO TRUNCATIONS

```
X-NWF-Z
                                                     X-WNWF-Z
                                                   X-LWNWF-Z
                                                  X-SLWNWF-Z
                                                 X-ASLWNWF-Z
                                                X-WASLWNWF-Z
                                               X-KWASLWNWF-Z
                                              X-DKWASLWNWF-Z
                                             X-LDKWASLWNWF-Z
                                            X-ELDKWASLWNWF-Z
                                           X-LELDKWASLWNWF-Z
                                          X-LLELDKWASLWNWF-Z
10
                                         X-ELLELDKWASLWNWF-Z
                                        X-QELLELDKWASLWNWF-Z
                                       X-EQELLELDKWASLWNWF-Z
                                      X-NEQELLELDKWASLWNWF-Z
                                     X-KNEQELLELDKWASLWNWF-Z
                                    X-EKNEQELLELDKWASLWNWF-Z
                                  X-QEKNEQELLELDKWASLWNWF-Z
15
                                  X-QQEKNEQELLELDKWASLWNWF-Z
                                X-NQQEKNEQELLELDKWASLWNWF-Z
                                X-QNQQEKNEQELLELDKWASLWNWF-Z
                              X-SQNQQEKNEQELLELDKWASLWNWF-Z
                             X-ESQNQQEKNEQELLELDKWASLWNWF-Z
                            X-EESQNQQEKNEOELLELDKWASLWNWF-Z
                           X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
                          X-LIEESONOOEKNEOELLELDKWASLWNWF-Z
20 -
                         X-SLIEESONOOEKNEOELLELDKWASLWNWF-Z
                        X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                       X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                      X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                     X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                    X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                   X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
25
```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides f the inventi n als include DP178like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTIS, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

10

15

20

25

30

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amin acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The 10 insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that 15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to 25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178 region of the gp41 protein.

D letions of DP178 (SEQ ID:1) r DP178 truncations are also within the sc pe of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, 10 as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

5.2. <u>DP107 AND DP107-LIKE PEPTIDES</u>

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1_{LAI} transmembrane (TM) gp41 protein, as shown here:

NH₂-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH (SEQ ID:25)

30

In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

inv lving coiled-c il peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group $(-NH_2)$ and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

25

10

15

20

30

TABLE II DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

X-NNL-Z X-NNLL-Z X-NNLLR-Z X-NNLLRA-Z X-NNLLRAI-Z X-NNLLRAIE-Z X-NNLLRAIEA-Z X-NNLLRAIEAQ-Z X-NNLLRAIEAQQ-Z X-NNLLRAIEAOOH-Z X-NNLLRAIEAOOHL-Z X-NNLLRAIEAOOHLL-Z X-NNLLRAIEAOOHLLO-Z X-NNLLRAIEAQQHLLQL-Z X-NNLLRAIEAQQHLLQLT-Z X-NNLLRAIEAQQHLLQLTV-Z X-NNLLRAIEAQQHLLQLTVW-Z X-NNLLRAIEAQQHLLQLTVWQ-Z X-NNLLRAIEAOOHLLOLTVWOI-Z X-NNLLRAIEAOOHLLOLTVWOIK-Z X-NNLLRAIEAQQHLLQLTVWQIKQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z 20 X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA DP178 (SEO ID:25) AMINO TRUNCATIONS

```
X-KDQ- Z
                                                    X-LKDQ- Z
                                                   X-YLKDQ- Z
 5
                                                  X-RYLKDO- Z
                                                 X-ERYLKDO- Z
                                                X-VERYLKDO- Z
                                               X-AVERYLKDO- Z
                                             X-LAVERYLKDO- Z
                                            X-ILAVERYLKDQ- Z
                                           X-RILAVERYLKDQ- Z
                                          X-ARILAVERYLKDO- Z
10
                                         X-QARILAVERYLKDO- Z
                                        X-LQARILAVERYLKDQ- Z
                                       X-QLQARILAVERYLKDQ-.Z
                                      X-KQLQARILAVERYLKDQ- Z
                                     X-IKQLQARILAVERYLKDQ- Z
                                    X-QIKQLQARILAVERYLKDQ- Z
                                   X-WQIKQLQARILAVERYLKDQ- Z
15
                                  X-VWQIKQLQARILAVERYLKDQ- Z
                                 X-TVWQIKQLQARILAVERYLKDQ- Z
                                X-LTVWQIKQLQARILAVERYLKDQ- Z
                               X-QLTVWQIKQLQARILAVERYLKDQ- Z
                              X-LQLTVWQIKQLQARILAVERYLKDO- Z
                             X-LLQLTVWQIKQLQARILAVERYLKDQ- Z
                            X-HLLQLTVWQIKQLQARILAVERYLKDQ- Z
                          X-QHLLQLTVWQIKQLQARILAVERYLKDQ- Z
20
                         X-QQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                        X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                       X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                      X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                     X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                    X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                   X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
25
                  X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                 X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"2" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier. group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTIS, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

10

35

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid 20 conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid 30 substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) t aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The 10 insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides. as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107 20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107 region of the gp41 protein.

30

35

PCT/US95/16733 WO 96/19495

10

20

35

Deletions of DP107 (SEQ ID:25) r DP178 truncations are als within the sc pe f the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to 15 modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

DP107 and DP178 ANALOGS

25 Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1LAI enveloped viruses, 30 non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

ability t m dulate intracellular pr cesses involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (i.e., other than HIV-1_{LAI}) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates.

DP178 analogs derived from the corresponding gp41 peptide region of other (i.e., non HIV-1_{LAI}) HIV-1 isolates may include, for example, peptide sequences as shown below.

NH₂-YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH2-YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF-COOH (SEQ ID:4);

 NH_2 -YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1_{SF2}, HIV-1_{RF}, and HIV-1_{MN} isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding positi n in the DP178 (SEQ ID:1) peptide. One such

35

10

15

20

DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV- $2_{\rm NHZ}$ isolate has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH2-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

of the HIV-2_{NHZ} DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH₂) and "Z" may represent a carboxyl (-COOH) group.

Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a

c valently attached macr molecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

TABLE III

HIV-2_{NDKZ} DP178 analog carboxy truncati ns.

X-LEA-2 X-LEAN-Z X-LEANI-Z X-LEANIS-Z 5 X-LEANISQ-Z X-LEANISOS-Z X-LEANISQSL-Z X-LEANISQSLE-Z X-LEANISQSLEQ-Z X-LEANISQSLEQA-Z X-LEANISQSLEQAQ-Z X-LEANISQSLEQAQI-Z 10 X-LEANISQSLEQAQIQ-Z X-LEANISQSLEQAQIQQ-Z X-LEANISQSLEQAQIQQE-Z X-LEANISQSLEQAQIQQEK-Z X-LEANISQSLEQAQIQQEKN-Z X-LEANISQSLEQAQIQQEKNM-Z X-LEANISQSLEQAQIQQEKNMY-Z 15 X-LEANISQSLEQAQIQQEKNMYE-Z X-LEANISQSLEQAQIQQEKNMYEL-Z X-LEANISQSLEQAQIQQEKNMYELQ-Z X-LEANISQSLEQAQIQQEKNMYELQK-Z X-LEANISQSLEQAQIQQEKNMYELQKL-Z X-LEANISQSLEQAQIQQEKNMYELQKLN-Z X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

25

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV HIV-2_{NDHZ} DP178 analog amin truncati ns.

```
X-NWL-Z
                                                    X-TNWL-Z
                                                   X-FTNWL-Z
                                                  X-VFTNWL-Z
                                                 X-DVFTNWL-Z
                                                X-WDVFTNWL-Z
                                               X-SWDVFTNWL-Z
                                              X-NSWDVFTNWL-Z
                                             X-LNSWDVFTNWL-Z
                                            X-KLNSWDVFTNWL-Z
                                           X-OKLNSWDVFTNWL-Z
                                          X-LQKLNSWDVFTNWL-Z
10
                                         X-ELQKLNSWDVFTNWL-Z
                                        X-YELQKLNSWDVFTNWL-Z
                                       X-MYELQKLNSWDVFTNWL-Z
                                     X-NMYELQKLNSWDVFTNWL-Z
                                     X-KNMYELQKLNSWDVFTNWL-Z
                                   X-EKNMYELQKLNSWDVFTNWL-Z
                                  X-QEKNMYELQKLNSWDVFTNWL-Z
15
                                 X-QQEKNMYELQKLNSWDVFTNWL-Z
                                X-IQQEKNMYELQKLNSWDVFTNWL-Z
                               X-QIQQEKNMYELQKLNSWDVFTNWL-Z
                              X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
                             X-QAQIQQEKNMYELQKLNSWDVFTNWL-2
                            X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                           X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                          X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20
                         X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                        X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                       X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                      X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                     X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                    X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                   X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
25
```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

PCT/US95/16733 WO 96/19495

> DP178 and DP107 analogs are recognized or identified, for example, by utilizing one r more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, 10 in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence 15 homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV).

20 Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or 25 otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et

35 al., 1991 Science 252:1162-1164) is inadequate for

identifying protein regions analog us to DP107 r DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

15

20

25

30

35

The computer search strategy of the invention, as demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database package, preferably PC/Gene.

A series of search motifs, the 107x178x4,
ALLMOTI5 and PLZIP motifs, were designed and
engineered to range in stringency from strict to
broad, as discussed in this Section and in Section 9,
with 107x178x4 being preferred. The sequences

PCT/US95/16733 WO 96/19495

> identified via such search motifs, such as thos listed in Tables V-XIV, below, p tentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed or braced amino acids is followed by a number in 20 parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

The ALLMOTI5 is written as follows: 25

15

```
\{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-
\{CDGHP\} - \{CFP\} (2) - \{CDGHP\} - \{CFP\} (3) - \{CDGHP\} - \{CDGHP\} - \{CFP\} (3) - \{CDGHP\} - \{CDGHP
   \{CDGHP\} - \{CFP\} (2) - \{CDGHP\} - \{CFP\} (3) - \{CDGHP\} - \{CDGHP\} - \{CFP\} (3) - \{CDGHP\} - \{CDGHP
      {CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
   \{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-
```

Translating this motif, it would read: "at the 30 first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except 3, F, or P is acceptable, at the fourth 35 heptad position (D), any amino acid residue except C,

D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTIS motif, a 35-mer search is preferred. viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino a cid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

10

15

30

35

The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is d signed to search for

four consecutive heptad repeats (thus the repeat of the first line four times), meaning that it search s for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in Table VII, below at the end of this Section, being preferred.

10

The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.

19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. Fr example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII 1sts viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table XIV lists viral sequences identified via P23TLZIPC search motifs The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention.

The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

20

25

30

The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178, above, in Section 5.1. For example, these peptides

may include any of the additional amin -terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section 5.2.

15 Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory 20 Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX presents Human Parainfluenza Virus 3 Fl region DP178 25 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped according to the specific virus which they inhibit, 35

including respiratory syncytial virus, human parainfluenza virus 3, simian immunodeficiency virus and measles virus.

TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

1 1 1 1 1 1 1 1 1 1	TALE WORLD	AP VECES OF STATE OF	Ī	ABLAR	ABEAS	3	777	4	1.62.	
POTENTIAL 198 KD PROTEIN POTENTIAL 198 KD PROTEIN DELTA ANTIGEN ANTITROCABINALINION PROTEIN ANTITROCABINALINION PROTEIN ALPIA TRANS-BOUCENG PROTEIN COAT PROTEIN VPI COAT PROTEIN COAT PROTEIN COAT PROTEIN COAT PROTEIN CO	PROTEIN		32		١	Γ				•
POTENTIAL 14 KO PROTEIN 11 15 KO PROTEIN 11 15 KO PROTEIN 11 15 KO PROTEIN 12 15 ANTIGEN DELTA ANTIGEN ANTIGEN ANTIGEN ANTIGEN ANTIGEN ALPIA TRANS-DEUCENO FACTOR ALPIA TRANS-DEUCENO FACTOR ALPIA TRANS-DEUCENO PROTEIN ALPIA TRANS-DEUCENO PROT	POTENTIAL 170 KD PROTECH	TOBACCO RATTLE VIRUS (STRAIM PSO)	T	314.348	101.446	644.678	1045-1079	1135-1176	1115-1376	
13 19 KO PROTEIN DELTA ANTIGEN ALPHA TRANS-BOUCHO FACTOR ALPHA TRANS-BOUCHO FACTOR ALPHA TRANS-BOUCHO FACTOR ALPHA TRANS-BOUCHO FACTOR ALPHA TRANS-BOUCHO PROTEIN ALPHA TRANS-BOUCHO	POTENTIAL 194 KD PROTEIN	IOBACCO RATTLE VIRUS (STRAIM SYNI	T	T	l					
DELTA ANTIGEN DE	STORE	GRPES SUPLEX VIRUS (TYPE 4 / STRAIN UGANDA-1102)		1						
DELTA ANTIGEN ALPIA TRANS-PROUCING FACTOR ALPIA TRANS-PROUCING PROTEIN ALPIA TRANS-PROTEIN ALPIA TRANS-PROUCING PROTEIN COAT PROTEIN V??	DET TA ANTIGEN	(EPATITIS DELTA VIRUS (ISOLATE AMERICAM)	1							:
DELTA ANTIGEN (LPNA ANTIGEN) DELTA ANTIGEN (LPNA ANTIGEN) DELTA ANTIGEN MATTIGEN MATTIGEN DELTA ANTIGEN DELTA PROTEIN VPI COAT PROTEIN VPI	STATE AND CEN	HEPATITIS DELTA VIRUS (ISOLATE DISO)								
DELTA ANTIGEN TANSE DECLUSION PROTEIN ALPIA TRANS-DECUCHO PROTEIN TANS-DECUCHO PROTEIN TO COAT PROTEIN V??	DELTA ANTIGENIAL PHA ANTIGEN	REPATITIS DEL TA VIRUS (ISOLATE ITALIAN)	1	- I						
DELTA ANTIGEN ANTITROCALUSION PROTEIN ALPIA TRANS-BOUCING PACTOR PUTATIVE A-TYPE BICLUSION PROTEIN ALPIA TRANS-BOUCING PROTEIN COAT PROTEIN V??	DELLA AVEICEN	IEPATITIS DELTA VIRUS (ISOLATE LEBANON-I)							<u> </u>	
DELIA ANTIGEN DE	DECIA ANTIGEN	REPATITIS DEL TA VIRUS (ISOLATE JAPANESE M-1)	2.48	8						: :
DELIA ANTIGEN ANTIGEN LI ED A.TYPE INCLUSION PROTEIN ALPIA TRANS-DEDUCING PACTOR ALPIA TRANS-DEDUCING PROTEIN COAT PROTEIN V?	DELIA AMILIARA	EPATITIS DELTA VIRUS (ISOLATE IAPANESE AI-3)	2.48	8						:
DELTA ANTIGEN DELTA ANTIGEN DELTA ANTIGEN DELTA ANTIGEN DELTA ANTIGEN DELTA ANTIGEN MATITHOLOGIN-LII KOMOLOG WATITHOLOGIN-LII KOMOLOG WATITHOLOGIN-LII KOMOLOG WATITHOLOGIN-LII KOMOLOG MATITHOLOGIN-LII KOMOLOG ALPIA TRANS-DEDUCING FACTOR ALPIA TRANS-DEDUCING PROTEIN COAT PROTEIN VP1	DELIA ANTIGEN	REPATITIS DELTA VIRUS (ISOLATE NAURU)	3.4	180						
DELTA ANTIGEN DELTA ANTIGEN DELTA ANTIGEN MATTIMOMEN-III HOMOLOG MATTIMOMEN-III HOMOLOG MATTIMOMEN-III HOMOLOG MATTIMOMEN-III HOMOLOG MATTIMOMEN-III HOMOLOG MATTIME ATTYRE INCLUSION PROTEIN ALPIA TRANS-DEDUCING FACTOR ALPIA TRANS-DEDUCING PROTEIN MATATIVE A-TYPE DICLUSION PROTEIN MATATIVE MATATIVAS-DIDUCING PROTEIN MATATIVE MATATIVAS-DIDUCING PROTEIN MATATIVE MATATIVAS-DIDUCING PROTEIN MATATIVE MATATIVAS-DIDUCING PROTEIN	DELIA ANTIGEN	(EPATITIS DELTA YIRUS (ISOLATE JAPANESE S-I)	-49	8						: !
DELTA ANTIGEN MATTITICAMENHI HOMOLOG WE KD A-TYPE INCLUSION PROTEIN LIE DA -TYPE INCLUSION PROTEIN ALPHA TRANS-BOUCING FACTOR ALPHA TRANS-BOUCING FACTOR ALPHA TRANS-BOUCING PROTEIN MATATIVE A-TYPE BOCLUSION PROTEIN MATATIVE A-TYPE BOCLUSION PROTEIN ALPHA TRANS-BOUCING	DELTA ANDICEN	GEPATITIS DELTA VIRUS (ISOLATE IAPANESE S-1)	•	8						: -
ANTITION OF THE INCLUSION PROTEIN II KD A-TYPE INCLUSION PROTEIN II KD A-TYPE INCLUSION PROTEIN ALPHA TRANS-INDUCING PACTOR ALPHA TRANS-INDUCING PACTOR ALPHA TRANS-INDUCING PROTEIN COAT PROTEIN VP1 COAT PROTEI	DELLA AUTICEN	HEPATITIS DELTA VIRUS (ISOLATE WOODCINICK)	7	8						: :
M KD A. TYPE INCLUSION PROTEIN ALPHA TRANS-PROUCHOR ACTOR ALPHA TRANS-PROUCHOR ACTOR ALPHA TRANS-PROUCHOR ACTOR ALPHA TRANS-PROUCHOR PROTEIN PUTATIVE A-TYPE INCLUSION PROTEIN ALPHA TRANS-PROUCHOR PROTEIN COAT PROTEIN V??	AND THE PROPERTY OF	FOWLPOX VIRUS (ISOLATE IIP-418)	١							:
11 I DA TYPE INCLUSION PROTEIN ALPHA TLANS-ROUCHOG ACTOR ALPHA TLANS-ROUCHOG PAOTEIN ALPHA TRANS-ROUCHOG PAOTEIN ALPHA TRA	AND A TYPE DATI DELIN PROTEIN	VACCIMIA VIRUS (STRAIN WR)		420.564	\$ 20-07.5					:
ALPHA TRANS-INDUCTION FACTOR ALPHA TRANS-INDUCTION FACTOR ALPHA TRANS-INDUCTION FACTOR ALPHA TRANS-INDUCTION FROTEIN ALPHA TRA	A AU ALLING INCOMPROTEDI	VANIOLA VIRUS	425-525	\$31.565	171.628					_ن
ALPHA TRANS-ROUCHOOF ACTOR ALPHA TRANS-ROUCHOOF ACTOR ALPHA TRANS-ROUCHOOF ACTOR FUTATIVE A-TYPE BACLUSION PROTEIN FALPAS-BADGENO PROTEIN FALPAS-BADGENO PROTEIN FUTATIVE A-TYPE BACLUSION PROTEIN FUTATIVE A-TYPE BACLUSION PROTEIN FUTATIVE A-TYPE BACLUSION PROTEIN FUTATIVE A-TYPE BACLUSION PROTEIN FUTATIVE BACTEN VP1 FUTATIVE A-TYPE BACTEN VP1 FUTATIVE A-TYPE BACTEN VP1 FUTATIVE A-TYPE BACTEN VP2 FUTATIVE A-TYPE BACTEN VP3 FUTATIVE A-TYPE A-TYP	THE STATE OF PURCHASE ACTOR	HERPES SIMPLEX VIRUS (TYPE I)	304.345							-
ALPHA TRANS BROUCHOUR ACTOR PUTATIVE A-TYPE BROLLUSION PROTEIN ALPHA TRANS-BROUCHOUR ACTOR ALPHA TRANS-BROUCHOUR PROTEIN A COAT PROTEIN VP: COAT	ALTENA TRANSCRIPTING FACTOR	HEADES SOULEX VIRUS (TYPE I)	102-139	201.14			1			!
ALPAN TITRE A-TYPE BACLUSION PROTEIN ALPAN TRANS-BOUCHOR SACTOR ALPAN TRANS-BOUCHOR PROTEIN (YAPWES) A COAT PROTEIN YPI CO	ALTIN TANK DESIGNO BACTOR	EQUINE KERPESVIRUS TYPE I (STRAIN ABAP)	101.141	264-331					-	· : !_
ALPIA TRANS-BUILDING PROTEIN ALPIA TRANS-BUILDING PROTEIN ALPIA TRANS-BUILDING PROTEIN (ALPIA TRANS-BUILDING PROTEIN VP) A COAT PROTEIN VP) COAT	ALTIN INC. THE BUT INION PROTEIN	VACCINIA VIXUS (STRAIN COPENHAGEN)	79-124	\$19.763						:
ALPHA TRANS-BROUCHOR FACTOR ALPHA TRANS-BROUCHOR FROTEIN ALPHA TRANS-BROUCHOR PROTEIN A COAT PROTEIN VP1 COAT PROTEIN VP1 COAT PROTEIN VP1 COAT PROTEIN VP2 COAT PROTEIN VP3 COAT PROTEI	TOTAL A TANK DO INCOME PROTEIN	VACCINIA VIRUS	19.124							: :
ALTHA INCREMENT OF THE ALLESTON FOURTH IN ALTHA TRANS-INCIDENCE PROTEIN (YAPWAS) IN ALTHA TRANS-INCIDENCE PROTEIN (YAWAS) IN ALTHA TRANS-INCIDENCE PROTEIN (POINTING A-117E INCLUSION PROTECTION	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	198-361	195-429						:
ALPIA TRANS-ROUCHO PROTEIN ("ALWAS) ALPIA TRANS-ROUCHO PROTEIN ("ALPIA TRANS-ROUCHO "ALPIA TRANS-ROUCHO "ALPIA TRANS-ROUCHO "ALPIA TRANS-ROUGHO "	ALPHA TRANS-INDUCTING FACTOR	VACCINIA VINUS	51-95							-
ALPIN TRANS-DEGICING PROTEIN (ALPIN TRANS-DEGICING PROTEIN VP) A ALPIN TRANS-DEGICING PROTEIN (ALPIN TRANS-DEGICIN VP) A COAT PROTEIN VP)	PULATIVE ALT THE INCLUSION PROTEDI CANALS	HERPES SDOLEX VIXUS (TYPE 2)	178-219	124-301						
ALPIA IRANS-DOUCHO PROTEIN ALPHA TRANS-DOUCHO PROTEIN ALPHA TRANS-DOUCHO PROTEIN ALPHA TRANS-DOUCHO PROTEIN ALPHA TRANS-DOUCHO PROTEIN A COAT PROTEIN VPI COAT PROTEIN V	ALPHA TRANS-INDICATE CROTEIN (NAME)	HERPES SIMPLEX VIRUS (TYPE 2)	177.272	124-161				1		
ALPHA TRANS-DEDUCEND PROTEIN ALPHA TRANS-DEDUCEND PROTEIN ALPHA TRANS-DEDUCEND PROTEIN A. TYPE PROLUSION PROTEIN A. TYPE PROLUSION PROTEIN A. COAT PROTEIN VP COAT PROTEI	ALTIA I KANS-INDUCINO INDICENTA	BOVINE HERPESVIRUS TYPE I	195-256							
ALPHA TRANS-INDUCINO PROTEIN (ALPHA IRANS-INDUCING PROJECT	EDUTAG HERPESVIRUS TYPE I	241-289					_		: -;-
MATTAL INCOLUSION PROTEIN MATTAL INCOLUSION PROTEIN MATTAL INCOLUSION PROTEIN MATTAL INCOLUSION PROTEIN MATTAL INCOLUSION PROTEIN VP MATTAL INCOLUSION PROTEIN MATTAL INCOLUSION PROTEIN MATTAL INCOLUSION PROTEIN PROTEIN PROTEIN MATTAL INCOLUSION PROTEIN P	ALTHA I MANSHAUCHAU PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	206-252							:
TALKECALTION ACTIVATOR BALFI TALKECALTION ACTIVATOR BALFI TALKECALTION ACTIVATOR BALFI TALKECALTION ACTIVATOR TO COAT PROTEIN VPI	ALTHA IRANSHINGA PROTION	COWPOX VIRUS	14.53	475-576	33.56	\$72.429	103-336			: : :-
TALLIER ACTIVATOR BALFI TALLICATOR ACTIVATOR BALFI THANGGLATOR VI THANGGLATOR THANGGLATOR T	PROTECULARIA SA	EPSTEIN-BAAR VIRUS (STRAÑ BOS-1)	8 ===			$\frac{1}{4}$				
### GOAT PROTEIN VP1 ### COAT PROTEIN VP1 COAT PROTEIN VP1	THE ANCORPORTION ACTIVATOR BRLF!	EPSTEIN-BARK VIRUS (STRAIN D95-1)	150-187							:
COAT PROTEIN VPI	COAT PROTEIN VP.	POLYGMANTUS BK	101-141							1
COAT PROTEIN VP1 COAT PROTEIN VP1 COAT PROTEIN VP2 COAT PROTEIN VP3 COAT P	COAT PROTEIN VP	POLYOMAVIRUS BK	103.141			\downarrow				
COAT PROTEIN VP1 COAT PROTEIN VP2 COAT PROTEIN VP3	COAT PROTEST VP	HAMSTER POLYOMAVIRUS	159-195							
COAT PROTEIN VP3 V COAT PROTEIN VP3	COAT PROTEIN VP.	SINIAN VIRUS 40	199.143			1		-	!	
COAT PROTEIN VP1	COAT PROTEIN VP3	BUDGERIGAR FLEDGLING DISFASE VIRUS						į	-	
COAT PROTEIN VP2 COAT PROTEIN VP3	COAT PROTEIN VP2	POLYOMANIRUS DK (STRAÍN AS)	2							<u>:</u>
COAT PROTEIN V71 COAT PROTEIN V72 COAT PROTEIN V71	COAT PROTEIN VP2	POLYOMAVIRUS BK								:
COAT PROTEIN VP 1 COAT PROTEIN VP 1 COAT PROTEIN VP 1 COAT PROTEIN VP 2 COAT PROTEIN VP 2 COAT PROTEIN VP 3 COAT PROTEIN VP 3 COAT PROTEIN VP 3 W COAT PROTEIN VP 3	COAT PROTEIN VP3	BOVINE POLYONIAVIRUS		100			<u> </u>			<u>:</u>
COAT PROTEIN VY 2 COAT PROTEIN VY 2 COAT PROTEIN VY 3 COAT PROTEIN VY 3 COAT PROTEIN VY 3 COAT PROTEIN VY 3 V COAT PROTEIN VY 3 COAT PROTEIN VY 3 COAT PROTEIN VY 3	COAT PROTEIN VP2	HAMSTER FOLYOMAVIRUS		136.116			 -		 -	
COAT PROTEIN V? COAT PROTEIN V COAT PROTEIN V COAT PROTEIN V COAT PROTEIN V COAT PROTEIN	COAT PROTEIN VP3	POLYOMAYINUS AC		1,66.304			L			
COAT MOTEN V72 COAT MOTEN COAT PROTEN COAT PROTEN COAT PROTEN COAT PROTEN	COAT PROTEIN VP3	LYBHOTROFIC POLTORIA VIROS	5							
COAT PROTEIN V72 COAT PROTEIN V72 COAT PROTEIN V72 COAT PROTEIN COAT PROTEIN COAT PROTEIN COAT PROTEIN COAT PROTEIN	COAT PROTEDN VP.1	MOUSE POLYONAVIRUS (31 KANA 1)		31:13		-				
COAT PROTEIN V73 COAT PROTEIN V73 COAT PROTEIN COAT PROTEIN COAT PROTEIN COAT PROTEIN COAT PROTEIN	COAT PROTEIN VP2	MOUSE FOLTONIAVIRUS		10.00					_	_
COAT PROTEIN VY2 COAT PROTEIN VY2 COAT PROTEIN COAT PROTEIN VY1 COAT PROTEIN VY1	COAT PROTEIN VP3	MOUSE POLYOMAVIRUS	27.5	13.21						
COAT PROTEIN VY2 COAT PROTEIN COAT PROTEIN COAT PROTEIN COAT PROTEIN	COAT PROTEIN VP2	MOUSE FOLYOMAVIRUS	1 3	228.262	28:31	ļ	L			
COAT PROTEIN COAT PROTEIN COAT PROTEIN VP. COAT PROTEIN VP.	COAT PROTEIN VP3	SPGAN VINUS 40								
COAT PROTEIN COAT PROTEIN VP.1 COAT PROTEIN	COAT PROTEIN	ABUTEON MOSAIC VIRUS (ISOLATE WEST INDIA				-				: -
COAT PROTEDI VPI	· COAT PROTEIN	APPLE CHLOROTIC LEAF SPOT VIRUS	100			-				_
COAT PROTEIN	COAT PROTEDI VP I	AEDES DENSONUCLEOSIS VINUS	34.30	11.00		-	L			
	COAT PROTEIN	ARTICHOKE MOTTLED CHIMALE VIAUS								
COAT PROTEIN	COAT PROTEIN	BEAN LEAFROLL VIRUS								

CCINE			Ī				7			
				4854	A PAR	1	1			
l.	NATURAL DESCRIPTION OF THE PROPERTY OF THE PRO	VIRUS	10.3	1						
١	CONTROL		163-197	1						
PCOAT BWY	S. S		163-197	1						1
COAT BYDY!	TOTAL STORY		164-196	1						
COAT BYDYN	COALTANTEN		164-198	1						
PCOAT BYDY	COAT PROJECT		26.90	114-733						
COAT BYDYR	COATPACIENT	(3) Marie	19:65	117.334						
PCOAT CUPYC	COAT MOTEUR		26.80	164-333						!
PCOAT CAMP	COAT PROJESIA	CAULIFLOWER MOSAIC VIRUS	8.3	184-333						:
PCOAT CAMPE	COAT PROTEIN	CALLIFLOWER MOSAIC VIRUS	19:05	187.234						!
PCOAT CALIVIN	COAT PROTEIN	CAULIFLOWER MOSAIC VIRUS	1							: 1_
PCOAT CAMVS	COAT PROTEIN	CARNATION MOTTLE VIRUS								!
PCDAT CAUNY	COAT PROTEIN	COUPEA CHI OROTIC MOTTLE VINUS							j	
YCOAT COAV	COAT PROTEIN	CABUATION ETCHED AING VIRUS								· ::-
200	PROBABLE COAT PROTEIN	STATE STATE BY BY SABIA CITLORELLA VIRUS I	207	1						_;
SCOAT COVE	MINIOR CAPSID PROTEIN	CASSAVA I ATENT VIRUS	197.231			-			-	
3 2 2 2 2 2	COAT PROTEIN	CASSACT AFERT VIRIS	167-231							
S C AVOC	COAT PROTEIN	CASACA MINISTER AND	133-167			-			-	
2000	COAT PROTEIN	COCOMISS ACCESS VINCEN	13)-167			1	-	_		:
100	COAT PROTEIN	COLUMBIA MORAL VIEWS	183-187			-				:
100	COAT PROTEIN	COCUMBER AND ALCOME	133-103					_		-
	COAT PROTEIN	COCUMBER PROJECT	153-187			-	-		L.	-
COAL CAN	STORY STORY	CUCUMBER MOSAIL TIMOS	183.187				ļ			: -
PCOAT CANAL		CUCUMBER MOSAIC VIRUS	328-365							ļ
PCOAT CARY	COAT PROTEIN	CUCUMBER MECROSIS VIRUS	104.315							 -
PCOAT CAV	COAT PROTEIN	CHE ORUS STRUATE MOSAIC VIRUS								i
PCOAT CSMV	COAT PROTEIN	CITAUS TRUSTEZA VIRUS	100.00						1	-
PCOAT CTVM	COATMOTER	CLOVER YELLOW MOSAIC VIRUS								1
PCOAT CYNY	COAT PROTEIN	ECCPLANT MOSAIC VIRUS		246-600						1
PCOAT EPMY	COAT PROTEIN	FELINE CALICIVIAUS	95 60	CAA.400						+
PCDAT FCVC	COAT PROTEIN	FFI INE CALICIVIRUS		100.001		_				1
PCOAT FCVF4	COAT PROTEIN	FELINE CALICIVIRUS	177.100	206.241	49.65					1
PCOAT FCVF9	COAT PROTEIN	FIGWORT MOSAIC VIRUS								1
PCOAT PAND	PROBABLE COAT PROTEIN	FOXTAIL MOSAIC VIRUS	27.00		L	-				1
MOAT FOON	COAT PROTEIN	TIME A DEDESCENT VIRUS	Ř			-				-
COAT DAVI	CAPSID PROTEIN	ENAIL RIM RUDESCENT VIRUS	2	1	1					4
PCOAT BIVE	CAPSID PROTEIN	CUIT O INDESCENT VIRUS	21.5							4
PCDAT IRV6	CAPSID PROTEIN	LA V SYMPTOM ESS VIRUS	32.70	A T			-			-
PCOAT LSV	COAT PROTEIN	AAAIDE STRIPE VIRUS	1.36		1		-	-		4
VIEW LACT	COAT PROTEIN	STATE CTREAK VALIS	187-221			-	-	-	-	_
TANK TANK	COAT PROTEIN	MALE STREAM VIETS	167-231			1				
WAY TANK	COAT PROTEIN	MAKE STAFFA CALLS	107-221		1	1				
100	COAT PROTEIN	MAUZE STREET THE STREET VIRUS	105.139			+				
POAT ORSV	COAT PROTEIN	BOVOR DARVOVIRUS	380-414	2	1	1	-			i
ONA TACOM	COAT PROTEIN VP2	SUSTRICT PARKOVALIS	497-531			 				
DAYS AVOICE	COAT PROTEIN VPI	CALIFE TAN TO VIEUS	13-114			\ 		-		
AUG TACK	COAT PROTEIN	PEA EXCEL PROPERTY	16-11		1		+			
POPAT POPAY	COAT PROTEIN	POLICE PROSPER AND MOTTLE VIRUS	104-138		1	+	+	-		
TACA TACA	COAT PROTEIN	FEFFEN MILL MO	11-11	2 2 2 2 2	1	$\frac{1}{1}$	+	-		
100	COATPROTEIN	POTATO VINOS	190-124		1		+			
PCOAL PVS	T	POTATO YELLOW MUSAIL VINUS	10.44	140-199			-	+	-	-
PCOAT PTMV	F	RASPBERIT BUNKT DWALL VINUS	272-306				+	-	-	-
ACOVI MON	T	RED CLOVER MELKUIN MUSIC LINES	34-68	83-120	20.00	1	$\frac{1}{1}$	-	-	
POOAT RUMM	T	NICE STRUTE VIKUS	190-224			1	-	1		
VOAT ISV	CONTRACTOR	SORO LES CONTRACTOR DE LA CONTRACTOR DE								

1000										
T.C.LAIL	PROTEIN	VRUS	81.3						1	
1000	COAT PROPER	SATELLITE MAIZE WHITE LINE MUSAN, TIMOS								
LOVE WATER	CONT. THE CONT. OF THE CONT.	SOYBEAN CHLOROTIC MOTTLE VIRUS	8			+		-		
COAT SOON	COALTROLEIN	SATELLITE TOBACCO NECROSIS VIRUS I	S.						-	
PCOAT STRVI	LUALTRUIEIN	SATELLITE TOBACCO NECROSIS VIRUS 2	?							
PCOAT STAVE	COALTROLEIN	TANDALO MOSAIC VIRUS	57				1	-		:
PCOAT TANV	GENCHA POLITICAL	TOMATO ASPERATY VIRUS					+			
PCOAT TAV	COAT PROTEIN	TOMATO BUSHY STUNT VIRUS	1	63:10		1	†		Ī	
PCOAT TBSVD	COAT PROTEIN	TOWATO BUSHY STUNT VIRUS	44.78	8.5			1	1	İ	:
MONT THIS VC	COAT PROTEIN	TIBNIP CADACLE VIRUS	13-46				+	+	Ī	:
PCOAT TCV	COAT PROTEIN	POMALATO CON DEN MOSAIC VIRUS	186-220				1	+	İ	:
PCOAT, TGACV	COATPROTEIN	PORACTO WITH DICREEN MOSAIC VIRUS	101-133				+		Ì	1
PCOAT THOMY	COATPROTEIN	TOBACCO MORAIC VIBILS	103-137				1	+		
PCOAT THAY	COAT PLOTEIN	TOBACCO MOSAIC VIBILS	103-137					+		
PCOAT THAT	COAT PROTEIN	CONTROL OF THE CONTRO	76-138				1	+		
PCOAT_TIMOCO	COAT PROTEIN	SOUTH TOTAL VIBILE	103-137				1	1		
PCOAT THANDA	COAT PROTEIN	SOURCE LINES IN CHAILS	103-137				1	+		
PCOAT_TMYER	COAT PROTEIN	POPACO MOSAN VIBILE	103-137					+		
PCOAT_THAMBL	COAT PROTEIN	SOMACCO LOCARE VIBILE	103-137				1	+		
PCOAT_TIMO	COAT PROTEIN	STORY CONTRACT CITY OF THE CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CITY OF THE CONTRACT CIT	103-137					+		
PCOAT THOOM	COAT PROTEIN	SOBACCO MOSAIC VIRUS	103.137				1			
PCOAT THEYTO	COAT PROTEIN	TOPACCO ATT E VIETS	71-109							
PCOAT TRVCA	COAT PROTEIN	STATE COLORS	69-103							İ
PCOAT TRVTC	COAT PROTEIN	SOBACTO VELLOW DWARF VIRUS	3.30					1	İ	1
PCOAT TYDYA	COAT PROTEIN	TOTAL OF THE POST	41.75				1			!
PCOAT TYNAY	COAT PROTEIN	TOWNS TELLOW MODELS TIMES	41.75							1
PCOAT TYNVA	COAT PROTEIN	TOTAL TELLOW FLOSALE TIMES	163.197						7	:
PCOAT WCLIVO	COAT PROTEIN	WHITE CLOVER PRODUCT VINCE	84-135					1		
PCORA HPBGS	CORE ANTIGEN	GROUND SQUINE IIII SILIII	11.140						İ	
PCORA HOBY	CORE ANTIGEN	THE A LINE AND THE VIBIG I	62.106					_		
PCORA WHVI	CORE ANTIGEN	WOOLANDER HERATIFIC VIRIA	13.10						-	
PCORA WIRVE	CORE ANTIGEN	WOODLINGE THE ATTENDED	198-232					-: 	:	
PD250_ASPB7	PROTEIN DISOR	A MILAN SWINE TO VIEW TO THE STATE OF THE ST	917.15	!				-	:	
PDACE ADECU	EALT ELA DNA-BINDING PROTEIN	HUNGAR ALCONOMIC TOPL C	201-336					-	:	
PONGS ADEBS	EASLY E2A DNA-BINDING PROTEIN	FORTER BARB VIBIS	215.352	116.752	974.10%	10:7:1068		_		
PONDI EBV	MAJOR DNA-BINDING PROTEIN	MANANCYTONE CAL DVIRUS	118.172	1013-107A			ר ו		:	
POPUL HOWA	MAJOR DNA-BROUNG FRUIEIN	LEBBER CARD BY CARIS	\$57.595	099.640	169-80)	1079-1140		-	!	
PDPMI HSVII	MAJOR DWA-BINDING PRUISIN	LEBER CACHER Y VIRUS	\$53.535	5.	164-803	1679-1140	_ 	-	:	
POPUL HSVIP	MAJOR DNA-BINDING PROTEIN	MEDDES SINGLE X VIRUS	\$57.505	577.640	764.80)	1079-1140		_	:	
POPOS HSVIK	MAJOR DRA-BINDING PROTEIN	BOUNG ICERPESUIRUS TIPE 3	183-581	199.611	1048-1131				:	
POWER HEAD?	MAJOR DRA-BINDING PROTEIN	SOUTH HERPESVINUS TYPE !	333.314						;	
PONDI HISVEI	MAJOR GRA-BINDING FROIDING	FOURTH INTERPESVIAUS TYPE I	617.658	1107.1149				-	į	
POWER HISVER	MAIGH DRA-BINDING PROTEIN	HERPESVIRUS SAIMIRI	111-119	130-367	506-357	173.207		<u> </u>		•
POPOSI MSVSA	MOCON DIVINITION OF THE PROPERTY OF THE PROPER	MUNTINE CYTOMEGALOVIRUS	184.618	31.12			1			
SA COL	MACON DAYS BOOM PROTECT	SDAIAN CYTOMEGALOVIRUS	125-562					İ		
i i i	NAME OF STREET PROPERTY	VALICELLA-20STER VIRUS	013-650	100.100			1	İ		:
CAZA IBACA	MACHINE STREET	AFAUCAN SWINE FEVER VIRUS	23:106					Ì		:
THE WAY	DAY DOVE	VACCINGA VIRUS	195-416							·-
PONG! VACCC	DAA LUAASE	VACCIMA VIRUS	105.416					1		:
AVC.	DAY LOASE	VALUOLA VIRUS	195-416							!
אסונדו אינו	DAY BY WELLS	MANAN ADENOVIRUS TYPE 2	667.74)							
TOTAL AUEN	MAN POLITICISM	HUDILLIN ADENOVIRUS TYPE 5	(52.74)					Ì		
NO COL	THE CALL PROPERTY.									

WO 96/19495

			٦	٦	T	AREA	ANA	3864	388.	
	A 1 MOTH	Apec (no potation)	J	A LANGE	7000	Г				
				91. 101						:
T		ONIOPOXVIRUS	T	2						
									1	
Τ		CHI. DAELLA VIRUS I	7	10.114	131-412				-	. . .
Γ			Ţ	٦					!	
L		(6)	Ī						į	
L										;
Γ			7	11110						
POPOL HORBIC		AI DUCK ISOLATE ST								
WORDH T		_		134.364	117.395					·
10703	DNA POLYNERASE		Ţ	101						·
DEPT TOTAL		PE A YW)	201-215							;
West Low			201-333			-				-
POPOL 10'BYZ		AIN 17)	21:520							
MAN MAN		GELOTTI	\$11-559			1				!
1000			\$11.559						İ L	
200	DAY BOX YACELASE		\$11-559			1				!_
DIOL HAVIN	SALA BOL WASHASE		313-360							j
OFG. RSVIS	THE STATE OF THE S		104.528							:
POPOL HSV21	UNA POLITICA SE		33-69	338.366	401-435	706-749	101-101			·
POPOL HSVEB	UNA POLITICIONE	т	999 505							-
POPOL HSVII	DNA POLTACIASE		433.483	730-818	120-662				}	į.
POPOL MPVAC	DNA POLYMENASE	т	437.461	136.	828-163					<u> </u> - -
POPOL VACCC	DNA POLYMERASE			940.813	827.061					<u> </u>
POPOL VACCV	DNA POLYMERASE	VALIDLA VIRUS								ij
POPOL VARV	DNA POLTHO MASC	VANCELLA-20STER VIRUS (STRAIN DUMAS)	301.174			i	-			
POPOL VZVD	DNA POLYMANASE	WOODCHUCK HEPATITIS VIRUS I	111,000			L				
DPOL WITH	DNA POLYNCHASE	WOODCHUCK HEPATITIS VIRUS 59	100							<u> </u>
DPOL WHYS	DNA POLYMENASE	WOODCHUCK JEPATITIS VIRUS 7	200.330							; -
PDPOL WHY?	DNA POLYMENASE	WOODCHUCK HEPATITIS VIRUS I	11,00							- -
OL WHY	DNA POLYMERANE	WOODCHUCK NEPATITIS VIRUS & (INFECTIOUS CLUNE)			-					-
PDPOL_WRV81	DNA POLYMEKASE	HEPATITIS B VIRUS (SUBTYPE AYW)	9		-	_				+
POPON HORBYY	DNA POLYMENASE		100			_				:
POUT HISVED		HERPESVIRUS SAIMIRU (STRAIN !!)	77-61							:
DUT HSVSA	PHAIR MALLE	MAKAN ADENOVIRUS TYPE 41	10			-				;
PEIA ADEAI	SAMLY BIA 27 KD PROTEIN	HI BAAN ADENOVIRUS TYPE 40	201.70		-	-	_			-i
FIBT. ADE40	EIB PROTEIN, LANGE T.ANTIGEN	INDIAN ADEMOVIRUS TYPE 2	6		-	-	! -			-
PRIMS ADEOL	EIB PROTEIN, SMALL T-ANTIGEN	LANGLAN ADEMOVIRUS TYPE S	6		-	1	 -	_		اُـــ
PETER ADEOS	EIB PROTEIN, SMALL T-ANTIGEN	LACANA ADSOCIATION TYPE 12	<u>=</u>		1	+	1			
PEIDS ADELL	EIB PROTEIN, SMALL T-ANTIGEN	HI BAAN ADENOVIRUS TYPE 40	8		-			_		j
PRINT ADEAD	EIS PROTEIN, SMALL T-ANTIGEN	LABORAN ADENOVIRUS TYPE 41	180-134	1	+	1	-	-		
PETER ADEA!	EIB PROTEIN, SMALL T.ANTIGEN	LOCKE ADSMOVIBUS TYPE I	19-13			-	-			
MOUNT ADEM!	EIS PROTEIN, SMALL T.ANTIGEN	LANGE AND APPROVIREDS TYPE 2	<u></u>			+	-		L	
Ans Ansol	EARLY EIB 14 KD PROTEDA	TOTAL A DEMOVIBILIS TYPE)	•		1	+	-			
ENIA ADEDI	EALLY ED 15.3 KD PROTERN	JANAN ADENOVILUS TYPE S	1	1	+	-	-			
PETTY ADEBS	EALTY ES 14 5 KD PROTEIN	INDIANA ADENDIVINIS TYPE?	77		+	+			_	
SENIA ADEGI	EALY ED 15.3 KD PROTEIN	ACCOUNT ADEMOVIEUS TYPE 35	ğ		+	+	-	-		
8130 ADE35	EALLY #3 70.3 KD GLYCOPROTERN	MANANA ADENOVIRUS TYPE 35	2		1					
1120	EARLY EJ 20 6 KD GLYCOPROTEDA	TOWNS ADDITION OF THE 2	3					}		
1000	PROBABLE EARLY E4 11 KD PROTEIN	HUMAN ACENOMIES TOPES	10.4			1	-	-		
PEALL ADEDS	PROBABLE EARLY E4 11 KD PROTEIN	HUMAN ADELS (STRAIN 895-8)	13)-13)		1	1	1	-		
	FARLY ANTIGEN PROTEIN R	ELTS IEIN-BANK AND A PARK AND MACHES	487-521					-	 -	-
					ļ	_		_		1

FEW ELVS ENV ENV ENV ENV ENV ENV ENV ENV ENV ENV		FARENS SPIEER FOCUS-FORATING VIRUS FARENS SPIEER FOCUS-FORATING VIRUS AVIAN SPLEEN FOCUS-FORATING VIRUS AVIAN SPLEEN FOCUS-FORATING VIRUS AVIAN SPLEEN FOCUS-FORATING VIRUS BANDON FORATING VIRUS (STAAN M.) BOVONE LEUKERIA VIRUS (STAAN M.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE II.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (ALGENCAN SOLATE I.A.) BOVONE LEUKERIA VIRUS (CLONE P.) 3-1) EQUINE PRECTIOUS ANEMIA VIRUS (CLONE P.) 3-1) EQUINE PRECTIOUS ANEMIA VIRUS (CLONE P.) 3-1) EQUINE BNECTIOUS ANEMIA VIRUS (CL	341-35 341-35 341-35 341-35 340-43 340-43 340-37 34	615-720 615-720 615-720 616-733 616-733 616-733 616-733 616-733 617-730 617-730	231-235 139-170 131-345 131-345 131-345	3304ID 330-384	109:401			
		TE 100) TE 117) ATE FLK.) GLATE GLATE TE LASS) TE LASS (TE LASS) TE LASS (T		18-122 18-123 18-123 61-736 61-73 616-513 616-513 616-513 616-513 616-513	231-235 139-130 311-345 130-130 130-130	330410 330410	199-601			
		TTE 106) ATE FLK) ATE FLK) ATE FLX) ATE FLX) ATE FLX) ATE FLX) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B13) ATE B133 ATE		11.122 11.122 11.120 11.120 11.130 11.130 11.130 11.130	131-185 131-185 131-185 131-185 149-185	390-410 319-38-4	635-491			<u> </u>
		(TE 196) (TE 196) (ATE IX) (AATE IX) (AATE IX) (615-720 615-720 615-730 616-513 616-513 616-513 617-613 617-613 617-613 617-613 617-613 617-613 617-613 617-613 617-613	121-255 131-175 131-175 116-105	330-410 230-284	635-491			<u> </u>
	PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR	TE 100) ATE FLK) ATE FLK) GLATE ATE FLK) ATE ALSO (TE LAND) ATE ALSO (TE LAND) ATE ALSO (TE LAND) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) E PJ 3-1) ATE WYOAIDAGO (T		16-122 16-123 16-123 16-123 16-123 16-123 10-123 11-128	135-135 135-130 131-341 145-341	330-410 330-334	635-691			!
	PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR PRECURSOR	ITE 106) ATE FLK) ATE FLK) ATE FLK) ATE FLS) ATE FLS) ATE FLS) ATE BS9		11-122 11-122 11-120 11	139-135 139-130 131-141 110-161 110-161	330-610	635-691			<u> </u>
		(TE 106) (TE 106) (TE 117) (TE 117) (TE LEX)		11-122 11-123 11-120 11-210 11-210 11-210 11-210 11-210 11-210	21-233 11-345 11-345 11-345 11-345	190-284	1.0.0707			
		(1) (1) (2)		11-132 615-730 616-735 616-735 616-735 616-735 616-735 617-736 617-736	131-345 131-345 139-319		Ī	33.5		
		1) (1) (1)		615.720 611.710 416.513 416.513 416.513 415.513 415.513	716-713		7			! !-
)))))))		615.70 615.70 615.70 615.71 616.71 616.71 617.52 617.53	716-71	_				!-
		1))		615-730 615-730 106-533 016-533 016-533 417-530	110-111					; :
		JAK)		615-730 611-718 616-733 616-733 616-733 617-730	710.765					<u>:</u> _
		Daki b)		615-720 611-716 436-523 436-523 437-520	31.36					<u>:</u>
				615-730 611-718 436-535 436-535 431-536	24.76					:
				611-710 611-711 436-515 436-515 431-526	14.10	j	- -	j		<u>.</u>
			_	611-718 436-525 436-525 436-525 437-526	119.303	143.155				:
				436-535 436-535 436-535 437-536	119.593	145.793				نـ
		NING)		436-525		961.316			İ	1
		MING		417-526	\$50.993	651-692				· ·
		MING)		437-526	550.593	658.716				- i
) DAIING)		414.435	500.504	659-663				<u>:</u>
		NING)			196.993	631.716			j	<u>:</u>
) DATENCI)	36.76	436.529	199.903	638.714				::-
				436-535	199-961	63E-71A				_
	ENV POL YPROTEIN PRECURSOR			436-533	196-656	658.716				.
	ENV POLYPROTEIN PRECURSOR		\$01.555	\$67.604	 -					_
	DAY POLYFROTEIN PRECURSOR	CACOL ATE PETAL IDEA)	069-019	215-756						: -
	DAVELOFE FOLYPROTEIN PRECURSOR	Τ	187-197	113.734						_
	DIVELOFE POLYPROTEIN PRECURSOR	T	177	989-009	714.735					<u>;</u>
	ENVELOPE POLYPROTEIN PRECURSOR		667.549	\$61.595						-
	ENV POLYPROTEIN PRECUESCA	W.1)	478-530	\$42.576						<u></u>
	A POLYPROTED PRECURSOR		408-550	\$62.596						<u> </u>
٦	ENV POLYPROTEIN PRECURSUR		475-527	530.573						-
T	ENV POLYPROTEIN PRECURSOR		<u> </u>	154.205	131-155	163-693	866-901			İ
	ENV POLYTHOTEIN	RAIN GARDNER-AUNSTEIN)	498-530	362-506						ļ
	ENV POLYMOTEIN PLECUASUR		478.530	\$42.576						1
1	DAY FOLT THE STEP SECTIONS		481.524	\$45.579						-
T	DAY FOLLTRO LEIN PRECINSOR	DEA.THEREN	44.532							ļ
PERV 73V31	ENV POLYPROTEIN PRECURSOR		523-575	287-621						1
	DAY POLYTROTEIN	HIDMAN T-CELL LEUKEMIA VIRUS TYPE I (STRAM ATK)	331.383							1
T	ENV POLYPROTEIN	3			$\Big $	-				ļ
	ENV POLYTROTEIN	SOLATE MI-7)	11.131			1				L
	ENV POLYPROTEIN PRECURSOR	HUMAN T-CELL LEUKEMIA VINUS I TPE II		116.518	764-845					
Γ	ENVELORE POLYPROTEEN GP160 PRECURSOR		785 709	216.019	747-443					L
П	ENVELOPE POLYPROTEIN GP146 PRECURSOR	Т	\$00.519	50.70	762-838		 -			Ц
	ENVELOPE POLYPROTEDI GP160 PRECURSOR	HUMAN IMPRODUCTION OF THE TOTAL TOTA	111.165	201.580	609-708	763:431				
PENV HVIBN EN	ENVELOPE FOLYPROTEIN GPIAO PRECURSOR (COM	RUMAN MANUNCUE ILIENCY VINUS 11TE 1 (SECTION ATE)	510.599	615.313	773-841					Ц
PENV, HVIBR EN	NVELOPE POLYPROTEIN CP160 PRECURSOR	153	142-376	\$10.606	626-724	779-855				
PENV HVICA EN	ENVELOPE POLYPROTEIN CPIES PRECURSOR		355.796	\$62.591	407.704	768.829				·
PEN WIEL EN	DAVELOPE POLYPROTEIN GP160 PRECURSOR	٦	20.50	810-712	767.836					
	ENVELOPE POLYPROTEIN GPI60 PRECURSOR	T	305-394	610-312	767-843					_ -
PENY HVIKD D	DAVELOPE POLYPROTEIN GP160 PRECURSOR	Т	11.15	\$17-605	623-723	778-443				
BN WID B	DAVELOPE POLYPROTEIN CP140 PRECURSOR	HUMAN IMMUNOUETICIENCY VANCE TYPE 1 (INCRE ISOLATE)	129-363	497-586	101-104	759-635				

	110000			1470	79.5		11991	911:118	177-648	
	ALCHICA	ΞI	٦	T		170-825				
THERM	CALL LAND POLYPROTEIN CPIEG PRECURSOR	ı	٦	T	T					
PEN HVIKE	ENVILORE POLY TO ROTE OF 160 PRECURSOR	Γ		٦	765-841	144.041				
FVIKA	ENVELOR OF CHANGE IN CPIED PRECURSOR	Г		306-595	T					
PENV HVING	ENVELORE BOT VEROTEIN CP166 PAECURSOR	SOL		٦		,,,,,				
PENV HVINO	ENVELORE POST STATE OF THE CURSOR		349-290		601-102	27-167				L
PENV HVINS	ENVELORE FOLITACINES OF PRECURSOR		336-370	447.593 6	610-711	766-143				
PENV ININD	ENVELOPE POLITICO COLOR DOSCITICOS	T	Γ	610-712	167-843					
PERV HVIOY	ENVELOPE POLYPROTEIN GET TO TALESTON	Ţ	Τ		619-721	258-944				
Adian Auge	ENVELOPE POLYPROTEIN OF 160 PRECURSOR	-	T	T	348.830					
FIGURE AND ADDRESS OF THE PARTY AND ADDRESS OF	ENVELOPE POLYPROTEIN CP160 PRECURSOR		٦	T	900	761.017				
	ENVELOPE POL YPROTEIN OP 160 PRECURSOR		٦	T		74.0				
PENV HVIST	TARE OF PAY YPROTEIN CP 160 PRECURSOR	Γ		498-594	217.					L
EDV HVIST	ENVELORE OF CHIEF OF PRECURSOR	9	331-365	498-594	611-712	787.678				_
PENV HVISC	ENVELOPE PARTY OF THE PRECURSOR		Γ	419.584	602-303	758-927	1			L
PENV HIVIWI	ENVELOR POLITICAL PROPERTY OF THE SOR	HAMAN DOMINODEFICIENCY VIRUS LYTE I WAS TOOL OF	Γ	165-205	610-709	764-831				
PERV HVIWS	ENVELOPE POLYTROTEIN OF TAN BRECHT SOR	1	Γ							
PENV HV123	ENVELOPE POLYPROTEIN GFIBU FALCONS	MANAN DAMPHODE FICIENCY VIAUS TYPE I (ZAIRE) ISULATED	T	107.75	111,009	764-840				
CIVIL VICE	ENVELOPE POLYPROTEIN OP 160 PRECURSOR	_	٦	T	***	461.716	774-831			
10124	ENVELOPE POLYPROTEIN GP166 PRECURSOR		٦	T		917.010				
	FAVEL OPE POLYPROTEIN GP160 PRECURSOR	9	322-594	1				L		
PENV MVICE	ELANET COR POLYPROTEIN GP160 PRECURSOR	-		٦	017-610		ļ		L	
PENY HVIER	TOTAL OF BOY VAROTEIN CP160 PRECURSOR	Г	\$12.597	619.709						_
FEN HY38E	ENVELUTE CONTINUE COLOR PRECURSOR	T		169-809			$\frac{1}{4}$			-
ENV HYJCA	ENVELOPE POLITICULE DE CONTROLLE SOR	Т:	140.471	\$62-587	609-609					1
EN HYZDI	ENVELOPE POLYPROTEIN GF 180 PACCONS	٦,		00V 00V						1
DEW HYZGI	ENVELOPE POLYTROI EIN OF TOTAL			300		L	_			1
ENV HYZNZ	ENVELOPE POLYPROTEIN GPISS PALLUNSON	HINAAN DOMINODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	211.378	90, 100	413.702	-				1
ENV HYZRO	ENVELOPE POLYPROTEIN GP160 FAELURSON	LIGHTAN MAGNADEFICIENCY VIRUS TYPE 2 (ISOLATE STOR IC	447.476	200						
ENV HV753	ENVELOPE POLYPROTEIN CP160 PRECURSOR	TABLES OF THE SELISY)	526-310	T	101.017			L		
PACK LIVING	ENVELOPE POLYPROTEIN CP160 PRECURSUR	STATES OF THE STATES OF THE STATE STATES TO STATE STATES TO STATES STATE	447-476	T		-				_
1000	ENVELOPE POLYPROTEIN GP146 PRECURSOR	TOTAL STREET, STREET, A.PARTICLE	367-433	463-327		1	 -	_	_	
N HV23	CAN ANY YOR OTHER PRECURSOR	MOUSE INTRACISIENCE AT THE POLICY OF IS	403-455	\$31-605			 	1		L
ENV UNIVE	SALVE TO VAROTE IN PRECURSOR	SHEEP PULMONANT ADENOMINATION OF THE PASS AND STATE OF THE PASS AN	473-525	17.571		$\frac{1}{4}$	1	1	-	-
ENV JSRV		MARK CELL FOCUS-FORMING PROMINE LEGISLA VIRIS (1501.A		538-572						-
ENV MOT	ENV POLITICAL IN SECTION OR ICOAT POLYPROTE	THE MINK CELL FOCUS-FORMING MUNINE LEGARETH		109-195						-
PENV MOTES		AKV MURINE LEUKEMIA VIRUS		\$62.596					1	 -
PENY MALVAV	ENV POLYTROTEIN PARCUASON	CAS-BR-E MURINE LEUKENIIA VIRUS		134.610						+
PENY MALVOR	ENV POLYTROTEIN PRELUASOR	FALEND MUNDE LEUKEMIA VIRUS (ISOLATE 57)	201.000	174.410						+
PENV MANTS	ENV POLYPROTEIN PRECURSOR	FRIEND MUTUNE LEUKENIIA VIRUS (ISOLATE FB39)	200-2076			-				
PENN NO VEF	ENV POLYPROTEIN PRECURSOR	COLEMP LATINE LEUKEAGA VIRUS (150LATE PVC-211)	250.364	310-010		-	 - -	_		4
450 00 000	ENV POLYPROTEIN PRECURSOR	SOUTH OF THE PETERNA VIRUS	504-551	201-201		-	-		_	_
92.00	ENV POLYPROTEIN PRECURSOR	HOMOLE RICKETT FERENCIA VIRUS	40-92	104-138		1				_
10 A A A	ENV POLYPROTEIN	KIRCHES FIRE FOR FAILS VIRUS	503-554	266-600		+	-	-	-	_
	ENV POLYPROTEIN PRECURSOR	MACCOSET PRODUCE CENTRAL VARIES	497-349	361-595		1	-	-	 -	
PENA PENA	ENV BOY VPROTEIN PRECURSOR	PADIATION MUMBER LEUNESHIN MALIS KAPLAN	497.549	\$61.595			+	-	-	<u> </u>
DA PA	CAN VORDITED PRECURSOR	RADIATION MUTUNE LEGITARIA VINCE CONTRACTOR	011:510	536-612			1			i 1-
PEN MENTA	CAN VENTED	MOUSE MANDIARY TUNIOR VIRUS (STRAIN DES)	477.530	156-612			-	+	1	; -
PEN MOUVE	OLUMBA STATE	MOUSE MANDIANY TUNDA VINOS LO INC.	401.476					4	-	-
PEN MOTIVO	DV FOLTFULLING	SOUNN MASON-PFIZER VIRUS	19.14	103.141				1		
PEN MONY	DAY POLITICAL	FBI MUNDE OSTEOSARCOMA VIRUS	7	111.223	664.746	780-816		$\frac{1}{2}$	-	 .:
PENV MSVFB	DAY POLYTHOLEIN	OVINE LENTIVIRUS (STRAIN SA-ONNV)	10.00	\$40.574				4	-	
PEN ORCANS	ENV POLYPROTEIN PRECURSOR	RAUSCHER MINK CELL FOCUS-INDUCING VIRUS					_			:]
PEN IMOV	DAY POLYFIOTER PRECURSOR	RAUSCHER SPLEEN FOCUS-FORNING VIRUS	2	91.101	154.205	5	189-638	A38-60)	14.92 14.92	į
PEN ISTIV	ENV POLYPROTED PRELUNDOR	SDAIAN FOAMY VIRUS (TYPE !)		80.33	110.33	36.78	100.191		_	- -
PEN STVI	ENV POLYPROTEIN	STATIAN FOAMY VIRUS (TYPE) / STRAIN LK!)	2		197	-	H		-	-
	PAY POT VPROTEIN	SOLATE)	269.310							
		THE WAY IN THE PARTY OF THE PAR								

		All Virgan (ne becteriosbates)	П						П	
PCCENE	PROTEIN		J	7	7	100	10	2000	Ι	į
THE FRAME	PRAYEL CHE POLYPROTEIN GPI40 PRECURSOR	V DIGAUNODEFICIENCY VIRUS (AGNI) ISOLATE)	T	44		,,,,,,	070		+	i
SENV SIVAL	FAVEL COR POLYPROTEIN GPISS PRECURSOR	CLONE CR	T	336-370				1	-	:
SEAV CIVAT	FLAVEL COPE POL YPROTEIN GP160 PRECURSOR			129-621	7.60	101	1100	1	-	!
PEN CIVEZ	ENVELOPE POLYPROTEIN GP140 PRECURSOR				317:30	2			Ť	:
PENV SIVOR	ENVELOPE POLYPROTEIN GP140 PRECURSOR	7	366-634				170		<u> </u> _	
PENV SIVAL	ENVELOPE POLYPROTEIN GP140 PRECURSOR	SIMIAN INDRINGOEFICIENCY VIRUS (ARIHA): 1) ISOLATE)	14:13	403.50				<u> </u> 	<u>-</u> -	:
STAN STAND	ENVELOPE POLYPROTEIN GPISS PRECURSOR	6	11:10					-	i	
PENV SIMAR	ENVELOPE POLYPROTEIN GP100 PRECURSOR							!	 !	
PENV SIVAG.	ENVELOPE POLYPROTEIN GP140 PRECURSOR		904-303		100	113.611			 !	
PENY SIVS	ENVELOPE POLYPROTEIN GPI66 PRECURSOR	SPANN BOAMONEFICIENCY VIRUS (F336/SNRM ISOLATE)	ADC-904			98	-	<u> </u> -	-	
PENY SINSP	ENVELOPE POLYPROTEIN GPISS PRECURSOR	SOURN DOUNODEFICIENCY VIRUS (PRINCE) ISOLATE)	4.00.31	20.150			_	-	:	_
PERV BOW	ENV POLYPROTEIN PRECURSOR	SOURREL MONKEY RETROVINUS (SMRV-H)	400-400				+			
IVEN VICE	ENV POLYPROTED ^N	SINIAN RETROVIRUS SAV-I	409.475				-		i.	
V 27 V 200	PAY POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 1514)	21-62	27.73	637.740	773-80-	-		-	_
IN IN AUG	ENV POLYPROTEIN PRECURSOR	VISHA LENTIVIRUS (STRAIN ISIA/CLONE LVI-IKSI)	27-22	2	97.148	100.00	-		:. 	
24 44 45	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 1914/ CLONE LV1-1KS2)	27-12	<u> </u>	12. SE			<u> </u>	 [
PERRY AVIET	FREA ONCOCENE PROTEIN	AVIAN ERYTIMOBLASTOSIS VIRUS (STRAIN ES4)	106-140				1	<u> </u>	 -	
PETEL FONDE	EABLY TRANSCRIPTION FACTOR TO KE SUBUNIT	FOWILOX VIRUS (STRAIN FP.1)	190-224	22).50				1	- 	•
SETTE CENTER	FARE Y TRANSCRIPTION FACTOR TO KD SUBURIT	SHOPE FIBROAIA VIRUS (STRAIN KASZA)	17.71	2	3,0-36		-	-	i	:
	EAST V THANKTRIPTION FACTOR 70 KD SUBUNIT	VACCIMIA MRUS (STRAIN COPENHAGEN)	13-71	20.54				<u> </u>	<u>.</u>	_
2000	FARE Y TRANSCRIPTION FACTOR TO KD SUBUNIT	VACCINIA VIRUS (STRAIN W.R.)	17:02	107-34					<u>.</u>	:
מבונו העוני	FARLY TRANSCRIPTION FACTOR 82 KD SUBUNIT	VACCINIA VIRUS (STRAIN COPENHAGEN)	\$2.03	72.7E					+	;
PETER VANCE	FARLY TRANSCRIPTION FACTOR 82 KD SUBUNIT	VANIOLA VIRUS	19.65	174.208			1		- <u>-</u> -	i :
A NO CAN A NO CAN	AT KAL INE EXONAICLEASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	10-114						i	:
SECON MENER	AT FAIL THE EXCHAINT FASE	EQUINE HEAPESVIRUS TYPE I (STRAIN ADAP)	19-141				+		<u>:</u> . 	:
PENCH NOVE	ALKAL ME EXONACLEASE	PSEUDORABLES VIRUS (STRAIN NIA-1)	02-130					1	<u>;</u> [:
CALL ROAD	AT KALINE EXONACLEASE	VANCELLA-ZOSTER VIRUS (STRAIN DURIAS)	109-157	10.10					i	:
PERSONAL ADEAD	AT A KID STREET PROTEIN	HUNKAN ADENOVIRUS TYPE 40	183-237						<u>:</u>	
PFIB3 ADE41	41 4 KD FIBER PROTEIN	HUNKAN ADENOVIRUS TYPE 41	183-223				+	<u> </u>	Ť	: !
PERP ADEO	FIDER PROTEIN	HUNGAN ADENOVIRUS TYPE 3	156-194				1	<u> </u>	+	!
YEBY ADEST	FIBER PROTEIN	HUMAN ADEMOVIRUS TYPE 1	26.210					-	İ	i
PEBP ADEA	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 40	26.02					1	Ť	1
PFEBP ADEA!	FIBER PROTEIN	HUMAN ADENOVIRUS TYPE 41	320-300						-	i
PFESP_ADEB3	FIREA PROTEIN	BOVINE ADENOVIRUS TYPE J	67-16	979-646			1		İ	:
PFOSX_MSVFR	V-FOSFOX TRANSFORMING PROTEIN	FUR MUMINE UNIECOARCORIA VIROS	51.00					-	<u> </u> _	!
PFOS AVDOX	PSEV-FOS TRANSFORMING PROTEIN	AVIAN RETRUVIRUS NAZA	100				-	<u> </u> 	- 	<u>ئۇ</u>
PFOS MSVTB	PSS-V-FOS TRANSFORMING PROTEIN	AND MUMPE USIECOS MECHANISMOS AND AND AND AND AND AND AND AND AND AND	3.10				-	-	<u> </u> -	<u> </u>
POAGC AVISC	PATGAGCEK) PROTECT	AND AN ENDOCEMONIC VIRILE EV. 1	57.5						<u> </u>	
POAG AVEVI	GAG POLYPRUIEIN	AVIAN ENDOPENDIS BOUS ASSOCIATED VIRUS-9	6.0							
POAD ANEVZ	OAG POLITICOLES	AVIAN MYELOCYTONIATOSIS VIRUS MC29	57.94							
POAG AVOAC	GAG POLITIKO LEIN	AVIAN MYELOCYTONIA TOSIS VIRUS IBI	57.P							
TOWO AVE	COURT DE CITED DIS	AVIAN SARCONA VIRUS (STRAIN UR2)	S7.84						٦	İ
2000	GAG FOL YPROTEIN	AVIAN SARCDNIA VIRUS (STRAIN Y?)	\$7.94					1	+	ĺ
TOTAL PROPERTY	GAG POL YPROTEIN (23)	BOYINE DARINODEFICIENCY VIRUS (ISOLATE 106)	17				-	1	+	İ
POAG EIAVY	GAG POLYPROTEDN	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL22)	91119				1		+	
POAD TVPE	GAG POLYPROTEIN	FELINE DOMUNODEFICIENCY VIRUS (ISOLATE PETALURIA)	9 10						1	
DOAD FIVED	DAG POLYPROTEIN	FELINE DIMUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	76-110				+	+	\dagger	
POAD FIVE	GAO POLYPROTEIN	FELINE INDAMMODEFICIENCY VIRUS (ISOLATE TAIL)	25.0					1	\dagger	
POAG FLV	DAG POLYPROTEIN	FELINE LEUKEANA VIRUS	496-537				+		\dagger	Ī
POAG FOAMY	GAG POLYPROTEIN	HUMAN SPUNIABETROVIRUS	30-186	301-433	93410	607-633	1		T	Ì
POAG 75W-B	OAG POLYPROTEIN	FELINE SARCOMA VIRUS (STRAIN MCDONOUGH)	28-574				1	-	1	

CCCUR ALLEADTR CROTTEN CROTT		All Viruses (no bacterropully)	AKIA	48544	1000	T	23,00			
CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN CAG POLYPROTEIN			57.94		1	T				_
GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN		LAI SARCOKA VIRUS	193-444		-	1				<u> </u> _
GAO POLYPROTEIN GAO POLYPROTEIN GAO POLYPROTEIN GAO POLYPROTEIN GAO POLYPROTEIN GAO POLYPROTEIN GAO POLYPROTEIN GAO POLYPROTEIN		tUS	Γ	194.320						ļ
GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN		Т		192-326						Ļ
GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN			Ī	292.326					1	Ļ
GAG POL YPROTEIN GAG POL YPROTEIN GAG POL YPROTEIN GAG POL YPROTEIN GAG POL YPROTEIN		T	T	293.336				j		_
GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN		T	Ī	100						! - ; -
GAG POLYPROTEIN GAG POLYPROTEIN GAG POLYPROTEIN		Ē	T	76, 50						-
GAG POLYPROTEDI GAG POLYPROTEDI			T							i
GAG POLYPROTEDI		<u>.</u>	T		-					-
				247.780						-
MINISTRUMENT AND AND A CALCU		Γ	11.131	293:336	+					_
UAU POLITICA STREET		Γ	20.13							-
٦		Т		295-320					1	
		Ş	Γ	292-326						+
		2	T	210.123]
			T	303.136						<u> </u>
POAG HVIND GAG POLYPROTEIN										-
Γ			٦	276.762						<u> </u>
Ī				147.720					_	
T		HIDIAN BANDACTICIENCY CIRILE TYPE 1 (STRAIN LICANDAN 67-12)	17.137							_
1		HOMAN BONDODE! KIENE THINGS TO THE TOTAL STEEL	292-336						-	
1		HUMAN DORMNODEFICIENCY VINUS LIVE WELL STATES	201.51	193.337					-	-
PGAG HVIWS GAG FOLTFRUIEN			303.124				1			-
		HUMAN BONDNODEFICIENCY VIRUS TYPE 2 (ISOLATE SOLIST)		130.157					-	-
	102.0	_								1
	RETROVIAUS-RELATED GAG POLYPROTEUR		67.103							4
POAG BALA RETROVINUS-RELA	RETROVINUS-RELATED GAG POL YPROTEIN		19:03				-			1
CAG PRIATE RETROVINUS AELA	RETROVINUS RELATED GAG POLYPROTEIN	RUS	470.50		1			_		1
T		BR6)	13-151	156-190			-	-		_
CAS LACTURE GAG POLYPROTEIN			15-131	Bi - 4X	†					-
Τ			117-760		†			-		
DAD FOL YPROTERY		SIMIAN PASON VIBIO COTO AIN PRACUE CI	13.04		1			-		
T		ROUS SACCOLIA CIRCLA (SCV.L.A)	103-139	100-201			-	-	-	-
	EN.	SACCHARONYCES LEAGUSIACE THE SACCHARONYCES CONTRACTOR OF THE SA	111-111	178-416	283-434		-	1		· -
OAG SCYLA		SDAAN FOAMY VIRUS (1978-1)	173.407	113-515	\$61-433					<u>. </u>
		SINIAN FOAMY VIRUS (TYTE J. STANIS 1501 ATE)	302.336				-	1	<u> </u>	<u>:</u> -
I		SIMILAN INDRINGOEFICIENCY VINOS (ANTIS)	106-340					-	 -	<u> </u>
1		SINGLAN INDICHODEFICIENCY VIRUS (ACM) 130CA 127, ONE CO	111.217	473.503	L			$\frac{1}{4}$		i
		SDAAN BOARNODEFICIENCY VIRUS (ISOLATE AUNIT CLOSE	10.136	-					1	+
		SDADAN DOMUNODEFICIENCY VIRUS (TYO-1 ISOLATE)	10.10	-					1	+
		CHIDA ANZEE INDAMMODEFICIENCY VIRUS (SIVICEZI)	100.00	223-267	203-317					i
		SIMAN IMACHODEFICIENCY VIRUS (ISOLATE COL)							1	<u>:</u> 1
		SIMIAN SARCOMA VIRUS	2	349.820						Ť
	2	HERPES SOUPLEX VIRUS (TYPE 1 / STRAIN 17)	3	111			_			+
	NSE	HERPES SIMPLEX VIRUS (TYPE 2/STRAIN HGS2)	700		(1984)				-	4
	ASE	HERPESYTRUS SATION (STRAIN !!)	138-201				_			+
	ASE	VARICELLA ZOSTER VIDUS (STRAIN DUMAS)	3	101	1		-	L		-
Γ	ASE	POUME CORONAVIRUS (STRAIN F15)	208-242							
	PENACOLUTINON-ESTERASE PRECURSOR	BOVING COMMANDIS (STRADA LY-136)	200-242						-	·
,	HEMAGGLUTDON-ESTERASE PRECURSOR	BOATE CONDUCTOR (STRAIN MEBUS)	308-242					-	-	
T	WENT A COLUMNIA ESTERASE PRECURSOR	BOVINE CONCORD STATE OF THE AND CONTRACT.	304-343					-		-
T	SELANCE UTINDE ESTERASE PRECURSOR	BOVINE CORONA VINOS (31100) COLOROS	208-242				1	+		-
T	ANY OCH ITTEM ESTEANSE PRECURSOR	HUMAN CORONAVIRUS (STRAIN CC.)	380-456				1			\mid
	PRECURSOR	INTLUENZA A VIRUS (STRAIN AALCHEZOS)	34.460					+	+	+
1	TO THE SOR	INSTLUENZA A VIRUS (STRAIN AUBANCIKON 1177)	178.454				$\frac{1}{4}$	$\frac{1}{4}$	$\left\{ \right.$	$\left \right $
PHENA INDAN HENADGLUTING	The Charles	INFLUENZA A VIRUS (STRAIN ABUDGERIGAL/HORKAIDOIN)								

		All Virges (se bettriopheges)	T	T	T			ABEAG	AREA 7	
PCCENE	ALLMOTIS		7	A LANGE	Tomas on the	1	Т	Τ	Γ	
CHEROME	HEMACCA LITTININ PRECURSOR		T	225.475	104-528					;
SIELLA LACEO	HEMAGGE LITININ PRECURSOR	-	T	Ţ						:
MENA IACKP	HEMAGGE UTININ PRECURSOR	INFLUENZA A VIRUS (STRATO ACHIERENTENTSTLYANIA)	T	487.512						
SENA IACKO	HEMAGGLUTDWW PRECURSOR		Τ	97.70						
PHENA IACKS	HEMACOLUTION PRECURSOR	T	Ι.	177.469						
PIESKA IACKV	HEMAQUEUTININ PRECURSOR	INFLUENZA A VIAUS (STRAIN ACITICARIA PERTAGRA)	Τ	-						
PIEMA IADA!	HEMACCLUTININ PRECURSOR	T	Γ	405-547						
HENA INDA	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIAUS (STRAIN AUGULIALMENTAGE)	Π	-						
MENA INDAS	HENLAGGE LITTING PRECURSOR		178-478	20-305						
PIEMA IADA	HEMAGGLUTOWN PLECURSOR	INFLUENZA A VIRUS (31 KAIP AUXILIANZELIAZIONEI DIVARIANIA)	174-454							
PIEMA INDCZ	HENLAGGLUTININ PRECURSOR	Т	31.55	111-111						
PHEMA IADE!	HEMAGGLUTININ PLECURSOR	Ī	14.440							
PHENA IADHI	HENLAGGLUTDRIN PRECURSOR	INTLUENZA A VIRUS (STRAIN ADUCENIUMA ALDONATI)	144.440							
PREMA MORE	HEMANGGLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN AUGALINURA NICO CHA)	244.40							
PHENA IADHU	HEMAGGLUTIPUR PRECURSOR	INTLUENZA A VIRUS (STRAIN ADDUCKHUKKAIDAN)								
PHEMA IADHA	HEMAGGLUTING PRECUISOR	BOLUEICA A VIRUS (STRAIN ADUCKHORRAIDOMIS)	200							
PHEMA IADHS	HEMACGLUTTHEN PRECURSOR	INTLUENZA A VIRUS (STRAIN ADUCKAIOKKAIDOZINZ)								
PHEMA IADHS	HEMACGLUTININ PRECURSOR	DELUENZA A VIRUS (STRAIN ADUCENIUR KAIDONIS)								
PHEMA JADH7	HEMAGGLUTINGN PRECURSOR	DELUENZA A VIRUS (STRAIN ADUL KNIOKRALIKU/1962)	157 965	135.45						
PUEVA IADRE	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN ANDICKIRELAND/I 11/13)		1						
INDVI VICE	HEMAGGLUTTINGN PRECURSOR	INFLUENZA A VIRUS (STRAÍN A/DUCIA/FIEA/PHIS/346/16	66-17							L
PACEMA TADIAZ	HEMAGGI, UTININ PRECURSOR	INFLUENZA A VIRUS (STRAÍN A/DUCKAIEMPHIS/938/74)	380-430							
PACELLA LADARY	HEMACCH UTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN A/DUCK/NEW YORK/12/13)	200							
MENT IANN	HEMACIC UTDAN PRECURSOR	INFLUENZA A VIRUS (STRAIN ADUCICNEW ZEALAND/11/16)	374.5							L
THEMS MAN	HEMACICA LITTRON PRECURSOR	INFLUENZA A VIRUS (STRAIN A/DUCKAIXRAINE/1860)	21-55							Ļ
THE PARTY	NEMACKE UTDON PRECUESOR	INTLUENZA A VIRUS (STRAIN A/DUCK/UXRAINE/1/83)	180-436							L
THE TANK	HEMADGLUTDUN PRECURSOR	INFLUENZA A VIRUS (STRAIN A/ENGLAND/121/77	180-438							L
PAGNA IAFPE	HEMAGGLUTTININ PLECURSOR	INFLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUS/RUS IOC.)								L
PIEMA LAGRE	HEMAGGLUTINGN PRECURSOR	INFLUENZA A VIRUS (STRAIM ACREST TEAL/AUSTRALIADOV)	130.67				-			
PHENA IAGU	HEMAGGLUTININ PRECURSOR	INTLUENCA A VIALIS (STRAIN ACCULUMANT LANGERS)	717-110							
PREMA IAGUA	HEMADOR UTININ PRECURSOR	INFLUENZA A VIRUS (STRAIM ACULLAS) INCARACAS	130-455							
PHENA LAHAL	HEMACGLUTININ PRECURSOR	INTUENCA A VIAUS (STRAIN ACQUINGALORIAS)	113.146	360-414	503-537					
PHENA IANCS	HEMADOLUTIVIN PRECURSOR	INTUENCA A VIRUS (STAKIT ACCOUNTS AND TO SELECTION OF THE PROPERTY OF THE ACCOUNTS AND ACCOUNTS	12:18	Γ	503.537					
PHENA INHC?	HEMAGGLUTDITO PRECURSOR	PART I PRAZA A VIRIOS (STRAIN AND AND UNION DETROITINGS)	160-484	503-537						
PHENA LAHOD	HEMAGGLUTININ PRECURSOR	TACH (SENZA A VIETS (STRAIN AFOUNE/DETROIT/1/44)	760-484	503-537						-
MEMA IMDE	HEMACCA UTININ PACE UNSUR	INTLUENZA A VIRUS (STRAIN AFQUINE/FONTAINEBLEAU/14)	379.455							
MENA INGO	SELVACIO INTO PRECIDEOR	INTLUENZA A VIRUS (STRAIN MEQUINEMENTUCKYOM)	179-455							1
THEMA WAY	VENACCI LITORIN PRECUASOR	INFLUENZA A VIRUS (STRAIN AEQUINERENTUCKYIIA)	178-455	Ī						
PHENA IAIO R	HEMADOLUTION PLECURSOR	RIFLUENZA A VIRUS (STRAIN A/EQUINEA/EXTINGTOW/M6)	9	Т						
PHEMA IMEO	HEMAGGLUTDAN PRECURSOR	INFLUENZA A VIRUS (STRAIN AEQUINEA CINDON (41671)	91.71	100-484	16.10					L
PHENA IMPO	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN ARQUINEARIANUM)	1000							
PIEMA MON	HEMACCLUTININ PRECURSOR	DATUENZA A VIRUS (STRAIN ARQUINEMEW ALAUXE 1/10)		Т	61.113					<u> </u>
PHEMA IANDON	HEMAGGLUTDAN PRECURSOR	INTLUENZA A VIRUS (STRAIN AEQUINEMEN MAKKE 1717.1)	200.710		(0)					
PIEMA WOR	HEMACOLUTION PRECURSOR	DALUENZA A VIRUS (STRAIN AEQUINE/PRAGUE)(28)	27.51	Τ						
PHEMA MARO	HEMAGGLUTIMIN PRECURSOR	INCLUENZA A VIRUS (STRAIN AEQUINERONATION)								L
PHEMA LAHSA	NEMACCLUTHIN PRECURSOR	INSTLUENZA A VIRUS (STRAIN ARQUINE/SAMTIACO/IM)		787 97	10.19					<u> </u>
MEMA IMISP	HEMAGGLUTIMIN PRECURSOR	INFLUENZA A VIRUS (STRAIN AEQUINESSAO PAULOVINS)		T	50.5					! !_
WIND ALISW	HEMAGGLUTDAN PRECUASOR	INTLUENZA A VTRUS (STRAIN ARQUINES WITZENLANDI)	39.64	Т						
PREMA WITH	HEMADGLUTDIN PRECURSOR	INFLUENCA A VIRUS (STRAIN ARQUINE) LENNESSEE STUD								
PIEDA MITTO	HEMAGGLUTDIN PRECURSOR	INSTLUDIZA A VIRUS (STRAIN ARQUINIZION TUTI)	117.00							
MAN AVENA	HENADOLUTION PRECUNSOR	INFLUENZA A VIRUS (STRAIN - VEGUINEUAUAUATTIAL)								

			-		H	П			ABUA
		All Varues (no bacteriuphages)	AREA I AR	AREA1 ABEA2	1020	- Parter	1		
PCCDVE	3			٤	-				
THERMAL	PROTEIN PREFITE OF		376-478 506	506-541	1				
MENA MA			376-478	206.54	1				
PHEDAM, LAKER		-	137.453			<u> </u>			
PIEDIA IALEN		VIIA NOTINE	182-458			1			
PHENCA JAMAA		Т	16.4%	-		+			
PHEMA INMAB			180-456			1			İ
PHEMA INMAO		т	100.4%	-		-			
PHENCA IANGEL		3	9777	<u> </u> 					:
PHENA IAMES		PARTIENZA A VIRUS (STRAIN AMERIMISANS)	T	1000	-				
STATES INVEST	HEMACGLUTININ PRECUISOR	ALIENZA A VIRIIS (STRAIN AAIINKUSWEDEWIN)	T						
	HELLA CICLLY THIN PRECURSOR	INTEGRAL STATE OF THE ANTI-MONE)	٦	1	1		_		-
THE PERSON NAMED IN	LELACCE (TRAIN PRECURSOR	POLUENCA VIACE (STEER OF WILL ENIANE) 194)		36.534		1			
PIGMA IANIE	TOTAL PRECITION	NATUENZA A VIRUS (STRAIN MATERIA	376-478	206-548		+	-		
PHEMA LAPIL	MDMACKED IININ TREESTINGS	MATUENZA A VIRUS (STRAIN AFUERIO RICORNA	378-454						
PHEMA IAPUE	IEMAGGLULININ PASCOSSO	POLUENZA A VIRUS (STRAIN ARUMAY TORAS TIMES	23.44			1			- : :::-
PHEMA INAUD	HEMACGLUTING PRECURSON	INTELLENZA A VIRUS (STRATH A/SEALMIASSACIIUSE)	Ī	58.35				1	
PHEMA LASE?	HEMAOGLUTINGN PRECURSOR	MENTANZA A VIRUS (STRAIN ASITEARWATERVAUSTRALIANT)	T	111 AAB					
PASTA IASH	HEMAGGLUTHIN PRECURSOR	SELECT A VIBILS (STRAFT ASTARL INCAICTORIASISATS)	٦						
PLEMA TASTA	NEMAGGLUTININ PRECURSOR	ASTITUTE A VIRUS (STRAIN ACTURKEYARELAND/1) 1041)	١	100	-				
	MEMACICAL UTTOWN PRECURSOR	INTEREST TO SELECT AND AVIOLET VALINAL SOLARISMO	176-454	1	I	-		-	-
V V V	HELLACKEL UTININ PRECURSOR	DOLUGAZA A VINCE (STR. 17 A ATTRICE Y/ONTARIO/7112/46)		5.50		1	-		_
NOW WATER	THE PRECUESOR	DOLUENZA A VINUS (SI MAIN)	338-454	661.540		1		-	-
HENA IATEO		MELUENZA A VIRUS (STRAL) A LUANE LOS	19.61	114.474		+		-	:
PIEDIA LATKI	HEMACOLUTION PRECORDOR	DIFLUENZA A VIRUS (STRAIN A/TURKE YORECONTI)	١	197.530					:
PHENA LATER	HEMADCLUTBIN PRECURSOR	MELLIENZA A VIRUS (STRAIN A/TURKEY/W:SCONSIWING)							: :
PAPETA IATEW	HEXAGGLUTION PRECURSOR	ANT HENYA A VIRUS (STRAIN A/TERN/AUSTRALIA/G10C/15)	2:3	+				_	!
PARTY INTRA	HEMAGGLUTININ PRECURSOR	A VARIS (STRAIN AUDOLAVIORA)	7						-
OUT VIEW	HEMAGGLUTHRIN PRECURSOR	THE LUCKER A VIBIL (STRAIN A/USSR/907)	٦	506.348	+				
	HEMAGGLUTINGS PRECURSOR	INTERCEMENT AND ANICTORIANS	381-457	1	1				:
100	HEMAGGEUTTININ PRECUNSOR	INTERIOR OF THE ACT AND ACT SON SAILTIVE	115-477	509-547			-		
A 1	MENACOL UTININ PRECURSOR	INTLUENCA A VINUS (311001)	380-456	-			-		
THE WAR	SELECTION PRECUASOR	DATUENZA A VIRUS (STRAIN SOS INSTRUMENTAL KONGALIAR)	364.440			<u> </u>	-	-	-
MENA MZCO	TOTAL STATE OF THE CURSOR	INTLUENCA A VIRUS (STALIN ASMINDADING PONCH 2003)	364.440				1	-	:
HEAL WIND	HOMACA COLUMN CO	INFLUENCE A VIRUS (STRAIN ASSWINE) CONTRACTOR	Γ	506.548				1	1
PHEDAN IAZHU	MENAGGLUTINIA PRECOMO	MELUENZA A VIRUS (STRAIN ASWINE/INDIAMALIZATE)	T	204.53		j			:
PIEDAN INZIN	MEMACAL DILINIA PLECCO	BOTUENZA A VIRUS (STRAIN ASWINEMEN JENSETTITO)						1	1
PHEDIA IAZNI	HEMAGGLUTININ PRECUASOR	DALUENZA A VIRUS (STRAIN ASWINEAUKKEUIMA		-	-				1 1 1
PHENCA MZUR	HENAGGLUTININ PRECURSON	INTI UENZA B VIRUS (STRAIN BAEITING IA)		-	-				: :
MENT PABE	MENAGOL UTRAIN PRECURSOR	INTLIENZA B VIRUS (STRAIN INDONNAS)	3 76-40			-			
PHENA BABBO	HEMAGGI UTIMIN PRECURSOR	INTELENZA D VIRUS (STRAIN DENGLAND/212/82)			-		L		
PIESA PREM	HEMAGGLUTDEN PRECURSOR	INTI INTIZA B VIRUS (STRAIN BAHONG KONGARTI)		+					
PHENA DIBIO	HEMAOGLUTONIN PRECURSOR	THE ITEM A B VIRUS (STRAIN BALEE/40)	307:473		-		-		
ALENA POBLE	HEMAGGLUTININ PRECUISOR	THE LIENZA B VIRUS (STRAIN BALARYLAND/SP)	377-462				-		
DABAA DOM	Ī	THE LENZA B VIRUS (STRAIN BACENDHIS MACA)	381.468	+	-		-		
PHENA DIBME	Ī	PATI (FNZA B VIRUS (STRAÍN BYOREGON/MO)	116-471		-		-		
PARTY DODGE	Ī	THE STATE OF STRAIN BUSINGAPORE/22/79)	386-471		+		-		
MONTH DOOR	HEMACOLUTININ PRECURSOR,	THE PARTY A BYTHIS (STRAIN BUSSIVICOR))	179-464	+	+	-	-		
	HEMAGGLUTENN PRECURSOR	CALCACTOR CONTRACTOR AND BANCT	381-466		+	1		-	
NEW YORK	HEMAGGLUTDAN PRECURSOR	INCOCKED TO STREET BYICTONIA 2017	368-473			-			
	T	INCLUENCE STATE (STEATH COLIFORNIA/TE)	483.571			1			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	T	INTLUENCA L VIROS (31 MAIN C/FINCL AND/92/83)	471-559						
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	T	INPLUENCE CATALOGUE AN CAREAT LAKES/116754)	471.559		-	-	\ 	 -	
A STATE OF THE PARTY OF THE PAR	T	INFLUENCA C VIANO (STRAIN CARVOCOLIA)	470-558			1		+	-
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	T	INPLUENZA C VINUS (STRAIN CHOLANNESBURG/1/86)	484-572			1		-	
100 V	T	INPLUENCE CARGE (STRAIN CKYOTO/4/R2)	470-558		1				
A STATE OF THE PARTY OF THE PAR	Τ	INTUENCA C TINGS (1)			•				
PHEMA LITTLE	1								

	PROTEIN PERVICELUTION PRECINSON PERVICENTAL PRECINSON PERVICENTAL PREC	(a)	$\Pi\Pi$	d d	70100			\mathbf{I}		
	LE) DASE DASE DASE DASE DASE DASE DASE	ERZ A C VRUS (STAAN CAISSISSEPURS) ERZA C VRUS (STRAN CANAVAS) ERZA C VRUS (STRAN CRIGOELINGVIRS) ERA C VRUS (STRAN CRIGOELINGVIRS) ERZ A C VRUS (STRAN CRIGOELINGVIRS)	100.51			+	\parallel	\prod	 	
W = > - 3 #	E) DASE DASE DASE DASE DASE DASE DASE		20.538	1	+		1	+	$\ $	
	LE) DASE DASE DASE DASE DASE DASE								1	
	LE) DASE DASE DASE DASE DASE DASE		466-179	\dagger		+	+		_	
	ASTES VIRUS (STRAIN HALLE) JACCALUTININ PLECUSIOR JACCALUTININ PLECUSIOR JACCALUTININ PLECUSIOR JACCALUTININ PLECUSIOR JACCALUTININ PLECUSIOR JACCALUTININ PLEUAAMINDASE JACCALUTININ PLEUAAMINDASE JACCALUTININ PLEUAAMINDASE JACCALUTININ PLEUAAMINDASE JACCALUTININ PLEUAAMINDASE JACCALUTININ PLEUAAMINDASE JACCALUTININ PLEUAAMINDASE		441-334	1		†	-			
	AAGGLUTRIN PRECINSOR AAGGLUTRIN PRECINSOR AAGGLUTRIN PRECINSOR AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE AAGGLUTRIN PREURAMINGASE							-		
	AACCA UTRININ PAECIA SOR AACCA UTRIAN-REMANITIOASE AACCA UTRIAN-REMANITIOASE AACCA UTRIAN-REMANITIOASE AACCA UTRIAN-REMANITIOASE AACCA UTRIAN-REMANITIOASE AACCA UTRIAN-REMANITIOASE		187							
	AAOGUUTININ-NEUTAANTIDASE AGGGUUTININ-NEUTAANTIDASE AAOGUUTININ-NEUTAANTIDASE AAOGUUTININ-NEUTAANTIDASE AAOGUUTININ-NEUTAANTIDASE AAOGUUTININ-NEUTAANTIDASE AAOGUUTININ-NEUTAANTIDASE	INTLUENZA C VIRUS (3 IRAIN CTANIACION)	06-90			-				
	AACCLUTNIN-HEUAANINDASS AACCLUTNIN-HEUAANINDASS AACCLUTNIN-HEUAANINDASS AACCLUTNIN-HEUAANINDASS AACCLUTNIN-HEUAANINDASS		04-97							
	AACCLUTEEN-BEILAANEDASE LACCLUTEEN-BEILAANEDASE LACCLUTEEN-BEILAANEDASE LACCLUTEEN-BEILAANEDASE LACCLUTEEN-BEILAANEDASE		46-87							
	VACCEUTRIN-NEURANIMIANS VACCEUTRIN-NEURANIMIANS VACCEUTRIN-NEURANIMIANSE	MEASLES VIRUS (STRAIM IF-J-LA)	16.67							
	AAGG UTRAN-VEUNAMMDASE MAGG UTRAN-NEUNAMMDASE		\$ 2							
	MAOQLUTININ-NEUMAMINIDASE	MARA VACCINE)	8.4.				Ļ			
	AAA CCU TITTI AND NING AND NIN		34.99							
			34.99							
_	HEMACOL UTININ-NE URANIMIDANE	(STRAIN AUSTRALIA-VICTORIAN)	1.52	477-529				1		:
	HEMADOLU I ININ-MEUKAMININASA	_	67-1					1	j	
T	HEMAGGLUTININ-NEUKARINIDASE		1.53					1		
1	HEMACOLUTININ-FEURANIMIAASE	ELA/SI)	1.53			1		+	1	
	MACCE OF THE WAR TO A VINITARY OF THE AVENUE OF THE AVENUE OF THE OWNER OWNER OF THE OWNER OWNER OF THE OWNER OWN	92	1-52			+				
Т	NEWACKEU INTERNATIONALISMENT AND ASE	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B /41)	1-49			1		+		
Ţ	ATTACAS CONTRACTOR AND ASSESSMENT	NEWCASTLE DISEASE VIXUS (STRAIN ULSTEAM)	1.53			+		+		
T	HEMALOGI ITTOMA ME MARMIDASE	PHOCINE DISTEMPER YIRUS	19-73			$\frac{1}{1}$		+		
1	TENACOL STROM META AMOUNTAGE	VIRUS (STRAIN WASHINGTON/1957)	011-99					+		
J	HENA COLUMNA META ANNUA SE		247-381			1	1	+	Ì	
THEMA TURN	ATTACC INTO NATIONAL PROPERTY OF THE PROPERTY	(STRAIN TOSHIBA)	247-281		1		1			
T	NEW ACCUSTOMENT OF AND STATE OF AND STATE OF A STATE OF		٦		1	1			1	
Ī,	HEMAGGI UTDININGUNANDHASE		٦	394-428	1		1	\dagger		
Ī	HEMAGGLUTININ-NEURAMINIDASE	٤	7	100	†	+	+	+		
Ī	HEMACCE, UTININ-NEURAMINIDASE			20.04	†	+			T	
Γ	HEMAGGLUTININ-WEURAMINIDASE			27		-		+	T	
	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAMPLUENZA I VIRUS (STRAIN 1EX) 120/1/10	T	167.00	+		-			
	HEMACCLUTINEN-NEURANDMIDASE		T	304-021	T	-				
7	ADMAGG UT DAN-NE URANGANDANE		\$4.88							
Т	ACMACCILITATION PRECIDENCE			256-290						
THESE BACK	HENA ACCE INTERNATIONAL METALANDATION SE	IUNDEAPEST VIRUS (STRAIN KABETE O)	46-87			+	1	+		
T	HEMAGGLUTIMIN-NEURAMINIDASE	RINDERVEST VIRUS (STRAM L.)	٥	101-233	+	+	1	\dagger	Ì	Ì
PHEMA SENDS HE	HEMAGGLUTININ-HEURANINIDASE	SENDAI VIRUS (STRAIN Z / HOST MUTANTS)	37-110			+	+	+		
Γ	HEMAGGLUTININ-WELDAAMNIDASE		2			\dagger	-	+	Ī	
	HEMAGGLUTDNIN-NEURANDMIDASE	JUS)		1	1	+	+	1		
Ī	HEDAAGGLUTININ-VEURANIINIDASE	/n		1	1					
T	HEMAGGLUTININ-NEURAHINIDASE	SENDAJ VIRUS (STRAIN Z)	27.110		1	+	-	+		
T	HEMAGGLUTTHEN HEURANGKEDASE	SDGAN YOUS 41	116-52	207:42		+		\dagger		
	HENLAGGLUTTHTH-NEUTANDHIDASE	SDEAN VIRUS 5 (STRAIN W3)	27.63	†		+	1		T	
Z	HEMAOGLUTININ-YEURANDHOSE	SDAAN VOUS S (ISOLATE SOMANAN)	2.0		1	+	1	+	T	
	HEMAGGLUTININ PLECURSOR		13.5			+	1	+		
T	PERIPENTONAL HEXON-ASSOCIATED PROTEIN		8.28			+	1	\dagger	1	
T	PERIPENTONAL HEXON-ASSOCIATED PROTEIN		90-134				+	+		
T	HEXON-ASSOCIATED PROTEIN		13.00		+	+	+	+	T	
Γ	EXON-ASSOCIATED PROTEIN	HIDAAN ADENOVIRUS TYPE S	***			+	+	\dagger		
T	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 1, AND IRMAN ADENOVIRUS TYPE (9)-130	87-178		1	1	1			

PCGENE TILE NAME PIEXY ADE!2	ALLMOTIS TROUGHER HEXON-ASSOCIATED PROTEIN HEXON-ASSOCIATED PROTEIN HEXON-ASSOCIATED PROTEIN			ABEA 1	7737	1020	1	4		
	SOCIATED PROTEIN									
HEXS ADEI2										
HEXS ADEI2		N ADENOVIRUS TYPE 12	67-126							
EXP ADEA!			1							
	i									
			Ī		***					
HEXP AUCK			-	433-407						
HEXS ADENT			330-379							
HEX ADEOL			Γ	408-449	553-587		-			
PHEX ADEOS		HINNAN ADENOVIRUS TYPE 40	Γ	\$55.580			T			
ANEX ADRAG		AND A DENOVIRUS TYPE 41	T		144.571	205.239				
		TUNION ADELIO TOPE 1	٦	113-41						
NEX ADEA		BOVINE AULMOVINGS 1112	320-395	455-489						
PHEX ADEBI		COWPOX VIRUS	130-151							
PHOLO COWPX		AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	Γ	171.419						
PITTE ASFR?		CALE TEL CASE ANDSAIC VIRUS (STRAIN DA)	T				_			
		CACLIFICATION OF STRAIN DARG 1)	179.470			-	-	_		
PERSON CAMAS		CAULIFLOWER MOSAIL VINOS (ST. CALIBEL)	7:1	378-419		-	1			
PIEND CANN		CALL IFLOWER MOSAIC VIRUS (3) KAIN CHITTE	1	378-419			-			
PIBLO CAMPC		CALL IFLOWER MOSAIC VIRUS (STRAIN DIT)		111419						
PIEMO CAMVO		CALIN IN OWER MOSAIC VIRUS (STRAIN BAC)		210 410						-
SIEVE CANVE		CALE IEL OWER MOSAIC VIRUS (STRAIN S.IAPAN)	2			-	-			
CANAL CANAL	INCLUSION BODY MATRIX PROTEIN	ALTER SACRAIC VIRUS (STRAIN NYBISS)	23	10-016		-		L		
2010	DACT LISTON BODY MATTUX PROTEIN	CAULTON CO. COMPILE (CTRAIN PV147)		374-419		1			_	
TIBLE CAME	ANY THINK MOON MATRIX PROTEIN	CAULIFLOWER PROSALL VINCE (STEAM CROURG)	1.3	371-419		1		-		_
PERIOD CANAN	THE PROTEIN	CAULFLOWER MOSAIC VIRUS (SIEMILE STIC	1,11							-
PIEND CANYS	INCLUSION BOOK ALVERY PROTEIN	CARNATION ETCHED RING VIRUS	15.	373-406				+		-
PUBAC CERV	INCLUSION BOOT PAYMEN	FIGWORT MOSAIC VIRUS (STRAIN DXS)		132.179	L					-
PERMO PAND	INCLUSION BODY MAINA THUS EN			300.134	498-532	-				-
VACOA SOCIAL	INCLUSION BODY MATRIA FROI EAR	MANAY CYTOMEGALOVIRUS (STRAIN AD169)			1	-				
AVACUA MICANA		TI NOTATION TO STEAD IT	331-365			1	\ \ +		L	
	PROTECTION AND TRANSPORT PROTEIN	HEADES SUPPLIES THE STATE AND ANGELOTTI)	331-365				-	-		
PICIE ISA	SACCESSION AND TRANSPORT PROTEIN	HEAVES SOUTHER VINOS (1176 1 / CTB ATA (1)	324-363				-	+		L
ALLE USALIA			466-500		_	1	-		_	L
TICIS MANIE	PROPERTY E PROCESSING AND TRANSPORT PROTEIN	BOVING RELICES VINCES	341-375			-	-	-		L
PICIS NOVEL	BEACH OF PROCESSING AND TRANSPORT PROTEIN	HEINESVIKUS LIVE I (130CA) ETT.	51.99	361-395		1	-	-	-	
PICIS HSVED	PRUBABLE PROCESSING AND TRANSPORT PROTEIN	HERPESVIRUS SABATA (STRAIN II)	60-112	290-340	169-299			+	1	+
PICIO HSVSA	PROBABLE PROPERTY AND TRANSPORT PROTEIN	ANDINE CYTOMEGALOVIRUS (STRAIN SALLIN)	6 360.111	101-137						+
PICIS MOAVS	PROBABLE PROCESSION AND TO ANGROLIT PROTEIN	APSEUDORABIES VIRUS (STRAIN INDIANA-FURINGAUSER) BEEN				L				-
PICIS PRVD	PROBABLE PROCESSING AND LINUX BEATEN ICPO	BOVING HERPESVIRUS TYPE I (STRAIN JURA)		-	-					1
MCPO HSVB!	TRANS. ACTING TRANSCRUTTORAL PROJECT	-	180-224		-					1
1000	TRANS. ACTING TRANSCRIPTIONAL PROJECT	-	1022-1036		$\frac{1}{4}$	-		_	L	
200	TRANS. ACTING TRANSCRIPTIONAL ACTIVATOR PR	٦t	920-954			1	-		-	_
	TRANS.ACTING TRANSCRIPTIONAL PROTEIN ICPA	7	207-241			1				_
200	THE ANGUREPHONAL REGULATOR IE61 HOMOLOG	HOMAN CTIOMECALOVING CTOATA	241-275					-	-	-
PIEGO HUMAN	TO ANYCHIPTIONAL REGULATOR (E63	HERPES SINCELEX VIXOS (LITTE 17 STEATH AND AND)	262-316				+			-
E PA	THE ANGUE PEGULATOR IEAS HOMOLOG	EQUING HELVESVINGS LITE (STEAM)	195-239	258-306				1		-
PEED HISVER	THANKE INTONAL REGULATOR (EAS HOMOLOG	VARICELLA-ZOSTER VIRUS (3 FRAIM DUMAS)	13.131	L				-	1	+
MEG VZVD	INCOME TO SERVICE OF S	EQUING HERIPESVIRUS 1 TPG 4 (31 KALIN 1744)	68-13							-
PIESS HSVES	DAME DATE OF STREET OF THE PROPERTY OF THE PRO	EQUINE HELDESVIRUS TYPE I (STRAIN ABAT)	1	-		_			1	+
PEESS HISVED	DOMEDIA I E-CALLI PROTEIN	HERPESVRUS SAMON (STRAIN !!)		-		L				1
PIEGI HSVSA	DOCDIATE EALT PROTEIN	HUBIAN CYTOMEGALOVIRUS (STRAIN AD169)	17.72	1	-				1	+
PUTOS HONA	HYPOTHETIS AL PROTESS IN 19	HIBAAN CYTOMEGALOVIRUS (STRAIN ADIES)				-				+
PIRIT HOWA	HYPOTHETICAL PROJECT TO ANSFORMANO PROT			-			-		-	+
PECABL FSVHY				20,000		-			-	1
PKABL MLVAB	TYROSINE PROTEIN KINASE LANSION						-			1
PICAKT MALVAT	AKT KNASE TRANSFORGENO PROTEIN	THE THE SARCOMA VIRUS (STRAIN GALDRER-ALMSTEIN)		1	1	-				$\frac{1}{1}$
PREES FSVGA	TYROSINE-PROTEIN KINASE I AVEFORE		707-817	1	913.840		-			+
PRECE FSVGR	TYROSDIE PROTEIN KINASA I INCLASOR	FEI ING SALCOMA VIRUS (STRAIN MCDONOUGH)	787-117		-	-				$\frac{1}{1}$
PKEAS FSVAD	PAS TYROSING KINASIS HANSON	THE SECT AND SARCOMA VIRUS (STRAIN PRCII)	4-60							
PKEPS AVISP	TYROSDIE PROTEIN KINASE TRANSPORT				٠					

	ALLAIOTIS TROSTANG-PROTEIN KRVASE TRANSFORAING PAOT THYAIDDRE KRVASE THYAIDDRE KRVASE THYAIDDRE KRVASE THYAIDDRE KRVASE THYAIDDRE KRVASE	YIRUS FURNAMI SARCONIA VIRUS AVERTA ANOMEI ENTONOPOXVIRUS	65:39 15:10	2 × × × × × × × × × × × × × × × × × × ×	148.398	6				; : ; !
	3 PROT	AG SARCONIA VIRUS		Τ		I				:
		POXVIRUS	-							: ! :
								L		
	MIDINE KINASE MIDINE KINASE MIDINE KOASE		38-83							
	MIDINE KINASE		228-263	431-472						:
	MODINE KOVASE		\$6134							:
		HENES STATES VINOS (1175 1/3/2011)	\$6.134							:
	TANADOME KINASE		80.134							;
	TUNAMENTAL KINA SE		134	-						•
	TANABLANK K DIASE		2 2	 						
	THE PROPERTY OF THE PROPERTY O	-								
	INTRICATE PRINCES		3							_
	MIDING KINASE	BOWNE IGE PES VIRUS TYPE 3 (STRAIN WC11)		1						:
	THYMIDING KINASE	KANTAGE LEED PERVISITY PE 4 (STRAIN 1942)	19.53	20.5						:
	THYMODIE KINASE	TOTAL SEPTEMBER 14 TOTAL AND ADAPT	19.53	178-130						:
	THYMIDING KINASE	EQUIPE SERVICES VINCE TO LICEPE CYBELS 1)	180-214							:
	THYMIDDAE KINASE	FELINE HEATES VIAUS (FELIN HEATES VIANO)	13.65					j		:
	THYMIDDG KOMSE	ALARANOSET HERPESVIRUS								
T	PUNCTIONAL KINASE	HERVESVIRUS SAINING (STRAIN 11)		t			L			
	TANADOG KINASE	PSEUDORABIES VIRUS (STRAIN NIA-3)	7117-101					_		
ľ	A STANKE THE CAME PROTEIN KINASE TRANSF	AVIAN RETROVIRUS LIII?	0,10	1						
		+=								i i
	GENE 19 PROTEIN ALCASE	HERPES STRIPLEX VIRUS (TYPE 1/ STRAIN 17)	٦	21.12						 -
1	WINE-TAN CIENT	ICTAL LINID HERPESVIRUS I		397-631				-		-
	CENE 14 PROTEIN KINASE		21-45							 -
	PINA		127-164							1
	30 KD PROTEIN KINASE MUNICALAN	CACCOUR COURTS (CTEATE WE)	137-168							: <u>!</u>
	30 KD PROTEIN KINASE HOMIOLOG	CALCINIA ASSESS	133-131						ļ	-
	30 KD PROTEIN KINASE HONIDLOU	VACCINIA VIBIR (CTLAIN COPENITAGEN)	147-181					4		:
	POSSIBLE PROTEIN KINASE BIZ	VACCINIA VIRIS ISTRAIN WRI	147.181					1		i
Ī	POSSIBLE PROTEIN KINASE BIL	VACCIONA VIRUS (STRAIN COPENHAGEN)	169-203							 -
1	POSSIBLE PROTEIN RIPASE FIV	VACCINIA VIRUS (STRAIN L-IVP)	136-170					-		-
1	POSSIBLE PROTEIN KINASE FIN	VARIOLA VIRUS	169.203				1			
	STOLE PROTEIN RIPAGE FIN	т	111-145							i
	AOS TYROSINE KINASE TRANSPURAIMO PROTEIN	AVIAN BETROVIBUS RPL30	13-66					1		-
	ASE TRAMSFURMI	VACCIDIA VIBILS (STRAIN WR) (STRAIN COPENHAGEN)	133-169							ļ
	DYNAMOYLATE KINASE		114-211					-		ļ
٦	INASE INANSPORTI		441-475				1	1		ļ
	LATS 100 KD PROTEIN	MANAM ADENOVISUS TYPE S	223-264				<u> </u>			1
	LATE 100 KD PROTEIN	HADAAN ADENOVIRUS TYPE 40	191-332	108 442		-		$\frac{1}{4}$		1
	LATE 100 KD PROTEUR	MANAN ADENOVIRUS TYPE 41							-	
	LATE 100 KD PROTEIN	INDIAN ADENOVIRUS TYPE 2	238-264	101-349			-	\downarrow		-
	LATELISTED	HIMAN ADENOVIRUS TYPE 5		301-348		1		\downarrow		1
	LATE LI 32 KD PROJEIN	EPSTEIN-BARR VIRUS (STRAIN 899-8)		294-318			-		+	-
٦	NE TERMINAL PROTEIN	SHOPE FIBROMA VIRUS (STRAIN KASZA)	54-152	623-656				1		1
T	MOUNT CATTING ENGINEER	VACCINIA VIRUS (STRAIN COPENHAGEN)		55.53		-	+	1		-
1	ADUA (APTIMO ENE THE	VACCINIA VIRUS (STRAIN WR)		623-657			1			
1	MUNA CATTAN CALIFORNIA	VARIOLA VIRUS		63.437			\downarrow]
T	MUNA CAPTURE EACT ME	VACCINIA VIRUS (STRAIN COPENHAGEM)		300				+		-
	ACUA CATING ENGINEE	VACCINIA VIRUS (STRAIN WR)	1	33.26				-		
J	MOUNT CANADA ENT YOUR	VALIGLA VIRUS	T	I						
	CONTRACTOR STATE	ASTUCAN SWINE FEVER VIRUS (STRAIN BATIV)		24.310	2	-	-			L
T	ALLA CASTER PROTEIN	ODONTOGLOSSUM RINGSPOT VIRUS	8.6			\downarrow	1	-		-
T	ACCOUNT PROTEIN	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	3				\downarrow			
PAGOVE PPAVS	MOVEMENT FACTOR	TOBACCO AMLD GREEN MOSAIC VIRUS (TAIV STRAIN U.)	300			-				

4							П	17	IΤ	
PCCENE	ALLAROTIS		AREAI	15380	SATA	2028	98562p	- Wild	707	120.00
TILE NAME	TROTEIN	POPACCO MORAIC VIRIS (STRAIN TONIATOR)	33-66				†			i
PAIDVE THATO	MOVEMENT PROTEIN		11-10							
PLIOVE TOMOVA	MOVEMENT PROTECT		33-60							
PHOVE TOWN	MOVEMENT PROTEIN		333-356							
ואענכו כאנאו	MODIFICATION NETHWASE CVIDE	CALUMETER AND STORY CHARGELLA VIRUS	116-164							
PATCE CHYPI	MODIFICATION METHYLASE CYLASS		129-266	175-419						
PHYTE AVBA	HYC TRANSFORMEN PROTEIN		230.367	174.10						
PLIYC AVDAC	MYC TRANSFORKING PROTEIN		230-267	176-420						
PAYC AVBID	MYC TRANSFORMING PROTEIN		111-111							
PLIYC AVDGE	MYC TRANSFORMING PROTEIN		126-261	370-414						
PAITC AVIOK	MYC TRANSFORMING PROTEIN	CEL PAR I FIREMIA VIRUS	193-417							
PHYTE FLY	MYC TRANSFORMING PROTEIN	THE PERMIT BEOVELLY FIT	161-417							
PAYC PLYTT	MYC TRANSFORMING PROTEIN	CORDINE CORONA VIETS MILY (STRATM A 39)	97 (
PNCA3_CVMAS	MUCLEOCAPSID PROTEIN		11:211							
PHCAP ATHOV	PUCLEOCAPSID PROTEIN	AINO VINUS	65	122-156						
PNCAP BEV	MUCLEOCAPSID PROTEIN	BATCHY SYNCYTIAL VIRUS (STRAIN AS1908)	63-104	163-200	348.303	10.00				
PNCAP BRSVA	NUCLEOCAPSID PROTEIN	PIPAY AND IS CERMISTON	176-228							
PNCAP BUNGE	MOCI EOCAPSID PROTEIN	P. D. VISING A CROSSE	136.229							İ
PHCAP_BUNGC	MUCLEOCAPSID PROTEIN	SUNTA VIEW CUANCINE ILARE	176-219							
PHCAP_BUNSH	MUCLEOCAPSID PROTEIN	BOATA WAS A VIBIL	135.231							
PNCAP BUNYW	NUCL EOCAPSID PROTEIN	CONDITION OF THE CORP. (150), ATE CORP.	111.106	427-461			j			
PHCAP CODGV	NUCLEOCAPSID PROTEIN		117.174	110.213	154-402					
PRCA CBVO	MUCLEOCAPSID PROTEIN	CANINE DISTRIPTE VIRUS (STRAIN ONITERSTEE COMP	10.00	131.369						-
PRCA CHAV	MUCLEOCAPSID PROTEIN	CHAMMINA VIKUS (STRAIN 1922) 14	140.161							
PNCAP CVBF	MUCL EOCAPSID PROTEIN	BOVINE CORCRAVIRUS (STRAIM F 12)	146.101							
PICA CVIM	MUCLEOCAPSID PROTEIN	BOVING CORUNAVIROS (STRAIN PREDOS)	165.227							
PHCAP CVCAE	MCLEOCAPSID PROTEIN	CANINE EMPENC CORONAVINOS (STOCKES ASSES)	149.313							:
PICAP CVHOC	MUCL EOCAPSID PROTEDY	FUNAN CORONAVIROS (SIENAIN OCCU)	97-2						:	:
PHCAP CYALIN	MUCLEOCAPSID PROTEIN	MUNITE CONCRAVINGS FILLS (STEEDENTED THE CORONAVIRUS (S	149.306							
PINCAD CVPTS	NUCL EOCAPSID PROTEIN		163.333							
THEAT CYPTU	NUCL EDCAPSID PROTEIN	PORCING INCREMISTRATE CONTINUE (CTRANGER 24/13/004 / RRIT	149.228						İ	-
PHCAP CVPRS	NUCL EDCAPSID P.OTEDM		169-238							-
PHCAP CVPILM	MUCLEOCAPSID PROTEIN		97							1
PHCAP CVRSD	NUCL EDCAPSID PROTEIN		148.383							!
PHCAP CYTKE	MUCH EOCAPSID PROTEIN		230.306							
PHCAP DUGBY	MUCI EOCALSID PROTEIN	TIGUS PERITONITIS VIRUS (STRAIN 79-1146)	151.204							
PICAP FIPV	NACE COLVERN PROTEIN		1.35	40.74	111.10					
PNCAP HANTY	MOCIECA SECTION PROTECT	ILAZALA VIRUS (ISOLATE IC280)	111.147							
MCA HAZVI	MOLECAN SECTION	AL VIRUS (SUBGROUP B / STRAS	62-143	5.78	249.703	2				!!
PACA PASVI	And tockets profess		\$ 2	±1.700	24.30 24.30	201.100	-			!
PACA HASVA	AND SOCIAL PROTEIN		106-227				1		- 	::::::
PICA IBVO	COLLEGE SECTION		22							-
MCAV GAY	SOCIAL DESCRIPTION		ا <u>چ</u>				+			-
PACAP PUNCA	SOLLEGE STATE OF THE STATE OF T		65-113	2. 1.2					 	
3	NOT TO COLVER PROTEON		2 = 1	12:17	25.50					i
2	A COLOR DE CATE DE		9						- -	- :
MCA LEG	MICH EGYAPETER	STRON		\$60.49			-		-	:
MCA LYCA	ANCHE COLANGE PROTEIN	HORIOMENINGITIS VIRUS (STRAIN WE)	-		460.47			İ		:
	AND EDITOR DEDTEON		T						1	!!!
ACC PARCE	AND ENCLOSED PROTEDN	170%)	T	10.45						i
1	NAME FOCAPSID PROTEIN	AGEASLES VIRUS (STRAIN HALLE)	T				-		Ī	i
2	NAME OF A PROPERTY	AFEASLES VINUS (STRAIN IP-1-CA)	189.736	161-41						Ì
MAN MEAN	NOTE OF THE OF				•					

		Control of the Contro					Т	Т	Т	
PCCENE	ALLAIOTTS		VECAL	1251	AREAL	AREA	2000	10190	2	
THERM	PROTEIN	ES VIRUS (STRAEN YANIAGATA-1)	٦	5.5			1			
PHCAP MEASY	MOCI EDCAPSID PROTEIN		901-59	11.303						!
PHCAP MOPE!	MUCL EOCAPSID PROTEIN	CETE AIN SOL. II		500-534						İ
PHCAP MAD!	MUCL EOCAPSIO PROTEIN	IARA VACCINE)	314.255							
PHCAP MARGIN	MUCL EOCAPSID PROTEIN		55.1	40.74	153.302					
PHCAD PHY	MUCL EOCAPSID PROTEIN	-	111-111	641-310						;
PRCA MIRC	MUCL EOCAVID PROTEIN	HINGTOWISS 1)	111.111	441.510						:
PCAP PER	MACL EOCAPSID PROTEIN	_	314-366	144.378					1	:
PICA PINT	MUCI EOCAPSID PROTEIN		100-401	144.410		İ	+			
PICA NUB	MUCLEOCAPSID PROTEIN	CSTRAIN MIT 47613)	13.135	308-366	144.401	440.491				
PHCA PUR	MUCLEOCAPSID PROTEIN		3	191.263]	1	
PHCAP PIANA	MUCLEOCAPSID PROTEIN		20.00	101-367					1	_
PNCAP PIOS	MACLEOCAPSID PROTEIN									
PHCAP MARY	MUCLEOCAPSID PROTEIN		Ī	125.359						_
PHCAP PIRTY	MUCLEOCAPSID PROTEIN	THE VIEWS AND THE PARTY AND THE PARTY.		40-75	133.30:					
THE PLEASE	MUCLEOCAPSIO PROTEIN			40.33	111.141			-		_
THE A PUBRIS	MUCL EOCAPSID PROTED		191-16	246.303	344-314				į	•
PHCAD PVH	MUCLEOCAPSID PROTEIN		_							_
PHCAP BABVA	NUCLEOCAPSID PROTEIN		Ī	141.664						
PACA SERIOS	NUCLEOCAPSID PROTEIN	MULANIS	Ī	104.14				i I		
FACAP SENDE	MUCL EOCAPSID PROTEIN	IDERS	Ī	141.601				İ		
PHCAP SENDE	MUCLEOCAPSID PROTEIN		Ť	****	111.180		l L			! :
PNCAP SEOUS	MACLEOCAPSID PROTEIN	RAIN SR-11)	T							.
PACAP SV4	MUCLEOCALSID PROTEIN		T	8						:
SACA SYNO	MICH EDCAPSID PROTEIN	IV MET VIRUS								!
AVI AVING	MAICH EDCAPSID PROTEIN			70.764						:
200	MACHEDICAPSID PROTEIN		215.240				1			
2002	MICH FOCAPSID PROTEIN		28-120					Ī		
PACAS TSWAY	MICLEOCAPSID PROTEDA	(SOLATE)	22.62				+			
PACAP TSWM	MICLEDCAPSID PROTEIN	TONIATO SPOTTED WILT VIRUS (STRAIN L.)	19.130	ĺ			1	Ī		: : :
PACAP LAR	MACLEOCAPSID PROTEIN	Ī	201-102							
PACAP VHSV0	MICLEOCA/SID PROTEIN	1	T							:
PNCAP VHSVA	MICLEOCAPSID PROTEIN		Ī	10.00			+			
PHCAP VSVID	MUCLEOCAPSID PROTEIN	VESICIALAR STORIATITIS VIRUS (SEROTYPE INDIANA / STRAIN U	B							
PHCAP VSVJO	MUCLEOCAPSID PROTEIN	135 1 2120								
PHCAP VSVSI	NUCLEOCAPSID PROTEIN	Τ								
PNEF HV3BE	NEGATIVE FACTOR	INDIAN BARBARETIEMY VIRUS TYPE 2 (ISOLATE DIP)	Ī							
PHES HYZDI	NEGATIVE FACTOR	T	31:21							
PNEJ HVZRO	MEGALIVE FACTOR	۶	109-150							!! !!
PACE HAVE	MEGATIVE FACTOR		101-149							:
PACE HAZS	MEDATIVE FACTOR	IE GR	96-140							
PRE SIVA	NEGATIVE FACTOR	SIMILAM DIGITAL DEFICIENCY VIRUS (F236/SAGH ISOLATE)		233.367						
PACE AL TABLE	MEIRAXMIDASE	LIANOUN	=				+			
CATAL LA CAS	MEIRANDIDASE	ACOLIA/12)	11.74							İ
PARAN IACIO	NEURANDIDASE	DIFLUENZA A VIRUS (STRAIN ACHILLEHM)	=				1			
CALL IN CALL	NEIRAMONDASE	INFLUENZA A VIRUS (STRAÍN ACHICKENPENNSYLVANIA/1) 10/1	140.183	1			+			
MAN MOKE	NEURANDASE	ANIA/BI29	19:10				1	1		
PARAM IADGE	NEURANDASE		T					Ì		
PHRAM MATW	NEUTANDADAS\$	USWEYBRU	T				1	T		
PHALM LAHED	NEURANDHASE	T	3	141.403			1		Ī	
PRAM LUBE	NEURAMMDASE	DEFLUENZA A VIRUS (STRAIN ANGUNERRENI ULATIVATI					 			
PHRAM IAKTE	NEURAAMVIDASE	7								

				-			\Box	П	1	i
		All Virgini (ne hacteriopheges)	AREAL	ABIAL	ABIAA	PRIVE	ALAL	TOTAL	4	-
		. To Standard a Potatili				†				!
٦	PROTEIN	ENZA A VIRUS (STRAM ALEMINORALISME)	11.9							
3		A PROPERTY OF STREET	100					1		
		DATLUENZA A VIRUS (STRAIN ARUDDY TURNSTUNENEW MENSI								
PHRAM IARUE NEU	MEURAMONDASE									
PHILAM IASH? NEU	NE UTCAMBIDASE	Т								
Ī	NEURAMINDASE	ŝ								:
PINEAM IATRA MEU	MEUTLANDRICASI	1								
Γ	NEURAMINIDASE	(E)/A4)	Ì							1
,	MEURAMONDASE	SELICIONA A VIRIS (STRAIN DIBEIDACIA?)	1							
T	NEIBALIDADASE	INTLUCATED THE STATE TO THE PARTY OF THE PARTY IN THE PAR	5.46	10.00						į
T	A LANGUA CE	DOLUENZA B VIRUS (BATANIA CTION	7	149-313						
٦	The company of the co		1	141-111						:
	IIAMINUASE	10010	T	148.11)						
	MEURANIDASE	DAT LIENZA B VIRUS (STRAIN BALARYLANDYST)	Ī	100,300						
٦	AEURAN MON SE	MALLENZA B VIRUS (STRAIN BAIEXIPHIS/MP)								
l	KEURALANDDASE	PART TENZA B VIDIUS (S FRAIN B-ORE GONUTED)								
١	TA AACD CIDAS &	INTLUENTS SEE AND MONICON PORTE AND AND AND AND AND AND AND AND AND AND	23	14.31						
١	MET BANDON SE	DATUENCA B VIRGO (SAN DA ROSE COLLONAL)	5.30	149-311						
١	AND AND ASE	DOLLENZA B VIRUS (STEAM POSSO)	5.10	348-312						
	7. CO. C. C. C. C. C. C. C. C. C. C. C. C. C.	INTLUENZA B VIRUS (STRALS BY IL TONIO	790-120							i -
PARAM DABVI	TEURANIAN PROTEIN PRECURSOR	BONBYX DENSONUCLEOSIS VIRUS	66.130	204-238						:
		DOPATIENS NECROTIC SPOT VIRUS (STRAFM NL. 07)								
PASS INSVIA	MON-STRUCTURAL PROTEIN	TOMINTO SPOTTED WILT VIRUS MAAZILIAN ISOLATE CPINITBIN								
	NON-STRUCTURAL PROTEIN	TOWATO SPOTTED WILT VIRUS (STRAIN L.)								
	HON-STRUCTURAL PROTEIN	A MEANTA MIDDRE I ENTONOPOXVIAUS	1		100, 517					-
Ţ	NUCL EOSIDE TRUPHOSPHATASE!	CHOSELLONGINA DIENNIS ENTONOPOXVIRUS	•	413-448						
	MUCI EOSIDE TRIPHOSPHATASE!	CHOMS CONTRACTOR MINGEN	36-90	241-217	349-344					
	MUCH EOSIDE TRIPHOSPHATASE I	VACCINIA WASSINGTON		146.210						
Γ	MACLEOSIDE TRIPHOSPHATASE I	VALLINIA VIII.		455-505						
T	MUCH EOSIDE TRUPIOSPIIATASE I	VARIOLA VINOS	119-123	649.735						
T	PROTEIN	ICENES SIMPLEA VINCOS IN CORECULACIONI	131-160							
T	ANI VIAL POLYNERASE CATALYTIC SUBUNIT	VACCINIA VIRUS 13 LANIA COL CITICO	131-160							i i
T	SOLVIA) POLYTICASE CATALYTIC SUBURIT	VACCINIA VIRIIS (STRAIM W.R.)	21:120							
	THE SUBURIT	VARIOLA VIRUS	13.16							
1	TOTAL THE THE ACT A TORY SUBUNIT	CAPAJPOXVIRUS (STRAIN KS-1)	94.114							
	POLY(A) POLYPRENASE SECUE AYORY SIGNANI	FOWLPOX VIAUS								:
	LY(A) FOLTMERASE FEOTOS ATORY SUBLINIT	VACCINIA VIRUS (STRAIN COPEMIAGEN)								:
	POLY(A) POLYACILASE REGULATORI S	VACCINIA VIRUS (STRAIN WR)	107							1
		VARIOLA VIRUS	100							ا
	POLY(A) POLYMERASE REGULATURE SOFFICE	ALTTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS		2						1
	13.1 KD PROTEIN IN PE STEUDIN	CARGYIA PSEUDOTSUGATA ANC TICAPSID POLYICEDAUSIS VIRUS	B.					L		: ::::::::::::::::::::::::::::::::::::
Γ	II S KD PROTEIN IN P26 STEGION	ATTICORAPHA CALIFORNICA NUCLEAR POLYMEDROSIS VIRUS		107.101						! !
	MAJOR BOIEDIATE EASE, Y PROTEIN	CARGOTA PSELIDOTSUGATA ACIL TICAPSID POL VIEDAOSIS VIRUS	9140-740							-
	MAJOR DIDIEDIATE EARLY PROFEIN	A ITTOCE A PHILA CALLFORNICA MUCLEAR FOLYHEDROSIS VIRUS	?							
[2	AND CALL A SET MOTSUGATA AND TICAPSID FOL YIEDROSIS VIAUS		3						
Γ	16 PATERGENIC NO	LEGALA ADENOVIRUS TYPE 7								
T	MATURATION PROTEIN	TOWNS TO THE TABLE TABLE	11.11							
Ī	PROTEIN VI PRECURSOR	TOPING TO	17.71				400.000	:100.2352	2368-2004	
Ī	PROTEIN VI PRECURSOR	HUNDAN ADENOVINOS TITES	139.363	143.773	E	183-177		1	3107.2330	1164-1401
٥	GENOME POLYPROTEIN I	BALLET TELLOW FILES AND SEESTING IN 1911	119.163	671.705	141:333	27.12				
T	CENTRAL POLYPROTEIN I	BALLET TELLOW MOSAL VINCOLITY VINCOLITY	130-161	912-591	230-373	117			1004-1041	
T	NA I POLYPROTED	HUNDAUAN GEAR VING CHANGE THE	110-313	615-007	636-677	661-333				-
T	ENA! POLYPROTED [®]	GRAPEVINE FARLEAV VINUS	223-270	616-616						
T	HAAL POLYPROTEIN	TOWATO BLACK HING TIRUS (STEWNS 3)	161-206							
T	NA 1 POL VPROTEIN	TOMATO MINESPOT VIXIUS (ISOLATE MAN SECONDA	340.281	669-333	139-173	707-678				
T	TAN TOWN VERNTEIN 1	BAJLEY YELLOW MOSAIC VINUS (GENSIAM ISOLATE)				:				
٦	EXOME TOTAL									
П	GENOME POLYPROTEIN 1	BAMES SEE								

diado		All Viruses (no bacteriaphages)	П		П	П	П	, , ,	Π	
PACE BANK]	1	T	1000	1	T	1	
THE EAST	CENTURE POR VEROTEIN 2	LEY YELLOW MOSAIC VIRUS (MANESE STRAIN II-1)	1	134-173	787-638					
TOTAL SATE	PACKAGE COLUMNIA		365-406	543-603						
200	Marchan State and State an	TOMATO BLACK RING VIRUS (STRAIN S)	4.38							
PROPERTY OF THE PARTY	ALL A DOL VED TECH	SPBERUXY)		134-368						
AND PORCE	COLONG BOL VERTER	BOVINE ENTEROVINUS (STRAIN VG-5-27)	149-116	1008-1064	1382-1416	1459-1507	1576-1617			
ACCOUNT OF THE	CENTRAL POLYPROTEIN	TE NADL)	244.219	- F	429-463	1033-1074	20.04	1392-1443	1869-1910	277
2000	COUNTY PROTEDY		245-289	446-491	(39-62)	1033-1074	1303-134	1392-1443	1779-1620	2/17-4/17
2000	OPPOSED TO VEROTERA	BEAN YELLOW MOSAIC VIRUS	96-130							
200	CENOME BOL VEROTEIN	COXSACKIEVIRUS AZI (STRAÎN COE)	6-43	562-596	664-698	1045-1100	1408-1546	1607-164R	1803-1839	701-1946
1	CENOME POLYMENTERS	COXSACKIEVIRUS AP (STRAIN GRIGGS)	15-49	1040-1036	1895-1940					
TO COM	CENOME POLITICAL	COXSACKIEVIRUS BI	15.49	1031-1067	1876-1921					
	CENTRAL COLUMNICATION	COXSACKIEVIRUS DI	13-49	1024-1070	1879-1924					
Prot Coxes	GENOME POLYROIEIN	CONSACRIBLE SA	15.48	189.64	1022-1068	1877-1922				
PPOLG COXBA	GENOME POLITICISM	COVENCE IN THE	15.49	1024-1070	1879-1924					
PPOLO COXOS	GENOME POLYPROTEIN	CONSTRUCTION VIBILE	120-154							
PPOLO CYVV	GERONIE FULTING	CENTER VIEW TYPE I (CTE AIN 196.1)	74-108							
POLG DENIE	GENOME FOL YPROTEIN	PENCIE VIEW TYPE I (STRAIN ALS 19.10)	74-108							
POLG DENIA	CENOME POLYPROTEIN		24.108							
PPOLO DENIC	GENOME POLYPROTEIN	E COTCADA	34.104	177-713	966-096	1142-1179	1366-1420	1614-1648	2518-2554	2946-3016
POLG DENIS	GENOME POLYPROTEIN		74-108	111.174	861.995	1143-1180				
PPOLG DENIW	GENOME POLYPROTEIN		448 402							
PPOLG DENTI	GENOME POLYPROTEDN		707 077							
PPOLO_DEN22	GENOME POLYPROTEIN	DENGUE VIXUS TYPE 2 (ISOLATE MALATSIA PIL)	14.100	276.273	200.130	1146-1180	1244-1280	1418-1452	1615-1649	1517-1551
PPOLO DEDIZA	GENOME POLYPROTEIN	DENGUE VIRUS I TPE 2 (STRAIN 1994)				1144-1110	1344-13780	1418-1452	1615-1649	2415-2551
PPOLO_DENZ?	GENOME POLYPROTEDY	DENGUE VIRUS TYPE 2 (STRAIN 16641-PDR33)	31-1	111-117						
PPOLO DENZO	CENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN DZ-04)								
POLO DEDZH	GENOME POLYPROTEIN	DENGUE YIRUS TYPE 2 (STRAIN TH:36)	34.			001.	34.	1410,1463	1415,1640	2412,2551
PPOLO DENU	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN JAKAICA)	B		C#-184	201				
PPOLO DEDGN	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN NEW GUINEA C)	313.24)	361-432				000. 770.	2071 0171	1416.1640
POLO DENZP	GENOME POLYPROTEIN	DENGUE VIXUS TYPE 2 (STRAIN PRISWSI)	74-108	728-777	832-875		1	0071-071	1010-1036	
POLO DESCT	GENOME POLYTROTEIN	DENGUE VIRUS TYPE 1 (STRAIN TONGA 1974)	448.497	332-393	617-13	200-200	200	1007-107		
PPOLG DEPOU	GENOME POLYPROTEIN	DENGUE VIAUS TYPE 2 (STRAIN PUO-218)	614-663						1000	7100.000
PPOLO DENO	GENOMG POLYPROTEIN	DENGUE VIXUS TYPE 1	830-872	959.903	1305-1419	2226-2238	1767-0002	2104-27.78	6/A7-04/3	1000
PPOLG DEN	CENONG POLYPROTEIN	DENGUE VIXUS TYPE 4	186.5	20.0	2514-2555	2701-2735	2	3877-3011		
PPOLG ECHG	GENOME POLYPROTEIN	ECHOVINUS II (STILAIN GREGORY)	213-239	1078-1113						
POLG EACV	GENOME POLYPROTEIN	ENCEPHAL OMYOCALDITIS VIRUS		1472-1518	1522-1570	100	1707-1820			
PYOCO EMCYB	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-B NONDIABETO		1	1974-1920	1374-1372				
PPOLO EMCYD	GENOME POLYPROTEDY	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-D DIABETOGEN	145-179	1076-1117	1474-1320	7/61-3761	2			
PPOLG ENMG3	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS (STRAIN 17A)								
PPOLG ENMCO	GENOME POLYPROTEIN	MENGO ENCEPHALOMYOCARDITIS VIRUS	221-01			5	1401.1631	3145.3300		
POLO FINDVI	GENOME POLYPROTEDI	FOOT-AND-MOUTH DISEASE VIXUS (STRAIN A10-61)	67-177	17.10	710-17			9164.9100		
PPOLO FACOVA	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN ALZ)	107-027	77.67	100					
PPOLO_FA@VO	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIL AND CIUTS)			201.4651					
פאסינים ביים	GENOME FOLYPROTEIN	FOOT-AND-MOUTH DISEASE VIKUS (STRAIN CI-SAMIA FAUIL-S								
PPOLG FABVT	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CI)	6		2					
POLG HCVI	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE I)	364-398							
AVOIL D. 1044	CENONE POLYPROTEIN	HOG CHOLERA VIRUS (STILAIN ALFORT)	40493	979-929	622-569	103)-1070	1190-1233	1307-1343	0281-6441	2136-2170
			366-3500	2515-1559	1647-2708	3037-3098	3133.38	3406-3440		
DON O HOME	GENOME POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN BRESCIA)	460-493	979-979	603-779	1033-1070	113-133	278-1870	1136-2170	311.3436
			2466-3500	2525-2559	1647-1708	3057-3098	3153-3195	1404-1440	1521-1562	
10 m	GENOVE POLYPROTEIN	IEPATITIS C VIRUS (ISOLATE DK)	157.191	2330-3365						
MOLO MCVEO	COUNT BOY VALOTEDA	HEPATITIS C VIRUS (ISOLATE ECIO)	62:99							
POLO H. VH	GENUME FULTENIEM									

		All Viruses (no bacteriophoges)	1000	ABFA 2	AREAS	AREA 4	AREAS A	AREA	AREA!	AREAI
PCCENE	ALTHOUGH	VIRUS	T	Γ	Γ	Γ				
TILLIAME	TAULTO SECOND	HEPATITIS C VIRUS (ISOLATE M)								
PROLO HOVE	GENOME POLITICAL	HEPATITIS C VIRUS (ISOLATE HCV-116)	26.39							
PPOLO HCVH7	GENOME FOLYTROTEUM	JEBATITIS CVRIS (ISOLATE HCT27)	216-270			1				
PPOLO_HCVHS	GENOMA POLYPROTEIN	THE ATTER C VIDEO (1901 ATE HET IS)	246-282				+		Ī	
PPOLO HCVIR	GENOME POLYPROTEIN	PERAILIS CHINAS (SOCIETY)	187.198							
PPOL C HCVD	GENOME POLYPROTEIN	HEPATITIS C VINOS (130CA) C 110 131	187.198							
PROTE OF HICKIS	GENOME POLYPROTEIN	MEPATITIS C VIRUS (1900A 1 E mo-14)	164.308							
ALVOU O SOME	CENTRAL POLYPROTED [®]	MEPATITIS C VIRUS (ISOLATE MC-13)	T	1714-1750	2062-2116					
	CONTRACTOR CONTRACTOR	HEPATITIS C VIRUS (ISOLATE HC-16)	1							
MOLO HCVI)		HEPATITIS C VIRUS (ISOLATE MC.IT)	1		7		6170 0175			
Proto HCVII	OENONG FOLTEROIELY	WEBATITIS C VIRIUS (ISOLATE HC-18)	_	1716-1750	ZOR Z-2110	Т				
PPOLO HCVIA	GENOME FOL YPROTEIN	SEASON CONTRACTOR ATE JAPANESE)	357-405	2331-2369			1			
PPOLO HCVIT	GENOME POLYPROTEIN	TELEVISION CONTRACTOR ATE MC.TD	357.391	2331-2365						
PROTO HEVTO	CENONE POLYPROTEIN	PERATITIS C VIROS (1900) IE DECEN	157.198	1328-2365	3444-3503		_			
CAVEL O 100 AV	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE INITIAL)	Γ	101.135	203-237	170-904	1021-1055	1117-1151		
TAY OF THE PARTY	CENOLOG POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 24A)	T	111.101	Γ	170-904	1021-1055	1117-1151		
2	CENTRAL PROTEDI	HEPATITIS A VIRUS (STRAIN 41C)	١		Ţ	20.00	1021-1055	1117-1151		
1		HEPATITIS A VIRUS (STRAIN 11F)		101-113			Т			
١	GENOME FOLTPRUISIN	HEPATITIS A VIRUS (STRAIN CRUSS)	3-43	101-135	103-237					
	CENCHA POLYPROTEIM	MERATITIC A VIRILS (STRAIN GATE)	90-114	183-216			Т			
PPOLO HPAYH	GENOME POLYPROTEIN	THE CALL CONTRACTOR AND INC. 1341	92	101-135	203-237	10.00	Т	107-101		
PPOLO HOAVI.	GENONG POLYPROTEIN	IRPAINIS A VINOS (SINGING)	3	\$61-101	203-237	100-008		1103-1131		
PACE O HOAVA	GENOME POLYPROTEIN	HEPATITIS A VIRUS (SIRVAIN LA)	Ī	101-135	203-233	870-904	1021-1055	1103-1158		
200	GENOME POLYPROTED	HEPATTHS A VIRUS (STILAIN MIBB)	Ī	101-110	307.241	106-678	1025-1059	1115-1155	1158-1191	
100	A STORE SOLVED TO	SDGAN IEPATITIS A VIRUS (STRAIN AGM-27)								
POLO POAVE	CENTRAL POLITICAL	SOCIAN IEPATITIS A VIRUS (STILATA CY-145)	Ç.	61.10		0.01				
POLO HAVIA	CENCHE FOLITACIONAL	HIDAAN BUIDOVIRUS 14 (PRV-14)	1020-1054	1207-1477	1012					
PPOLO HOVIA	CENTRAL FOLLTRA	HUMAN RUINOVIRUS IA (PORV-1A)	362-396							
PPOLD IQVIB	GENOME POLITICAL	HELLAN RIGNOVIRUS IB (PGIV-18)	387-421	163.904	133-1161					
PPOLO HAV2	GENOME FOLTEROIEM	HERAN RHINOVIRUS 3 (PGIV-2)	156-897	2012	1882-1883					
PPOLO HENNE	GENOME POLYTRUIZIN	INTERNAL BHINDVIRUS S9 (PGV-89)	3							
PPOLO HUEVI	GENOME FOLYPLOIDIN	THE PARTY BOYINGS TO (STRAIN 1670/11)	159.197	176-917	1033-1088	1403-1441	1230-1374			
PPOLG BIDVO	GENOME POLYPROTEIN	ACCESS OF THE STREET STREET STREET STREET	134-168	180-281	475-520					
POLO IAEVI	STRUCTURAL POLYPROTEIN	AVIAN INTELLIOUS BURSAL USEASE STATES	Γ	21.28	339-576	9101-086	1409-1450	1461-1497	2739-2777	2762-2823
PPOLG JAEVS	GENOME POLYPROTEIN	IAPANESE ENCEPRALITIS VIRUS (SI IKAIN SATIT)	322.338	3307-3428						
				,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	119.174	920.1014	1409-1450	2463.2493	2719-2773	1782-1873
SPECIAL DISTRICT	CENDME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA(V))	277	107.701			Т			
					636.636	980-1014	1409-1450	2463-2493	1719-2777	2783-2823
SECOND LATINA	GENOME POLYPROTEDY	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAUANSWAS)	11111111	1117.1478			Т			
					467-504	908-943	1337-1378			
MWIN O WHE	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIKUS (STIKUN MAKATAMA)		36.29	361.00	2464-2490	Г	2740-2778	3335-3359	1319-3423
DAY 1 0 100	CENCACE POLYPROTEIN	KUNUN VIRUS (STRAIN MILMOIC)	2				Г	2534-2591	1967-3001	1003-1017
	CONONE BOI VEROTERI	LANGAT VIRUS (STRAIN TP21)	701-107				Т			
			3102-3143							
71.0	CENOME POLYPROTEIN	LANGAT VIRUS (STRAIN YELANTSEV)	64-103							
TOTAL CANA	CENONE POLYPROTEDN	LOUPING ILL VIRUS (LJ)	62-123							
170	CENOME POLYPROTEIN	LOUPING ILL VIRUS (STRAIN SB 536)	2	200	1048 3087	2610.2689	1016-1095	1390-3341		
	CENOAGE POR VPROTEON	MOSQUITO CELL FUSING AGENT (CTA FLAVIVIRUS)	20.00	Z I	200	1101	1402.1440			
PPOLO HVEV	SETURE OF VEHICLE	MUDICAY VALLEY ENCEPHALITIS VIRUS	67-115	20.5	1	1				
200	CENTRE POLYMENTED	ORNITHOGALUM MOSAIC VIRUS	100		00177100		Τ		1031-101	1167-1201
TOTAL LEGIS		PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	33-100	207:76	1141	101-171	200	0104	7101.1011	
PPOCO POCIN	UEMOME TOLITACIES		1468-1529	71	1948-1942	777	201	100		
	OFLICATE BALL VOID TO	POLIOVIRUS TYPE I (STRAIN MAHONEY)	Ī	200	101-101		Т	iele ie	100-1042	1904-1949
100	COLONG BOLYBOTED	POLIOVIRUS TYPE I (STRAIN SABIN)	3		1007-1102		Т	1400.1640	1106-1140	1902-1947
MOLO POLI	CENTRAL FOR THEORY	POLIOVIRUS TYPE 2 (STRAIN LANSING)	573	13.03	1047-1100		7			
POLO POLZW	GENOME FULTIFICIES									

MAINTER MAINTER MAINTER MAINTER			-	_				
GENOME POLYMOTER PALADORES PALADORES PALADORES PALADORES	IX3 (no escientipueges)	AREA 2	AREAJ	AREA	AREA 3	AREAS	AREA?	ABEAR
GENOME FOLY PROTEINE FOLK DOWING STEER STEAMS IN GENOME FOLK PROTEINE PA	VIRUS TYPE 2 (STRAIN W-2)	168-768	1045-1100	1413-1447	1503-1547	1608-1649	ŝ	1903-1947
GENOME ONLY PROTEINS TOLAD POLICY DIVINITIES UNIVERS TOLAD PROPERTY SECRETARY 164-294 164-195 164-195 164-204		866-930	1044-1098	1412-1446	1498-1546	1607-1641	1805-1839	1901-1046
CENOME OF TWOTTEN		896-930	1044-1099	1412-1446	1498-1546	1607.1648	1805-1839	1901-1946
GENOME FOR TRROTTER PLAN POS POTYVILLE STANDER LALAND LALA		441-503	126-769	13:467	921-955	1741-1782		
CENOGE POLYMOTERN PLANK DECENTIVE STALLS IN THAT IN THE 38 40.141		384-818	1146-1197					
CENOME POLYMOTERN PLAN FOR SOUTH (STRAN PLANTER) 113-31 135-319 130-319		403-433	20 S	77.76	22	20-924	740-1781	
CENOGE POLYMOTEN		403-433	640-502	727.768	914-666	20-026	1340-1381	ļ
GENOME POLYMOTERN VAAA'A BANGSOV VIRIS (STALM PODI) 131-319 131-319 131-319 GENOME POLYMOTERN PAAA'A BANGSOV VIRIS (STALM PODI) 131-319 13		134-468						
GENOME POLYROTEIN PAYA'A BAKENOT VALUE (STAAN POP) 133-315 135-319 GENOME POLYROTEIN PAYA'A BAKENOT VALUE (STAAN POP) 131-319 135-319 135-319 GENOME POLYROTEIN POTATO VALUE (STAAN IN-CALLAN) (17-10) 137-319 131-319 GENOME POLYROTEIN POTATO VALUE (STAAN IN-CALLAN) 127-319 111-319 GENOME POLYROTEIN POTATO VALUE (STAAN IN-CALLAN) 127-319 11-329 GENOME POLYROTEIN POTATO VALUE (STAAN IN-CALLAN) 11-329 11-329 GENOME POLYROTEIN POTATO VALUE (STAAN IN-CALLAN) 11-329 11-329 GENOME POLYROTEIN POTATO VALUE VERTACAL IN-CALLAN IN								
CENOGE POLYMOTEIN PEA SEED-BOODE HOLACE (STAAIN DPD) 133-131								
CENOME POLYMOTERN POTATO VRUS Y (STAAN) 111-119	(STRAIN DPD!)	_	529-5119	935-976	964-1018	1040-1177	1361-1627	1808-1860
CENOGE POLYROTEN FOTATO VIRUS Y GITAAN O 111-194 701-131 GENOGE POLYROTEN FOTATO VIRUS Y GITAAN IN ORGANIAN 140-191 701-131 GENOGE POLYROTEN FOTATO VIRUS Y GITAAN IN SEVELE) 160-196 211-134 GENOGE POLYROTEN POTATO VIRUS Y GITAAN IN SEVELE) 160-196 211-134 GENOGE POLYROTEN POTATO VIRUS Y GITAAN IN SEVELE) 160-196 211-134 GENOGE POLYROTEN PASSIONERIUW VOODDRESS YALKS GITAAN IS PRUGHTY 160-197 211-134 GENOGE POLYROTEN STASSIONERIUW VOODDRESS YALKS GITAAN IS PRUGHTY 160-197 101-107 GENOGE POLYROTEN STASSIONERIUW VOODDRESS YALKS GITAAN IS PRUGHTY 160-197 101-107 GENOGE POLYROTEN STASSIONERIUW VOODDRESS YALKS GITAAN IS PRUGHTY 160-197 101-107 GENOGE POLYROTEN STASSIONERIUW VOODDRESS YALKS GITAAN IS PRUGHTY 160-197 101-107 GENOGE POLYROTEN STASSIONERIUW STASSION IS STAAN I			2712-2746	1870-2907				
GENOME POLYROTEN POTATO VIRUS Y (STAAN HONOLALM) 114-111 701-130 GENOME POLYROTEN POTATO VIRUS Y (STAAN H) 116-118 211-130 GENOME POLYROTEN POTATO VIRUS Y (STAAN H) 116-118 211-131 GENOME POLYROTEN POTATO VIRUS Y (STAAN H) 116-118 211-131 GENOME POLYROTEN PASSIONERUIT WOODRESS YAUS (STAAN HS IN) 116-118 211-131 GENOME POLYROTEN PASSIONERUIT WOODRESS YAUS (STAAN HS IN) 116-118 211-131 GENOME POLYROTEN PASSIONERUIT WOODRESS YAUS (STAAN HS IN) 116-118 111-131 GENOME POLYROTEN SWEE VESICLAA DISSASE VAUS (STAAN HS IN) 116-118 111-131 GENOME POLYROTEN SWEE VESICLAA DISSASE VAUS (STAAN HS IN) 11-12 116-119 GENOME POLYROTEN TICK-BOANE ENCENALLITIS VAUS (STAAN HS IN) 11-13 116-119 GENOME POLYROTEN TICK-BOANE ENCENALGARTELITIS VAUS (STAAN HS IN) 116-111 116-111 GENOME POLYROTEN TICK-BOANE ENCENALGARTELITIS VAUS (STAAN HS IN) 116-111 116-111 GENOME POLYROTEN TICK-BOANE ENCENALGARTELITIS VAUS (STAAN HS IN) 116-111 116-111		701-735	103-154					
CENOME FOLYPROTEIN POTATO VILLS Y (STRAIN I) 146-184 111-141		201-335	101-163	901-949	1401-1441	1492-1526	1728-1772	1777-1818
CENOME POLYPROTEIN POTATO VIRUS Y (STRAIN O) (1979-1970 111-343 CENOME POLYPROTEIN POTATO VIRUS Y (STRAIN STREEL) 102-127 111-343 CENOME POLYPROTEIN PASSIONFRUIT WOODDRESS YULUS (STRAIN STREEL) 102-127 111-343 CENOME POLYPROTEIN PASSIONFRUIT WOODDRESS YULUS (STRAIN STREEL) 102-127 102-127 CENOME POLYPROTEIN PASSIONFRUIT WOODDRESS YULUS (STRAIN STREEL) 102-127 102-127 CENOME POLYPROTEIN ST. LOUIS ENERHALLI WOODDRESS YULUS (STRAIN STREEL) 102-127 102-127 CENOME POLYPROTEIN ST. LOUIS ENERHALLI STRUIN (STRAIN STAIN) 11-49 102-127 CENOME POLYPROTEIN TICK-BORNE ENCEPHALLINS YRUS (STRAIN STAIN) 11-49 102-127 CENOME POLYPROTEIN TICK-BORNE ENCEPHALLINS YRUS (STRAIN STA								
CENOME POLYBOTEN		211-345	701-735	102-163	1401-1441	1492-1526	1728-1772	1177-1818
CENOME POLYPROTED CENOME FOLYPROTED POSATO VALIA Y GETALNO STEVALE) 10-137								
CENOME POLYPROTEIN PASSIDNYRUITY WOODDRESS VRUIS (STRAM PRICHT) 201-217 GENOME POLYPROTEIN FASSIDNYRUITY WOODDRESS VRUIS (STRAM MSLT) 184-218 1811-117 GENOME POLYPROTEIN FASSIDNYRUITY WOODDRESS VRUIS (STRAM MSLT) 184-219 1811-117 GENOME POLYPROTEIN ST. LOUIS BECENHALITIS VRUIS (STRAM MSLT) 184-19 1811-187 GENOME POLYPROTEIN STR. LOUIS BECENHALITIS VRUIS (STRAM MSLT) 184-19 181-10 GENOME POLYPROTEIN STR. LOUIS BECENHALITIS VRUIS (STRAM MSLT) 184-19 181-10 GENOME POLYPROTEIN TICK. BORNE ENCEPHALITIS VRUIS (STRAM MSCRT) 184-19 181-10 GENOME POLYPROTEIN TICK. BORNE ENCEPHALITIS VRUIS (STRAM MSCRT) 184-13 184-13 THELERS MAINNE ENCEPHALITIS VRUIS (STRAM MSCRT) 184-13 184-13 184-13 GENOME POLYPROTEIN TREALESS MAINNE ENCEPHALONTELITIS VRUIS (STRAM GOVILINE) 184-13 184-13 GENOME POLYPROTEIN TREALESS MAINNE ENCEPHALONTELITS VRUIS (STRAM GOVILINE) 184-13 184-13 GENOME POLYPROTEIN TREALESS MAINNE ENCEPHALONTELIS VRUIS (STRAM GOVILINE) 184-13 184-13 GENOME POLYPROTEIN TREALESS		211-245	701-735	801-856				
GENOME POLYPROTERN PASSIONFRUIT WOODDRESS VALUS (STAAIN HEID) 100-131 111-117 GENOME POLYPROTERN ST. LODIY PELLOY RECK YINJS (STOAIN HEID) 104-10 611-10 GENOME POLYPROTERN ST. LODIY BELEAS YELLOY RECKTAND (STOAIN HEID) 11-49 101-10 GENOME POLYPROTERN SWING VESTIALAN SOFTH) 11-49 101-10 GENOME POLYPROTERN SWING VESTIALAN SOFTH) 11-49 101-10 GENOME POLYPROTERN TICK-BOLNE ENCEPHALITIS VRUS (STAAIN SOFTH) 106-10 211-17 GENOME POLYPROTERN TICK-BOLNE ENCEPHALITIS VRUS (STAAIN SOFTH) 106-10 211-17 GENOME POLYPROTERN TICK-BOLNE ENCEPHALITIS VRUS (STAAIN SOFTH) 106-10 211-17 GENOME POLYPROTERN TICK-BOLNE ENCEPHALITIS VRUS (STAAIN SOFTH) 106-10 211-17 GENOME POLYPROTERN TREBEESS MUDNE ENCEPHALITIS VRUS (STAAIN SOFTH) 106-10 211-17 GENOME POLYPROTERN TREBEESS MUDNE ENCEPHALITIS VRUS (STAAIN SOFTH) 106-10 211-17 GENOME POLYPROTERN TREBEESS MUDNE ENCEPHALITIS VRUS (STAAIN SOFTH) 106-10 211-11 GENOME POLYPROTERN TREBEESS MUDNE ENCEPHALITIS VRUS (STAAIN STAAIN ST								
GENOME POLYPROTEIN PARANDY VELLOW FLECK VARUS (GTAANI HELT) 184-218 111-117 GENOME POLYPROTEIN ST. LOUIS ENCETHALITIS VARUS (STRANI HELT) 164-107 104-1070 GENOME POLYPROTEIN ST. LOUIS ENCETHALITIS VARUS (STRANI HELT) 11-49 1021-1070 GENOME POLYPROTEIN TICK-BORNE ENCEPHALITIS VARUS (STRANI HELT) 11-49 1021-1070 GENOME POLYPROTEIN TICK-BORNE ENCEPHALITIS VARUS (STRANI HELT) 11-49 1021-1071 GENOME POLYPROTEIN TICK-BORNE ENCEPHALITIS VARUS (STRANI BAN) 104-1070 104-1070 GENOME POLYPROTEIN TICK-BORNE ENCEPHALOWYELITIS VARUS (STRANI BAN) 104-1011 104-101 GENOME POLYROTEIN TICK-BORNE ENCEPHALOWYELITIS VARUS (STRANI BAN) 104-101 104-101 GENOME POLYROTEIN TICK-BORNE ENCEPHALOWYELITIS VARUS (STRANI BAN) 104-101 104-101 GENOME POLYROTEIN TICK-BORNE ENCEPHALOWYELITIS VARUS (STRANI BAN) 104-101 104-101 GENOME POLYROTEIN TICK-BORNE ENCEPHALOWYELITIS VARUS (STRANI BAN) 104-101 104-101 GENOME POLYROTEIN WEST MILE YARUS (STRANI HANDS (STRANI BAN) 104-101 104-101 GENOME POLYROTEIN </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>								
GENOME POLYPROTEIN 11-401 1011-101		1111-1172	1379-1413	1838-1199	1930-1931	1101-111		
CENOME POLYPROTEIN SWING VESICULAL DISEASE VALUS (STRAIN 1077) 113-49 1024-1070		673.707	20.73	975.100	- FOR			
GENOME POLYPROTEIN TICK-BOINE ENCEPHALITIS VRUS (STRAIN URCATAT) 15-49 1034-1030		1024-1070	1779-1813	1890-1924				
CENOME POLYMOTEN TICK-BORNE ENCEPHALITIS VIRUS (PRESTERN SUBTYRE) 60-140 231-237		1024-1070	1890-1974					
GENOME POLYPROTEIN TICK-BORNE ENCEPHALITIS VRUS (WESTERN SUBTYPE) 644-599 1011-1092		21.17	53 463	138-152	101-102	1929-1966	3103-2216	3535.2590
CENOME POLYTROTEN TICK-BOANE ENCEPTALLITIS VIRUS (WESTEAN SUBTYTE) 44-140 211-212 44-122 4		1051-3092	3100-3143					
THEILER'S MAINDE ENCEMALOMYTELTIS VINUS (S TOBACCO ETCH VINUS THEILER'S MAINDE ENCEMALOMYTELTIS VINUS (STRAIN BEAN 1364-1702 1741-1713 GENOME POLYTROTEIN THEILER'S MAINDE ENCEMALOMYTELTIS VINUS (STRAIN GEN') 1364-1710 1741-1713 GENOME POLYTROTEIN THEILER'S MAINDE ENCEMALOMYTELTIS VINUS (STRAIN GEN') 1364-1710 1741-1713 GENOME POLYTROTEIN THEILER'S MAINDE ENCEMALOMYTELTIS VINUS (STRAIN GEN') 1364-1710 1741-1713 GENOME POLYTROTEIN THEILER'S MAINDE ENCEMALOMYTELTIS VINUS (STRAIN GEN') 1364-1710 1741-1713 GENOME POLYTROTEIN WATERAGEON MOSAIC VINUS 1741-1713 1741-1713 GENOME POLYTROTEIN WATERAGEON MOSAIC VINUS 1741-1713 1741-1713 GENOME POLYTROTEIN WATERAGEON MOSAIC VINUS 1741-1713 1741-1713 GENOME POLYTROTEIN WATERAGEON MOSAIC VINUS 1741-1713 1741-1713 GENOME POLYTROTEIN WATERAGEON MOSAIC VINUS 1741-1713 1741-1713 GENOME POLYTROTEIN WATERAGEON MOSAIC VINUS 1741-1713 1741-1713 GENOME POLYTROTEIN WATERAGEON MOSAIC VINUS 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN WEST PILL OW FEVER VINUS (STRAIN FASTELIN TO-BO) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN PEDATITIS E VINUS (STRAIN BARDA) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN PEDATITIS E VINUS (STRAIN BARDA) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN PEDATITIS E VINUS (STRAIN BARDA) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN REPATITIS E VINUS (STRAIN BARDA) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN REPATITIS E VINUS (STRAIN BARDA) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN REPATITIS E VINUS (STRAIN BARDA) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN REPATITIS E VINUS (STRAIN BARDA) 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN 1741-1713 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN 1741-1713 1741-1713 1741-1713 1741-1713 MONSTRUCTURAL POLYTROTEIN 1741-1713 1741-1713 1741-1713 1741-1713 1741-1713 1741-1713 1741-1713 17	_	131-171	23-463	138-114	1431-1692	1911-1966	1336-2391	1967-3001
THEIL ERST MANDRE ENCEMALOAPTELITIS VIRUS (\$ TOBACCO ETCH VIRUS TOBA		3053-3094	\$ 7.50 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1					
CENOME FOLYTROTEN THEREN'S ANDRE ENCEPHALOMYELITIS VIAUS (STRAIN BEAN) 1304-1301 1401-1316	TOBACCO ETCH VIRUS	164-22	\$40-584	770.712	120-025	1141-1192	14141460	1494-1515
GENOME POLYTROTEIN THELEN'S MALDRE ENCEPTALLOGYTELTIS VRUS (STALM DA) 1441-134 GENOME POLYTROTEIN THELEN'S MALDRE ENCEPTALLOGYTELTIS VRUS (STALM GOVI) 106-1340 1441-1344 GENOME POLYTROTEIN THELEN'S MALDRE ENCEPTALLOGYTELTIS VRUS (STALM GOVI) 106-1340 1441-1344 GENOME POLYTROTEIN THELEN'S MALDRE ENCEPTALLOGYTELTIS VRUS (STALM GOVI) 106-1340 1441-1344 GENOME POLYTROTEIN WATER-MELON MOSAIC VRUS 44-40 44-40 44-40 GENOME POLYTROTEIN WATER-MELON MOSAIC VRUS 44-40 44-40 44-40 GENOME POLYTROTEIN WATER-MELON WATER-MENON WAT		1747-1781	1797-1820	7787474	2787-7872			
CENOME POLYPROTEIN THEREA'S MURINE ENCEPTALGONTELITIS VALUS (STAAM COVI) 104-1114		7	1601-1633					
GENOME POLYPROTEIN THRILD'S MULLINE VIRUS 114-151	THEILEY'S MURINE ENCEPHALOMYELITIS VIAUS (STRAIN DA.) 1994-1911	┱	200					
CENOME POLYTROTEIN TOBACCO VERN MOTTLING VIRUS 14-46 41-46 4	THE LEAST MULLINE ENCEPTAL CONTELLIS VINUS (STRAIN GOVINISOF 1340	+	1001-1007	346.410	1441.1477			
GENOME POL YPROTEIN WATERAGLON MOSAC VIRUS 1646-1735 2016-234	ALC: SABIRE	977	38. 007		100-100	21013	2011-102	443.1677
GENOME POL YPROTEIN WATERMELON MOSALC VRUS II 64-165 702-134 GENOME POL YPROTEIN VEST MILE VRUS 74-169 702-131 GENOME POL YPROTEIN YELLOW FEVER VRUS (STRAIN PASTEIN 17D-704) 718-131 718-134 GENOME POL YPROTEIN YELLOW FEVER VRUS (STRAIN PASTEIN 17D-704) 716-131 718-133 GENOME POL YPROTEIN YELLOW FEVER VRUS (STRAIN 1994) 716-161 716-131 GENOME POL YPROTEIN YELLOW FEVER VRUS (STRAIN 1994) 716-161 716-163 NON-STRUCTURAL POL YPROTEIN YELLOW FEVER VRUS (STRAIN 1994) 716-161 1047-110 NON-STRUCTURAL POL YROTEIN YELLOW FEVER VRUS (STRAIN 1994) 716-171 104-110 NON-STRUCTURAL POL YROTEIN YELLOW FEVER VRUS (STRAIN 1994) 716-171 104-110 NON-STRUCTURAL POL YROTEIN YELLOW STRUCTURAL POL YROTEIN YELLOW STRUCTURAL POL YROTEIN 115-179 115-179 NON-STRUCTURAL POL YROTEIN HEPATITIS E VRUS (STRAIN 197A) 311-379 1115-116 NON-STRUCTURAL POL YROTEIN HEPATITIS E VRUS (STRAIN 197A) 311-379 1115-116		\top	1701-2749	201-201				
GENOME POL YPROTEIN WEST PILL OW TEVER VILUS (STIALM 17D) 19-108 703-131 GENOME POL YPROTEIN YELLOW TEVER VILUS (STIALM PASTEIN 17D-704) 411-431 711-434 GENOME POL YPROTEIN YELLOW TEVER VILUS (STIALM PASTEIN 17D-704) 411-431 711-143 GENOME POL YPROTEIN YELLOW TEVER VILUS (STIALM PASTEIN 17D-704) 71-163 711-143 GENOME POL YPROTEIN YELLOW TEVER VILUS (STIALM PASTEIN 17D-704) 71-163 71-163 NON-STRUCTUALL POL YPROTEIN YELLOW TEVER VILUS (STIALM PASTEIN 17D-704) 71-163 104-110 NON-STRUCTUALL POL YPROTEIN YELLOW TEVER VILUS (STIALM TENDAD) 71-173 119-117 NON-STRUCTUALL POL YROTEIN YED TRANS (STIALM TEADAD) 71-173 119-117 NON-STRUCTUALL POL YROTEIN YED ATTITIS E VIRUS (STIALM BEDADO) 711-779 111-179 NON-STRUCTUALL POL YROTEIN HEP ATTITIS E VIRUS (STIALM BADOO) 711-779 1119-1176 NON-STRUCTUALL POL YROTEIN HEP ATTITIS E VIRUS (STIALM BADOO) 711-779 1119-1176		т						
CENCINE POL YPROTEIN YELLOW FEVER YIRUS (STALIN 17D) 116-313 315-343 316-344		207-251	1847-881	173-100)	1413-1449	3461-3495	3535-2574	2737-2775
GENOME POL TPROTEIN TELLOW FEVER VILUS (STALIN 17D-304) 411-433 131-543 GENOME POL TPROTEIN TELLOW FEVER VILUS (STALIN 17D-304) 411-433 131-543 GENOME POL TPROTEIN TELLOW FEVER VILUS (STALIN 17D-304) 15-116 411-433 GENOME POL TPROTEIN TOLOVILUS THE VILUS (STALIN 17D-304) 15-116 411-433 GENOME POL TPROTEIN TOLOVILUS THE STALIN 17D-304 14-133 HON-STRUCTURAL POL TPROTEIN TELDRE CALLICYBAUS (STRAIN TRINIDAD) 143-312 191-313 HON-STRUCTURAL POL TPROTEIN TELDRE CALLICYBAUS (STRAIN BURALA) 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLICYBAUS (STRAIN BURALA) 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLICYBAUS (STRAIN BURALA) 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLICYBAUS (STRAIN MYANGALA) 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLICYBAUS (STRAIN MYANGALA) 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLICYBAUS (STRAIN MYANGALA) 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLIS STRAIN FAKISTAN 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLIS STRAIN FAKISTAN 131-319 HON-STRUCTURAL POL TPROTEIN TELDRE CALLIS STRUCTURAL P	6516-9400	3385-3426						
CENDAG POL YPROTEDI YELLOW FEVER VILLS (STIAM PASTELIN 17D-200) 411-451 113-143 GENDAG POL YPROTEDI POLLOWILIS TRES (STIAM 19941) 15-116 416-113 GENDAG POL YPROTEDI POLLOWILIS TRES (STIAM MARONEW) 1-11 110-514 NON-STRUCTURAL POL YPROTEDI FELDRE CALICIVARUS (STRAM TRANDED) 14-5 196-110 NON-STRUCTURAL POL YPROTEDI FELDRE CALICIVARUS (STRAM BURAL) 110-544 110-544 NON-STRUCTURAL POL YPROTEDI FELDRE CALICIVARUS (STRAM BURAL) 110-540 110-117 NON-STRUCTURAL POL YRROTEDI MEPATITIS E VIRUS (STRAM MYANGAR) 110-117 110-119 NON-STRUCTURAL POL YRROTEDI HEPATITIS E VIRUS (STRAM MYANGAR) 110-119 110-119		123-563	738-768	1388-1444	2211-2276			1097-1143
GENOME FOLLYPROTEIN YELLOW FEVER VIRUS (STAJN) 199/N1) 35-116 418-432 GENOME FOLLYPROTEIN POLLOWINE TYPE I (STAJN MANOREY) 8-43 1067-1103 MONSTRUCTURAL POLYPROTEIN FELDRE CALICYRUS (STAJN CFUS FV) 316-54 108-332 MON-STRUCTURAL POLYPROTEIN FELDRE CALICYRUS (STAJN CFUS FV) 4-45 316-54 MON-STRUCTURAL POLYROTEIN FELDRE CALICYRUS (STAJN FV) 14-5 316-110 MON-STRUCTURAL POLYROTEIN HEDATITIS E VRUS (STRAIN MANORAR) 311-379 1139-117 MON-STRUCTURAL POLYROTEIN HEPATITIS E VRUS (STRAIN MANORAR) 318-379 1139-116 MON-STRUCTURAL POLYROTEIN HEPATITIS E VRUS (STRAIN MANORAR) 318-379 1139-116	R 17D-204)	135-563	721.768	1380-1444	3711-1176	2477-2565	2916-2926	3097-3143
GENOME FOL YPROTEIN POLIDYBLIS TYPE I (STIAM MAIGHEY) 8-43 1047-1102		410-453	525-563	71.72		┪		
NONSTRUCTURAL POLYROTEIN VEMEZUELAN EQUINE ENCEPILALITIS VIRUS (STAAN TAMIDAD) 145-313 198-933 NON-STRUCTURAL POLYROTEIN FELINE CALICIVADUS (STRAIN CT/08 FV) 146-544 146-540 NON-STRUCTURAL POLYROTEIN FELINE CALICIVADUS (STRAIN ENDAM) 131-379 113-179 NON-STRUCTURAL POLYROTEIN HEPATITIS E VIRUS (STRAIN MYANGAR) 331-379 113-179 NON-STRUCTURAL POLYROTEIN HEPATITIS E VIRUS (STRAIN MYANGAR) 331-379 113-179	POLIOVIRUS TYPE I (STRAIN MAHONEY)	1047-1103	1415-1449	1501-1549	1610-1651	1000-1042	1904-1949	
NON-STRUCTURAL POLYROTED FELDÆ CALICYMBUS (STRAM GFUG FIV) 110-544 NON-STRUCTURAL POLYROTED FELDÆ CALICYMBUS 4-45 146-110 NON-STRUCTURAL POLYROTED HEDATITIS E VBUS (STRAM BURAA) 131-139 113-117 NON-STRUCTURAL POLYROTEN HEDATITIS E VBUS (STRAM MYANAKA) 131-319 113-319 113-116 NON-STRUCTURAL POLYROTEN HEDATITIS E VBUS (STRAM MYANAKA) 131-319 113-116	VENEZUELAN EQUINE ENCEPILALITIS VIRUS (STRAIN TRINIDAD)145-312	101-033	1945-1979					
NON-STRUCTURAL POLYROTER FELDRE CALICIVIRUS (STRAIN F9) 4-45 186-410 NON-STRUCTURAL POLYROTER HEPATITIS E VIRUS (STRAIN BURMA) 311-379 113-179 NON-STRUCTURAL POLYROTER HEFATITIS E VIRUS (STRAIN MYANALA) 311-379 NON-STRUCTURAL POLYROTER HEFATITIS E VIRUS (STRAIN MYANALA) 331-379 NON-STRUCTURAL POLYROTER HEFATITIS E VIRUS (STRAIN PAKISTAN) 331-379	FELDE CALICIVIAUS (STRAIN CFUSI FIV)							
NON-STRUCTURAL POLYROTEIN HEPATITIS E VIRUS (STRAIN BURLA) 111-179 NON-STRUCTURAL POLYROTEIN HEPATITIS E VIRUS (STRAIN MYANALA) 131-379 NON-STRUCTURAL POLYROTEIN HERATITIS E VIRUS (STRAIN MYANALA) 131-379 NON-STRUCTURAL POLYROTEIN HEBATITIS E VIRUS (STRAIN PAKISTAN) 131-339		369-410	946-1020	1003-1061				
NON-STRUCTURAL POLYPROTEIN HEPATITIS E VIRUS (STRAIN MEDICO) 331-339 NON-STRUCTURAL POLYPROTEIN HEBATITIS E VIRUS (STRAIN MYANALA) 331-339 NON-STRUCTURAL POLYPROTEIN HEBATITIS E VIRUS (STRAIN PAKISTAN) 331-339		1139-1177						
NON-STRUCTURAL POLYBOTEIN HEPATITIS E VIRUS (STRAIN MYANALA) 138-379 NON-STRUCTURAL POLYBOTEIN HEPATITIS E VIRUS (STRAIN PAKISTAN) 1315-331								
NON-STRUCTURAL POLYPROTEIN HEPATITIS E VIRUS (STRAIN PAKISTAN) 137-373		1139-1164						
	STRAIN PAKISTAM	1138-6176						
NONSTRUCTURAL POLYTROTEIN MIDDELBURG VIRUS	MIDDEL BURG VIRUS							

				ĺ		ABTA	, Y	2		
PCCENE	ALLMOTIS		Ī	1	7010			Γ		
TILEMANE	PROTEIN	NO-NYONG VIRUS (STIVAIN GULU)	1	•	707	1467.1314				
PPOLN INDV	NONSTRUCTURAL POLYPROTEIN		186-234	304-347	409-457	100				
POLN RAVA	NON-STRUCTURAL POLYPROTEIN		626-568	1928-1962	2414-2467					
POLY REVT	NONSTRUCTURAL POLYPROTEIN			1043-1136						
POLN RUBYT	NONSTRUCTURAL POLYPROTEIN	8	1506-1540	1551-1585	1730-1767	0481-2081				
PPOLN SPV	HONSTRUCTURAL POLYTROTEIN	Ē	1094-1128	2358-2393						
PPOLY SDADO	NONSTRUCTURAL POLYPROTEIN	E OCKET BO / STRADY EDSBYN 82-5)	116-616	1491-1525	1961-1996	3444-3476				l
ADOS N TOMA	NONSTRUCTURAL POLYPROTEIN		=	1959-1994	2443-2476					
VACE R PACV	NONSTRUCTURAL POLYPROTEIN	130	199-933	1137-1161						1
PROFE EPPV	RNA REPLICASE POLYPROTEIN		Γ	914-951						1
500	CTRI SCHIRAL POLYPROTEDY	EASTERN EQUINE ENCEPHALITIS VINUS	137.407	015.052						
	CHAINCTING AT BOX VOROTEIN	7	950				L	L		
POLS EEVY	SIROCIONE CENTRAL	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STIADN TC-11)	2071-017						L	
POLS EEWT	STRUCTURAL POLITICAL	죍	1216-1230							L
Procs BDV5	STRUCTURAL POLICEMENT	AVIAN INTECTIOUS BURSAL DISEASE VIRUS (STRAIM 12/10)	136-168	231-780		-				L
PPOLS IBDVA	STRUCTURAL POLYFROILIN	3	134-168	27:78	470-323					
PPOLS IBDVC	STRUCTURAL POLYTROTEIN	AND THE CTIONS BURSAL DISEASE VINUS (STRAIN CU-1)	134-161	2 26	470-323					L
PPOLS BIDVE	STRUCTURAL POLYPROTEIN	Γ		231-316	304-340					ļ
PPOLS IBDVP	HONSTRUCTURAL PROTEIN VP4	G-98)	115.149	192-212	451-504					1
PPOLS IBDVS	STRUCTURAL POLYPROTEIN	Τ	134-168	249-283	470-523					\downarrow
PPOLS DWV	STRUCTURAL POLYPROTEIN	EE	69-103	23.715						4
NAME & POST	STRUCTURAL POLYPROTEIN		716-786							4
CANANO S SOS	STRICTURAL POLYPROTEIN	(3) (3) (3) (3)	1121-121							4
5	STRUCTURAL POLYPROTEIN	OC.0)	97.1							4
200	STEEL THE POLYPROTEIN		107 074	018.071						
POCS PAYE	Manual Por Volume	92)	100-401					_		
POLS KKY	STANCE OF VENTER	AOSS MVER VIRUS (STRAIN T40)	674-466							
PIOLS MUSVIN	STANCTION OF VERNING	RUBELLA VIRUS (VACCINE STRAIN HPV77)	201-60							Ц
PPOLS RUBYR	STRUCTURE AT BOX VPROTEIN	RUBELLA VIRUS (VACCINE STRAIN RAZIO)	979-1030							
TOTAL POPULATION	CONTRACTOR ALL BOX VPROTEON	RUBELLA VIRUS (STRAIN THERIEN)	200					L		_
THOSE STORES	CTRICTIONAL POLYPROTEIN	SINDBIS VIXUS (SUBTYPE OCKELBO / STRAIN EDSBTN 12-3)	20, 20,			-	-			Ц
	GINE L'THE AT POLYPROTEIN	SINDBLS VIRUS (STILAINS HASP AND HALP)	2					-		
אמונים אינוים	CTS INTIMAL POLYPROTEDY	SINDBIS VIRUS (WILD TYPE SB DERIVED FROM STRAIN ACLT)				-		_		
2	PROJECTITE AT BOLIVEROTEDA	WESTERN EQUINE ENCEPHALITIS VIRUS		15.55	304.913	1001-1042			L	
HOT BY	ANI VEROTER	BABOON ENDOGENOUS VIRUS (STRAIN M7)					-	-		Ц
THE PERSON	BOL BOL VAROTED	BOVING LEUKEMA VIKUS (AUSTRALIAN ISOLATE)	1			-			_	L
10.01	SOLVED TEN	BOVING LEUKENDA VIDUS (IAPANESE ISOLATE BLV-1)	200		-	-			L	_
POL CAEVC	TOUR TOUR WHO TEN	CAPRING ARTHURTIS ENCEPHALITIS VIRUS (STRADI CORK)	117-714		1	-	-	-		L
	THE POST OF STREET	CALLELOWER MOSAIC VIRUS (STRAIN DAI)	117-11		777 408	10.074	194.930	1310-1351		L
Prof. Corp.	ENGINEER ON VIEW	COMPRELINA YELLOW MOTTLE VIRUS	171.7							L
PPOL ELAVO	TOTALIVE PARTIES	EQUINE INFECTIOUS ANEWIA VIRUS (CLONE 1349)	30.360	ecal Property	\downarrow	-	\mid			-
PPOL EIAVC	POLINGIEM	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL22)	\$13-366	201-103				1		L
PPOL ELAVY	POLITICAL EIN	ECKING DIRECTIOUS ANEXAN VIRUS (ISOLATE WYOMAING)	\$12.565	1021-103			-	-		╀
POL FEWI	POL POLYPROTEIN	FFI INE ENDOGENOUS VIRUS ECE!	533-600	63,639	6 ×			1		╀
PPOL FIVE	POL POLYPROTEIN	TET THE DAMINODEFICIENCY VIRUS (ISOLATE PETALUMA)	429-473	<u>§</u>		-		-	\downarrow	╀
PPOL FIVSD	POL POLYPROTEIN	FEI INE DAAUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	428-473	2 2 2 3 3			$\left \right $	+		╀
PPOL, FTVT3	POL POLYPROTEIN	FET THE THAT HADDEFICIENCY VIRUS (ISOLATE THAT)	428-472	395-662		4				ļ
PPOL_FIAVD	POL POLYPROTEIN	ELEGINOS T. MOSAIC VIRUS (STRAIN DXS)	403-437					-	\downarrow	+
PPOL FOAMV	ENZYMATIC POLYPROTEIN	INDIAN CHIMARETROVING (FORMY VIRUS)	140-174	217-256	215-326		$\frac{1}{1}$	$\frac{1}{4}$	+	\downarrow
PPOL GALV	POL POLYPROTEIN	TORANA ABERENTA VIEW	528-562	673-740				$\frac{1}{1}$		+
PPOL HTLIA	POL POLYPROTEIN	CERTAIN A CELEBRATA VINIT TYPE I (STRAIN ATK)	111-019	L						\downarrow
PPOL HTLIC	POL POLYPROTEIN	HUBAN I LELL LEUKENA VINIS 1175 I (CARDARAN ISOLATE	E 670-711		_					4
PPOL HVIA	POL POLYPROTEIN	RUMAN 1-CELL LEGISSION VINUS I I I C. (COLLEGIS I SOLA)	E 501-537	130 kg					1	4
POL HVIBI	POL POLYPROTEIN	HUMAN DOMINIONE TAKES THE CONTROL AND SELECTIVE (SELECTIVE)	513-549	619-676	-	Ļ	_	_	_	

WO 96/19495 PCT/US95/16733

071000	1.0 a. a. a. a. a. a. a. a. a. a. a. a. a.	All Wanted fan herindanhamat				_				
PTI P NAME	PROTEIN		AREAL	AREAL	AREAJ	AREA 4	AREA S	AREAS	AREA!	AREAI
POL HVIBE	POL POLYPROTEIN	N INDALMODEFICIENCY VILUS TYPE I (BHS ISOLATE)	\$13.549	91979				Г		
POL HVIEL	POL POLYPROTEDY	ITAKAN DOMINODEFICIENCY VIRUS TYPE I (BRU ISOLATE)	513.54	618-676						
POL HVIID	POL POLYPROTEIN	Г	300-536	626-663						
POL HVIR	POL POLYPROTEIN		501-537	101-664						
POL HVIMA	POL POLYPROTED	0	505-541	99-019						
POL HVING	POL POLYPROTEIN	٦	476-536	\$						
PPOL HIVINS	POL POLYPROTEIN		T	199-609						
POL HVIND	POL POLYPROTEIN	링	Т	30.20						
POL HVIOY	POL POLYPROTEIN		T	100						
PPOL HVIPV	POL POLYPROTEIN	HUMAN DANIUNGLE HELENCY VIAUS 177E I (UTI ISULATE)	10.10	100-004						
PPOL HVIEW	FOL POLITICION	ĺ	717-05	100 AK1						
TOTAL PARTY	NA. POLITACIEN	74	Τ	197 199						
THE BALL	TOL FOLLOWING		Τ							
True nythe	TOTAL CONTINUE OF THE PARTY OF		Τ	107.707	451.407	13.831				
PROF HOUSE	POL POL VPROTEIN	Ţ	ļ	Г	632-466					
TOO BY	TOUR DOLL VAN OTEGE	Т	907-400	Τ						
PECE LOCACI	NO. POLYPROTEIN	T	3848	116.524	138.177	633-687				
PPOL HYZNZ	POL POLYPROTEIN	15	464.562	633-667						
PPOL HYZRO	POL POLYPROTEIN		44.78	356-380	464-529	19967				
PPOL HYSSB	POL POLYPROTEIN	Г	157-391	Г	634-468					
PPOL HV2ST	POL POLYPROTEIN	13	Γ	Γ	633-467					
POL DIA	POL POLYPROTEIN		484-518	512-577	653-487					
PPOL JSRV	PUTATIVE POL POLYPROTEIN	HAMSTER INTRACISTERMAL A-PARTICLE	462-503							
POL MLVAK	POL POLYPROTEIN	TOSIS VIRUS	190-231							
POL MALVAV	POL POLYPROTEIN		185-197							
POL MENTS	POL POLYPROTEIN		677-764							
POL MEVEF	POL POLYPROTEIN		612.749							
POL MANTP	POL POLYPROTEIN		642.749	7						
POL M. WAO	POL POLYTROTEIN	MEND MONTE LEUNENIA VIAUS (ISULATE LAC-111)								
HOL MINED	FOL FOL THIOTEIN									
200	NOT DOLVED TEN	ISTRAIN KAMAM	43.130	T						
PIOL ONIVIS	POL POLYPROTEIN	Ī	Ī	316.613						
PPOL RSVP	POL POLYPROTEIN		470-505	133-910						
PPOL_RTBV	POL POLYPROTEIN	(GUE C)	,					П		
PPOL RTBVP	POLYPROTEIN			29.96	101-135	76-236	Т	7	1003-1039	1405-1439
Prof. SFVI	POLYTROTEIN	ALCE TUNGAU BACILLIPONM VIRUS (ISOLATE MICLIPPINES)	100.000	8	101-135	1,42,36	23:30	200	1003-1039	1403-1439
PPOL SIVAL	POL POLYPROTEIN	SIRAINLKII	Τ	Τ	530					
PPOL SIVA2	POL POLYPROTEIN	I SOLATE)	Γ	L	111-111	938-979				
PPOL SIVAG	POL POLYPROTEIN	0	45.24							
POL_SIVAL	POL POLYPROTED ^N	SINGYN IPIDYINODE KCIENCA AIKOS (YCM) ISOCYLE)		П						
PPOL SIVAT	POL POLYPROTEIN	LONE GR			641-700	942-983	1020-1054			
PPOL_SIVCZ	POL POLYPROTEIN			187-781						
PPOL_SIVGD	POL POLYPROTEIN	(=	П	П					
PPOL_SIVAI	POL POLYPROTEIN			П	629-673	703-627	912.946			
PPOL, SIVACK	POL POLYPROTEIN	ATE)	П	819-059						
PPOL, SIVS4	POL POLYPROTEIN			119-159			·			
HOT SINS	POL POLYPROTED	6		617-651						
POL SOCIA	POL POLYTROTEIN	BI/BC(1) ISOLATE)	1	620-654						
PPOL SRVI	ENZYMATIC POLYPROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	247-795	34.6	1					

PPOL VEVI PPOL VEVI PPOL VEVI										_
OL VILVI	ZI-LC-		20.64	23.413		L				
AC VEVI	SOUTH THE PARTY OF			174.036						
FOL VELVI	POLITICAL CONTRACTOR C	41514)	485-324	22.010						L
POL VILVA	POL POLYTRUIE	CLONE LVI-IKSI)	419-524	174-979						
AVACH FINE	POL POLYPROTEIN	VICEN I ENTIVERIS (STRAIN 1514/ CLONE LVI-1KS1)	489-524	24.93						
		CONTRACTAL OVERITY (STRAIN AD169)	21-51	167-221						L
PPRTJ MOSTIVE	LARGE STRUCTURAL PHOSPHOPROTEIN PP 150	CONTRACTOR TO THE CONTRACTOR CITED (STRAIN DRG)	182-200							
PRETS MONTIVE	PROTEDI PR.73	MUUSE MARKET TOTAL TOTAL TOTAL TOTAL	20.78							
PRATI LOCTIVO	PROTEIN PA 73	MOUSE MANDANT TOMON VINCO (STORY OF STATE OF STA	\$. 5	143-201						1
PPR TI NOCTVO	PROTEIN PR73	MOUSE MANDAMY TOMON VINOS (STROME)	145-204	130-311						1
DATE LOCKYO	PROTEIN PRID	MOUSE MANDIARY TUMOR VIKUS (S. I.A.M. C.P.)	141.700	266-307						
	PROTEIN PR.13	MOUSE MANORARY TUMOR VIRUS (STRAIN OR)								
	NO VARIOUS PRECISEOR	BOMBYX MORU CYTOPLASMIC POLYNEDROSIS VIRUS								
PYNE KVAC	TOT INCOME.	AUTOGRAPHA CALIFORNICA PUCLEAR POLYHEDROSIS VIRUS	7							L
PPYIND NEVAS	KALTHEDIAN	AGROTIS SEGETUM NUCLEAR POLYNEDROSIS VIRUS	272							L
PYID NIVBM	POLYNEDIUM	ROMBYX MORI NUCLEAR POLYNEDROSIS VIRUS	13:54							L
PPYND NPVBS	POLYNEDRIN	ANTIMA SUPPRESSARIA MUCLEAR POLYHEDROSIS VIRUS								ļ
PYND MAYLD	POLYMEDRIN	SALANTHIA DISPAR MIN TICAPSID NUCLEAR POLYHEDROSIS V	14-48							\downarrow
PAYED MAYOR	POLYMEDRIN	CONTRACTOR MARCHES POLYMEDROSIS VIRUS	14-46							1
PPYIND INPVOP	POLYNEDRON	CACCAL PERIMOTERICATA AND TICAPSID POLYNEDROSIS VIRUS 13-47	17-11							ļ
PYND MIVOS	POLYHEDRIN	CACITA TECHNOLOGY CANCER CAPED MICI EAR POLYNED	17.							1
PYIND NOVIE	POLYNEDADY	ORGITA PSEUDOI SUCALA SILVELLA CICA PRID POL YHEDROSIS			L					1
PRYNCE NOVSE	POLYHEDRIN	PANOLIS FLANCAEA MULITURE NUCLEUCA SID FUCHIESTES	14.48							4
TOWN CONTRACT	WESTERN.	SPODOPTERA EXIGUA NUCLEAR FOLTHELIRUSIS VINUS (SINCE					L			
SAME OF SAME	With Vienna	SPODOPTERA FRUGIPERDA NUCLEAR POLTHEDAUSIS VIRUS			-					
10000	NACOBINA COL	SPODOPTERA LITTORALIS NUCLEAR POLTREDADSIS VIAUS					_	L		
TIASK MOVE	THE AMERICAN PROTEIN 21	KIRSTEN MUTUNE SARCOMA VIRUS					-		_	L
PREV BIVE	Marcal	BOVINE DOLUNODEFICIENCY VIRUS (ISOLATE 127)								L
THE V ELAT	March and March	EQUINE DIFECTIOUS ANEMIA VIRUS (CLONE 1169)	40-16	1	\downarrow					Ļ.,
MEV ELAVO	PEC PROTEIN	EQUINE INFECTIOUS ANEARA VIRUS (CLONE CL22)								L
	20100	EQUINE INFECTIOUS ANEADA VIRUS (ISOLATE WTONING)								
MEV HVIIS	BEV PROTED	HUMAN INDAMPODEFICIENCY VIRUS TYPE I (CLONE 12)		1			-	_		Ц
ביי ביי ביי ביי ביי ביי ביי ביי ביי ביי	PEN PROTEIN	HUMAN INDAMMODEFICIENCY VIRUS TYPE I (AXV 237 I SULATE						-		
PREV HVIBI	ACT TROUBLE	HUMAN INDAMINODEFICIENCY VIRUS TYPE I (BIIIO ISOLATE)	20.00			+				L
PREV HVIBS	The Thousand	HUMAN DEMONDEFICIENCY VIRUS TYPE I (BHS ISOLATE)	25-32		1					L
PREV HVIBN	MEN TROITER	HUMAN DOMINODEFICIENCY VIRUS TYPE I (BRAIN ISOCATE)	55.22		\downarrow		\downarrow			L
PREV HVIBA	MEV PROTEIN	INDIAN INDIANDEFICIENCY VIRUS TYPE I (BRU ISOLATE)	15-69				-	-		-
PREV HVIEL	REV PROJECT	HABLAN DAMPHODEFICIENCY VIRUS TYPE I (ELI ISOLATE)	33-64				1			-
PREV HVIND	REV PROTEIN	HIDALAN DOALMODEFICIENCY VIRUS TYPE I (HXD2 ISOLATE)	÷				1			Ļ
PREV HVID	REV PROTEIN	HUMAN BOALMODEFICIENCY VIRUS TYPE I (THI ISOLATE)	19-61		$\frac{1}{4}$		$\frac{1}{4}$			╀
PREV HVIR	AEV PROTEIN	HIMAN BARBADDEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	31-64						1	+
PREV HVIMA	REV PROTEIN	MANAN BARRACOEFICIENCY VIRUS TYPE I (NAL ISOCATE)	31-44			4			\downarrow	1
PREV HVINO	AEV PROTEIN	MANAN ILAGANODEFICIENCY VIRUS TYPE I (ACM ISOLATE)	35							\downarrow
PREV HVIOY	AEV PROTEDY	INTERNATIONAL PROPERTY OF THE I (OVI ISOLATE)	12-69			4			\downarrow	╀
PREV HVIPV	REV PROTEDY	HARIAN ISARINODEFICIENCY VIRUS TYPE I (PV22 ISOLATE) AN	35-69				\downarrow		1	+
PREV HVIST	REV PROTEIN	HAMAN BERRINODEFICIENCY VIRUS TYPE I (SF1) ISOLATE)	15-69					+		╀
PREV HVISC	REV PROTEIN	MINAAN INDANNODEFICIENCY VIRUS TYPE I (SC ISOLATE)	33-49			1	-	1	\downarrow	+
PREV SIVAI	REV PROTEDY	CHANAN BARANDEFICIENCY VIRUS (ACMISS ISOLATE)	26-77			4	\downarrow			\downarrow
PREV SIVAG	AEV PROTEIN	SEMAN BARRINGDEFICIENCY VIRUS (AGAI) ISOLATE)	26-77			-	4	-		+
PREV SIVAL	REV PROTEIN	SPAIN BRANDDEFICIENCY VIRUS (ISOLATE AGM / CLONE GR					1			╀
PREV SIVAT	REV PROTEIN	SIMIAN PARTIMODEFICIENCY VIRUS (TYO-1 ISOLATE)	18.75					+		\downarrow
PREV SIVCZ	AEV PROTEIN	CULL O ANZEE DANIMODEFICIENCY VIRUS	13-61						1	1
PREV VILV	AEV PROTEDI	COCKA I ENTINABLIS (STRAIN 1514)	21-62							\downarrow
PRIDE ASPAD	AEV PROTEIN	AB AFRICAN SWINE FEVER VIBUS (ISOLATE MALAW) LIL 201)	7	16.133	635-483			1	1	+
PARI EDV	AMONDICI EOSIDE DIPHOSPHATE NEDUCIASE	A PROTECT DATE COMMENTED AND SOCIAL	113.247	649-723						4

W 96/19495 PCT/US95/16733

		All Victoria betrackers								
PCGENE.	ALCHOILS	YRUS	AREAJ	AREA.	AREA?	AREA	2.42.6	AREAS	ABEA1	AREAS
THE CASE	PROPERTY ENGINE SIGNATURE SEDIETASE LAR	IAN CYTONEGALOVIRUS (STRAIN ADISS)	633-568							
AST LICYER			26-110							
ACT IN THE PERSON OF THE PERSO		HEBSECHBUS CANCIDE STRAIN III	124-365							
2000 AND 1818			367-402							
TALK VALLE	PROMICE COSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	167-402							
CALL CALL	AMOUNT FORDS DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	367-402							
PRIES FRV	REPONDET FOSTOR DEPHOSPHATE REDUCTASE LAR	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	123-257							
PALTAZ HISVIDS	ADDRUCT EOSIDE DUHOSPHATE REDUCTASE SKA	EPSTEIN-BARR VIRUS (STRAÍN 895-8)	161.00							
PRITE. HSVEB	REDONUCLE COSIDE DIPHOSPHATE REDUCTASE SNA	BOVINE HERPESVIRUS TYPE I (STRAIN 34)	101-135							
PEUR. HSVSA	RIBONUCLEDSIDE-DIPHOSPHATE REDUCTASE SMA		106-140							
PLIN SFVKA	AURONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMA		651-561							
PRIN VACCE	REDOMUCLEOSIDE-DIPHOSPHATE REDUCTASE SMA	SHOPE FIBROMA VIRUS (STRAIN KASZA)	91-13							
PILILY VACCP	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SALA	VACCINIA VIRUS (STRAIN COPENHAGEN)	261.06							
VEUR. VACCV	ILBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SAIA	VACCINIA VIRUS (STRAIN L-1VP)	26-132							
PRIRZ VARV	NBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMA	VACCINIA VIRUS (STRAIN WR)	2(1.10							
PRE I HSV2H	RUBONUCLEOSIDE. DIPHOSPHATE REDUCTASE SNA		11:15							
Part VACEV	NEUROVIRULENCE FACTOR	HERPES SIMPLEX VIRUS (TYPE 2/STRAIN HGS2)	111-313							
PRIMA VARV	RNA-POLYMERASE-ASSOCIATED TRANSCRIPTION S	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN	116-150	465.500	757.791					
MUOI VACCC	RNA-POLYNGRASE-ASSOCIATED TRANSCRIPTION	VANOLA VIRUS	41-75	91-120	465-540	757.791				
PRPOI VACCV	DNA-DIRECTED RNA POLYMERASE 147 KD POLYTE	VACCINIA VIRUS (STRAIN COPEMIAGEN)	143-291	622-656	754-791	954-988	1004-1057			
PEPOI VARV	DNA-DIRECTED RNA POLYMERASE 147 KD POLYPE	VACCINIA VIRUS (STRAIN WR)	162-672	959-229	154.791	934-988	1024-1058			
PRIOS CAPVK	DNA-DDRECTED RNA POLYMERASE 147 KD POLYPE	VALUOLA VIRUS	162-101	959-229	154-791	954-988	1006-1057			
PAPO2 COMPX	DNA-DIRECTED RNA POLYMERASE 133 KD POLYPE	CAPRIPOXYIRUS (STRAIN KS-1)	99-61	114-155	389-630					
PUOL VACCV	DNA-DELECTED RNA POLYNGRASE 133 KD POLYPE	COWPOX VIRUS	311-348	359-400	833-874					
PRIJO2 VARV	DNA-DDLECTED RNA POLYNGRASE 131 KD POLYPE	VACCOMA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN)	311-345	000-650	113-034					
PRIVON VACCC	DNA-DIBECTED RNA POLYMERASE 111 KD POLYPE	VARIOLA VIRUS	211-245	159-400	133-674					
PRIOR VACCV	DHA-DOLECTED RNA POLYMERASE 35 KD POLYPEP	VACCINIA VIRUS (STRAIN COPENHAGEN)	62-116							
PRIPOR VARV	DNA-DIRECTED RNA POLYMERASE 15 KD POLYPEP	VACCINIA VIRUS (STRAIN WR)	62-116							
PRPOS VACCC	DNA-DUECTED RNA POLYMERASE 15 KD POLYPEP	VARIOLA VIRUS	97-116							
PRINOS VACCV	DNA-DIRECTED RNA POLYNGRASE 30 KD POLYFE	VACCIMIA VIRUS (STRAIN COPENHAGEN)	=							
PRPOS VARV	DNA-DIRECTED RNA POLYACIASE 30 KD POLYPEP	VACCINIA VIRUS (STRAIN WR)	-							
PIPOS VACCV	DNA DOLECTED KNA POLYNGASSE 10 KD POLYPEY	VACUAL VIEW STREET, AND STREET	07.10							
PRPOS VARV	DNA-DRECTED INA POLTAGASSE 11 AU POLTAGE	VALUE A VIETE	87.50							
PREOF VARV	DNA-DIRECTED BNA POLYMERASE 19 KD POLYPEP	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN)	43-93							
PRPOR LELY	DNA-DIRECTED NAA POLYMEKASE 19 KD POLYPEP	VARIOLA VIRUS	43.63							
PRIPOL EAV	RNA-DIRECTED BNA POLYNGRASE	LELYSTAD VIAUS	1833-1867	1721-1758	1958-1992	2109-2157				
PRUPI LANN	RNA-DIRECTED RNA POLYMERASE	EQUINE ARTENTIS VIRUS	1003-1117	1477-1518	1633-1673					
PRUPI LABEL	ANA-DIRECTED RNA POLYMERASE SUBUNIT PI	INTLUENZA A VIRUS (STRAIN AVANN ARBONOVO)	171-342	279-313						
MUDAY (AXIV	ANA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN ABELINGA) 1736)	2		130-391					
PRRPI JAGUZ	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN ADUNEDINAM)	2							
PRUPI INTO	ANA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN AGULLAKARYLAND/NOG/7)	20.5	279.2					T	
PRUPI LAHTE	ANA-DOLECTED HAN POLYMERASE SUBURIL P.	DATUERS A VICE (STRAIN ACQUINCTURISMENT)	200							
PILLPI LAKEE	THA DUCCTED HAS FOLDERANG SUBJECT 11	INFINITED A VIEW (STRAIN ARIEVISOR)	171.201	1						
PRESENT LANCE	INA DIRECTED BNA POLYMERASE SUBUNIT PI	DIFLUENZA A VIRUS (STRAIN AKOREAM2668)	171-242	279-313						
141 53	THA DIRECTED BNA POLYNGRASE SUBUNIT PI	1457)	131.303	138-313						
am in	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	DOLUEYZA A YIRUS (STRAIN AALENINGRADVI)4417/57)	131-343	179-313						
MAN INTH	RIVA-DIRECTED RNA POLYNGRASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN AALENINGRADVI)444757)	131-343	179-313						
PRUPI IAMES	RNA-DIRECTED RNA POLYMERASE SUBURIT PI	INFLUENCA A VIRUS (STRAIN AMALLANDINEW YORKS13071)	131-343	376-313						
PRUPI_IANT6	RNA-DIRECTED RNA POLYMENASE SUBUNIT PI	SAM1)	2	11.313						
PARPI INPUE	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	INTLUENZA A VIRUS (STRAIN ANTAGGA)	2	116-613]

	NOTES	All Viruses (no bacteriophages)	AREAL	AREAL	ABEAl	AREA	AREAS	ABLA	444	4
PCCLAC.		VIBUS	14-242	279-313						
400 V			171-242	179-313						
PRED TATION		OTAMINAO	171-242	179-313						
14/17		Г	171-242	279-313						
Part tanes			160-242	279-313						
1000	BMA.DRECTED RNA POLYNGRASE SUBUNIT PI		165.242	179-313						
200		Ī	187-242	179-313						
	BWA. DIRECTED BWA POLYMENASE SUBUNIT PI		131.343	178-313						
PROF. IACUT	SAA BORECTED BAA POLYMERASE SUBURIT PI	T	97.61	236-313						
MUNI INCII	ANY PRECITED BUY BOLYMERASE SUBIDITY PI	11.000								
PRUPI INSTAC	MA-DIRECTED POST OF STATE AND A CE CHILDRIT PI	Т	47.00							
PLUS DEAD	MA DIRECTED ANA POLITICANA SUSTAINED	WILD-TIPE	208-249				-			
PILLE DIBLE	ANA DOLECTED RINA POLTMERASE SUBUMITY		208-249							L
PELD DICH	RNA-DIRECTED RNA POLYNGRASE SUBURIT PI		150-384	648-686	707.752					
PREP! LANN	RNA-DIRECTED INA POLYNGRASE SUBURIT PI	ARDOR/660)	110-144	177-216				1		
PERFY IADAD	RNA-DIRECTED RNA POLYMERASE SUBUNIT P3	Variab)	110-144	177-218						ļ
1450	RNA-DIRECTED ANA POLYMERASE SUBUNIT PI	INFLIENZA A VIRUS (31 KAIN ADDUCATIONIONIO VIETA ACITE	110-144	177-218						1
	THE THE PART POLYMENASE SUBURIT PE		110.144	177.218						
אומיין האומין	THE STREET WAS POLYNORASE SUBUNIT P.	INFLUENZA A VIRUS (STRAIN AGULL/MARTLAMILAMI)		31.516		-				
MAN INGO	KNA-DUCC IED NICK FOR SER CEREBAT PA					-	-	_	L	
PREST LAYER	RNA-DBECTED ANA TOL INCANA CO CITAL DATE PO		10.14			-	-			
PILLY LAKOR	NA-DIRECTED RAY POLITICASS SUSCESSION		10.144							L
PRUP INLEI	RNA-DIRECTED RNA POLTMERASE SUBJECT FE		110-144	177:218		1				L
PIUM INED	RNA-DOLECTED RNA POLYMERASE SUBUNIT P.	_	110-144	177-218		1	1	-		L
PREPT LAMAN	RNA DIRECTED RNA POLYNGRASE SUBUNIT PA	(37.027.8)	110-144	177-210				1		ļ
MAN IANTE	INA-DIRECTED RNA POLYMEDASII SUBUNIT PT	•	110-144	117.218						1
May 14 Bin	BWA.DIRECTED RNA POLYMERASE SUBUNIT P?	Ī	110-144	177.216	L					1
TANK TANK	RNA DOBECTED RNA POLYMERASE SUBUNIT P2		101144	177-218						1
2004	NA AMPRITED BNA POLYAGBASE SUBUNIT PS			177-2118						1
	ANA THE ETTED BNA POLYMERASE SUBUNIT PT	DAPLUENZA A VIRUS (STRAIN ARGUDT 10 MS1 CALL		177.210						1
1	NAME OF BELLIA SHA POLYMERASE SUBURIT PI	DIFLUENZA A VIRUS (31 FAIR ANSIMOACARDINA)		177-218						1
F 100 100 100 100 100 100 100 100 100 10	BAYA, DIRECTED BAYA POLYAGRASE SUBUNIT PT	,	100	13.21						1
	BAY DIRECTED BAY POLYACEASE SUBUNIT PT		11014	117.711						\downarrow
MUZ IAWIL	SALL PROFESSION POR VACIBASE SUBURIT P2	T		11.2						
PREMI INCHE	MAN DUCKER BAN POLYMORASE SUBUNGT P1	INTLUENZA A VIRUS (STRAIN ASWINGAIONG KONCOSI778			-					
MAZYI WZMI	MANOUS SUBLINE SAN PAR VAGENCE SUBLINGT PS	INFLUENZA A VIRUS (STRAIN A/SWINE/HONG KONOVIENTA)								
MAN WZII	MACOURT IN THE WAR SUBURIT PE	DOTLUENZA A VIRUS (STRAIN A/SWINE/IOWA/1970	1			-				
PRETT INZTR	MAN-DEEC IED MAN TON COME A SE STRINGT PE	INFLUENZA A VIRUS (STIJAIN A/SWINE/TENNESSEE/24/77)	1			-	-	_		
PRUPY D'BAC	NA-DOLECTED KNA POLI PERASE SUBINIT PO	INSTITEMEN BYTHUS (STEAM BYANN ARBONING COLD ADAPTE	=	349-380		+	-		-	_
PRUT DIBAD	ANA-DUECTED RNA POLYMENAN SUBURITY	THE LIENZA B VINUS (STRAIN BAIN ARBONING [WILD-TYPED 111-196	<u>\$</u>	26.38		1	-	-		L
אונונים בעונע	NNA-DDECTED INA POLTMEAASB SOSCIED	INFI HENZA B VIRUS (STRAIN BISINGAPORE/11779)	247-11	749-311				-		L
PREST LAND	INA-DOSCIED BNA POLYMENASE SUSCIENTED	INTI LENZA A VIRUS (STRAIN AVANN ARBORNES)	3	363-402	10.00		306 300	-	-	L
PILLY INDUD	INVA-DIRECTED RNA POLYMERASE SUBURILLY	INTER TENTA A VIRUS (STRAIN ABUDGERIGARATION KAIDON (7)	7	163.462	433-514				1	ļ
PRAPY IACHT	ANA-DIRECTED ANA POLYMENASE SUBURILLY	TATE I TENTA A VIBING (STRAIN ACHILE 1/17)	? 71	363-403	4354	207-735	+	-	-	ļ
PRUP) LAFFR	ANA-DIRECTED RNA POL YAERASE SUBURILLY	THE LEGIS A VIRIS (STRAIN AFOWL PLACUE VIRUS ROSTOCK	173	363-402	473-514	207-133			-	ļ
PRINT INTW	RNA-DIRECTED RNA POLYMERASE SUBURIT P.	THE STATE OF THE PARTY AFOUR PLAGUE VIAUSAWEYBRID	7710	363-402	473-314	107.735			-	1
MAN IAGIN	ANA-DETECTED BNA POLYMERASE SUBLIMIT P.	INTUENCY A VINCE (THE CALL ACTION AND COOK)	173	363-402	473-514	707.755				1
ALD I TAGE	INA DOLECTED RNA POLYMENASE SUBUMIT PO	INTURNEY A VICE AND AND AND AND AND AND AND AND AND AND	7	363-403	413-514	707-755				1
PORPT TANKE	INA-DIRECTED RNA POLYMERASB SUBUMIT PO	DOLUMEZ A VIRUS (STRAIN ANDLUMENTINE VORGO)	13	207-007	13:55	101-155				1
O DIAL LAGOR	ANA DIRECTED RNA FOL YMURASE SUBURIT P?	INTERESTA A VIKUS (STRAIN ACQUING REALISMENT)	2	363-402	473-514	201-155				1
2000	BMA DIRECTED RNA POLYNCRASE SUBURIT P.)	INTLUENZA A VIRUS (STILAIN ARCQUINELLORDON INC.	: :	161.402	473-514	721-755	_			4
PRUPI IANUA	SAY DRECTED BUA POLYNGBASE SUBURIT P.	DIFLUENZA A VIRUS (STILAIN ALEQUINE/FICACUE 1734)		141.402	473-514	707-755				4
1	ANA PRECITED RNA POLYMERASE SUBUNIT PA	DIFLUENZA A VIDUS (STRAIN ARTEVISWIN)		141.402	473-514	707-755				-
100	BAY DORECTED RNA POLYNGRASE SUBURCT PT			107.131	3.54	207-755	-			4
L COL	AND THE CITED BUY POLYMERASE SUBUNIT P.	INFLUENZA A VIRUS (STRAIN ALENINGRAD/13457)	1			356	-		_	
, 1						72:-12:			_	

FILE MAINE					A DEA		ABFAG	ATTA		
The state of the s	PROTEIN	1]	4	7					
PRINT LAMAN	ANA-DORECTED RNA POLYMERASE SUBUNIT P)	7	T	7007	316-17	2000				
PRUP) JANEE	RMA-DIRECTED RNA POLYMERASE SUBUNIT PI	/ YORUCATSOTIS	363-402	473-514	707-758					
PREST LANGE	RNA-DIRECTED RNA POLYNGRASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN AMERIPHIS/W18)	741		473-514	707.755				
PREST LAPUE	RNA-DDIECTED RNA POLYNERASE SUBUNIT PI		1-43		473-514	707-755				
PREST IABLED	BNA DIRECTED RNA POLYNGRASE SUBUNIT PI		142		473-514	707.755				
PRU) IASE2	RNA-DIRECTED RNA POLYNGRASE SUBUNIT PI	$\overline{}$	1-43		473-514	701.755				
PELLY LASON	RNA-DIRECTED RNA POLYNGBLASE SUBUNIT PI		142		473-514	707.755				
PLUZY IATION	ANA-DIRECTED BUYA POLYMERASE SUBUNIT PI		1-43		473-514	707.755				
PRUP LAVIT	RNA-DIRECTED BUY POLYMERASE SUBURGT PI	OTARIJAN)	143		473-514	107.75S				
PRUS LAWA.	RNA-DIRECTED MA POLYMERASE SUBUNIT PI	Г	7		173-514	107.755				
PRED TAZII	RMA-DIRECTED RNA POLYMORASE SUBUNIT PI	DOPLUENZA A VIRUS (STRAIN AAVILSON-SMITHO)	77	163-402	113-614	121.135				
PRIEST LAZTE	RNA-DIRECTED RNA POLYNGRASE SUBURIT P.)		7	363-402	113-514	221.101				
PAULT DOBAC	ANA-DOLECTED ANA POLYNGRASE SUBUNIT PI	71.00		363-402	473-514	701-755				
PRINT DIBAD	RNA-DIRECTED RNA POLYNGRASE SUBUNIT PI	DIFEUENZA B VIRUS (STRAIN BANN ARBONING (COLD-ADAPTE (SE-53)	458-533							
PAREL DATE	RNA DIRECTED BNA POLYMERASE SUBLANT P.	DISTLIENZA B VIRUS (STRADI BIANN ARBONING (WILD-TYPE))	450.533							
	ANA DESCRIPTION OF SACROAGE CITATIONER P.	т	235.260	275.109						
THE PARTY	MAN-DIRECTED MAN FOR IMPERAGE SCHOOL P.		Τ	275-316						
A STATE OF THE STA	ANA-DIRECTED ANA POLITICIONAL SUSPENIOR PER		Т							
FRUE CVIII	MAN-DIRECTED AND POLITICAL SOCIAL STATES	VIETE CETE A PU 330E)	1	495-571	1742-1776	1971-7008	3664-3724	3913-3946		
PARTA CVINCA	BNA DIRECTED BNA POLYMERASE	Con	Γ	1364-1398	1769-2803	3584-3620	3821-385	4075-4121	0319-4350	
1000	BAY WELTER BAY BOX WARE ASS		T	Т	943-1009					
TRACE CVINA	BWA DIRECTED BWA DOLYNGRASE	DNAVIRUS MON (STRAIN A59)	8	-	1457-1694	1692-1726	2629-2670			
	ANY DIRECTED BUY DO WATER ACE		1129-1170	1303-1337	1433-1494	1490-1724	2627-2668			
MUTE IBVB	BUT DORCHED BUT DO WASHASS	LAIN BEALIDETTE	Т	10.493	1460-1494	1509-1548	224-1287			
ALAN MANA	BNA DIRECTED BNA POLYNCRASE	Г	Γ					L		
PREPL BUNCOV	NAN-DELECTED MA POLYMERASE		308-342		135-903	1031-1076	1114-1201			
THUL COVO	RNA POLYMERASE			10-114	308-363	171-412	1704-1741	1802-1861	189.1935	
PRUPL HANTY	ANA POLYMERASE BETA SUBUNIT	IN ONDERSTEPOORT)	20-54							
MUR. HUSVA	INA POLYMERASE	HANTAAN VIRUS (STRAIN 16-118)	96-139	134-208	172-431	187-591	633-696	131-163	905.949	1376-1310
			1419-1433	1342-1776	1993-2027					
PRINT, HABYH	RNA POLYMERASE BETA SUBLINIT	VIRUS (STRAIN A3		127-061	1131-1179	1185-1230	1465-1517			
PRUTE MABYP	RNA-DIRECTED RNA POLYNERASE	KE)	597-631	1046-1092	190-153	1804-1838	2028-2063	2194-2266		
MUNI MEASE	NNA-DIRECTED RNA POLYMERASE			2	1490-1553					
PRUPL MUNDIN	NUA POLYMERASE BETA SUBUNIT	AGEASLES VIRUS (STRAIN EDMONSTON)	107-231		669-903	1064-1109	1303-1317	212-1212		
FRUT, NOVB	ANA POLYMERASE DETA SUBUNIT	MUNIPS VIRUS (STRAIN MIYAHARA YACCINE)	╗	П	267.304	176-627	133-607	1331-1286	1447.1481	1627.1531
			1366-1600	2191-2225			2010			
PREAL PINE	INA POLYMERASE BETA SUBUMIT	2	Т	Т	107-404	107-101	7			
MAN, PITH	INVA POLYMERASE DETA SUBUNIT	IIDMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSIIIDA)	Т	575-628	750-765	126-126	16.53	147-1479	1364-1630	1687.1721
	TIME TO THE TOTAL OF THE PARTY	STANDARD OF STANDARD	1901-1933	107.161	100.00	147.70	1044.133	1201.1356	1100.1114	1024.2014
TOTAL POOR	INA PULTMENASE BELA SUBURI	T		Ī					477.076	
MUNITARY	MAN-DIRECTED MAY FOL TALKASE		1742.1774	T,	1001.7013					
2744	BAY BAY WATER ASE BETA CITAINIT	RABITS VIRUS (STRAIN PV)	21.0	Т	666-730	1134.1222	1522-1580	1384-1411	2064-2123	
700 1000	BAA BOY VACEBACE BETA STRIBIT	98(9)	T		694-730	749-783	1174-1222	1522-1580	1504-2133	
PREM RVEVZ	BNA DORECTED RIVA POLYMERASE		Γ	Γ	14-67	910-913	1017-101			
PLEAT. SENDS	NA-DEECTED RNA POLYMERASE	A VIRUS (STILAIN 2H-549 MI3)			133-467	1001-1115	1633-1647	1819-1870		-
PLUM. SENDE	NAMA POLYMEDIASE BETA SUBUNIT	SENDAJ VIRUS (STRAIN Z / HOST MUTANTS)	109-343	340-600	613-456	147-781	1064-1119	1239-1260	9881-8601	2000-2034
			2146-2216							
MRM. SENDZ	ANA POLYMERASE BETA SUBURIT	SENDAJ VTRUS (STRAIN ENDERS)	138-163	057090	4)3-476	103-734	134-979	1059-1100	1319-1356	1030-1154
							-			

PCGENE		Y CAN WAR THE STATE OF THE STAT	7 7 7 9 7	ABFA 2	AREA 3	AREA	AREAS	7	Ť	
			T	200	84.1	Ī	1064-1119	1239-1210	1499-1535 2	2000-2014
THE MANUE		I VIRUS (STRAIN Z)	Т	200		T	1			
PRINT, SEOUR	ANA POLYNCIASE BETA SUBURIT		2146-2216			Т	Т	1949,1976	1047.1911	1003-2027
		9 CO TO TO TO TO TO TO TO TO TO TO TO TO TO	98-139	174.204	557-591	Т	Т	1	Т	
PREPL SYSWR			\$47-627	147.781	1225-1280	1318-1333	Т	т		
VVV 1888		4 W		125-159	977-1014	1089-1137	1978-2032	┑	7	
1		SONCHUS YELLOW NET VIRUS	T	100 411	510.571	\$19-634	(\$11-6111	1195-1236	1321-1379	1310-1333
PROT. 13WVB		TOWATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPHHIBE)	7		1010	T.	Г	3313-3346	2378-2419	2808-2843
PRIME UNK	NA DIRECTED RNA POLTMEANSE	_	1684-1725	1157-1198	2013-2121		Т	Т	2061-2098	
				2	136-074	1030-001	Т	Т		
PRINT, VSVIR	RNA POLYMEDIASS	CORUNIEM VINOS		674-315	720-763	1323-1567	200			
OLVEN VEND	RNA POLYNŒAASE BETA SUBUNIT	VESICULAL STORATIONS VIROS (SEACTION TO THE CENT OFFIA	Γ	674.715	120-763	3031-1836				
10000	BHA POLYNGRASE BETA SUBURIT		Τ	130,363	1019-1034	1742-1799	2046-2107			
1	AND AND AND ACT BETA STREET	VESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	Ţ		99.	1				
PREPO ACLSV	MA FOLD THE SECTION OF		٦	***	Name of the last					
PILLO BWYY	ANA-DIRECTED IDNA POLITHERANS	LATE FL-1)	304-341							
PRING BYDVI	PUTATIVE RNA-DIRECTED INA POLYMENASE	1154	234-215							
PREPO BYDYP	PUTATIVE RNA-DIRECTED RNA POLYAGRASE		234-265							
WOYE OF STATE	PUTATIVE RNA-DIRECTED RNA POLYMERASE		236.285		L					
	MIT A THUR BUA DIRECTED RNA POLYNERASE	KUS (ISOLATE P-PAV)								
PIUDO CAUSA	MINITED THE THE PART OF WELKE	CARNATION MOTTLE VIRUS	_				1445.1470			
THE COM	PROBABLE INA-URECTED MAN TO THE	CHITAMER GREEN MOTTLE MOSAIC VIRUS (WATERMELON STR74)			446-480	1				
PRIMO GIDVS	PUTATIVE RNA-DIRECTED RNA POLYMERASE	COCCEMENT OF BEAT DISEASE VILLES (STRAIN 5270)	384-432	446-434						
PRRPO IBDVA	PUTATIVE RNA-DIRECTED RNA POLYNERASE	AVIAN INFECTIOUS BURSAL DISEASE WHIS ISTERAN ALISTRALE	144-185	266-307	109.157	111.809				
INC.	PLITATIVE ANA-DIRECTED RNA POLYMERASE	AVIAN INTECTIOUS BURSAL DISEASE VINOS (STRAIN		368.407	\$01.535	150-803				
2	MANA TAVE BNA DIRECTED BNA POLYNERASE	INTECTIOUS PANCAEATIC NECROSIS VIRUS (SERGITPE JASTER) 147-114			15.16	253.602				
MUNO THINKS	POINTING MAN SOUTH BOX YOUR BASE	INTECTIOUS PANCHEATIC NECROSIS VIRUS (SEROTYPE SP)	147-181				1216 0005			
PRING LYCVA	MIATIVE MANDINECTED MAN OF	LYNAPHOCYTIC CHORIONENINGITIS VIRUS (STRAIN ARMISTRON		803.4 803.4	926-960	1304-1343				
PREMO LYCVW	RNA POLYMENASE	I YAPHOCYTIC CHONONENINGITIS YIRUS (STRAIN WE)	301-345					_		
PRUPO MONV	INA POLYMERASE	ALASTE CLI DECTIC MOTTLE VIRUS	181-315	697.731						
PRILITO PEASAN	PROBABLE RNA-DIRECTED RNA POLYMERASE	AND THE CHARGE AND ADDRESS OF THE CHARGE AND	331-358							
PREPO PLEVI	NA-DOECTED INA POLYMERASE	PEA ENAITON MOSAC VANS	136.373	433-457	-					
WALK OF SER	MITATIVE MA DIRECTED MA POLYACRASE	POTATO LEAFROLL VIRUS (SIRAIN I)	117111	25.0						
	MITATIVE BNA-DOLECTED BNA POLYNGRASE	POTATO LEAFBOLL VIRUS (STRAIN WAGENIMBEN)		3	197(19	162-196	L	_		
	MIT A TIVE BAY. DIRECTED RIVA POLYMERASE	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN	781-176					L		
2	Т	RED CLOVER NECROTIC MOSAIC VIRUS	000		-	-			L	
PRINTO REGAD	Т	REOVINUS (TYPE 3 / STRAIN DEARING)	310-361		+				_	
PRINO REOV	Τ	REOVINUS (TYPE 1 / STRAIN DISJONES)	ž die	\downarrow	+					
PREPORE OF	MAN-DIACTOR NAME AND AND AND AND AND AND AND AND AND AND	REDVIRUS (TYPE I / STRAIN LANG)	310-301				1980	439-416	690-724	171-805
PRINTO ROTER	RNA-DUELIED MA POLITICA ACE CIMINET VOI	ROWING ROTAVIRUS (STRAIN R.F.)	8.09	3:18	204-240	1		707 007	200	201-152
PRING ROTBU	RNA-DIRECTED INVA POLITIMENASE SCHOOL	ACCESS ROTAVIRUS (STRAD) UK)	20.00	137-167	ŽŽ	27.75				
PRING ROTPC	RNA-DIRECTED RNA POLTMELANA SUBGRIT	CONTRACTA VIRUS (GROUP C/ STRAD) COWDEN)	74	155.299	335.387	476-510	2			
PRILITO ROTTO	ANA-DIRECTED RNA POLYMERASE SUBUNIT VE	POWER BOTAVILLE (STRAIN COTTFRED)	63.96	113-167	236.37	201-631		3		
PRINO ROTS!	NAN-DOLECTED BYA POLYMERASE SUBUNIT VP	TORCING NOTA WHITE (STEAM SAIL)	94·95	133-167	535-569	177-631	20.00	22.73	6	
PLUTO SBACV	RNA-DIRECTED RNA POLYNGRASE SUBURIT VPI	SINGLAN II KOLA VINOS (SERVINOS SERVINO	628-665							
4 500	PRODADLE RNA-DIRECTED RNA POLYMERASE	SOUTHERN DEAN MOSAKC VIRUS		101.674	-					
	ANA DISSERTED BNA POLYNERASE	SACCHAROMYCES CEREVISIAE VIRUS L-A			317.35	100	191-925	1030-1081	1265-1319	1981-2015
אומנים ואר	T	TACANDE VINUS	25.58	200						
TRES TAGAS	T	TOBACCO MELD GREEN MOSAIC VIRUS (THAY STRAIN UZ)	401-49	682-730	103-110	+				
את סטמי	PUTATIVE DIA JUNE LIED MAN TON	TOBACCO MOSAIC VIRUS (VULGANE)	=	Ş 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	£	+	1	1		
PRILITO THANKS	T	TOBACCO MOSAIC VIRUS (STRAIN KOREAN)	1:33	401-433	663-698		1	<u> </u>	-	L
PRUPO_TLAVTO		TOUR LOCAL COMMENT OF TOWARD TOWARD IN	=	401-453	160-134					
DANG TAVO	Г	TOBACCO MODAIL VINUE 13 INCHI I VINCE CO.					l			

WO 96/19495 PCT/US95/16733

PCCENE	ALLMOTIS	All Viruses (no bacteriophages)	T	٦	1	Т	Т	Т	1	
TILE WANT	PROTEIN		T	AREA!	7	1	7000	1000	N N N N N N N N N N N N N N N N N N N	4
PRATP BASVA	RNA-DIRECTED RNA POLYMERASE	٦	103-144							
PREPP COVO	ANA POLYMERASE ALPHA SUBUNIT	BOVING RESPIRATORY SYNCYTIAL VIRUS (STRAIN AS 1908)	99-158	160-216					1	
75 FE FO	INA POLYMERASE ALPHA SUBINUT		312-373							
PREPS HECVI	ANA POLYMERASE ALPHA SUBLATT		851-66	160-216						
VANAL BEER	BWA POLYNCEASE ALPHA STRINGT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAI) 99-158	951-66	160-216						
N 60 0000	THE POLYMER AS AT PILA STREET	HUMAN RESPUNTORY SYNCYTIAL VIRUS (STRAIN AZ)	99-150	160-216						
PRESENT ACTION	ENA POLYMORASS ALPHA SIMINAT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAUPS-158	Г	160-216						
PREPARATE AND AND AND AND AND AND AND AND AND AND	THE POLYMERACE ALPHA STRIBUT	MEASTLES VIRUS (STRAIN EDMONSTON)	315-374	\$60-099						
PRESE MEASY	ANA POR YACEBASE AL PHA SUBLINIT		315-374	\$69-099						
PRESP ACIDA	ANA POLYMERASE ALPHA SUBLAUT	ATA-I)	315.374	460-495						
TOURS INDIGE	BNA POLYNGBASE ALPHA SUBIDIT		149-183	213-275						
Maraya Maray	BNA POLYMERASS ALDHA SUBURIT	5	214-276							
PREP MOVA	BMA PCT YNGBAST AL PHA STRUNT	LA VACCINE)	214-276							
EVON SORRE	BNA PCLYAGRASE ALPHA SUBURIT	NEWCASTLE DISEASE VINUS (STRAIN AUSTRALIA-VICTORIANI) 100-134	100-134							
Willia de se	ANA POLYACTBASE AL PHA SUBLINET	NEWCASTLE DISEASE VIAUS (STRAIN BEAUDETTE CAS)	100-136							
PRESE PLINE	BNA POLYMERASE ALPHA SUBUMIT		10-114	c 190-cu	175-437					
CHILD STATE	RNA PCI. YACERASE ALPHA SUBUNT		P11-09	C 191-CIC	375-437					
PRINT PRINTS	RNA POLYMERASE ALPHA SUBUNT	HUMAN PARAINFLUENZA I VIRUS (STRAIN CI-577)	111-00	113-364	175-417					
PREPS PERH	BWA POLYNGRASE ALPHA SUBUNGT	6	96-114	112-111	113-364	375-437				
PRESE PERMIT	ANA POLYMERASE ALPHA SUBURIT		182-818							
PREST PUB	RIVA POLYMEDASB ALPHA SUBUNIT	(STEADY TOSKUBA)	216-281							
PERTY PIDEN	INA POLYACIASE ALPHA SUBURT		31-130	414-470						
PRRIP PIAHA	ANA POLYMERASE ALPHA SUBUMT		8							
PRINT PIAND	RNA POLYNŒRASE ALPHA SUBUNIT	١٧)		222-225						
FRUT FRY	INA POLYNŒRASE ALPHA SUBUNT	LAINFLUENZA 4B VIXUS (STRAIN 60-313)	222-205							
PRESP. RABVA	ANA POLYMENASE ALPHA SUBUNIT		137-174					1	1	
PRUP RABVC	RNA POLYNGRASE ALPHA KUBUNIT		93-137					1	1	
PAUL TABVE	INA POLYNERASE ALPHA SUBUNIT		93-127					1		
FREE LABYP	INA POLYMERASE ALPHA SUBUNIT	A), AND (STRAIN PM)	721-27	+						
SARVI JANU	RNA POLYNGRASE ALPHA SUBUNIT		121-18							İ
PRAPS SENDS	INA POLYMENASE ALPHA SUBURI	SECURITY OF STREET SAN SIN	11.16	200711						
PULT SEND	NA POLINGLASE ALTIN SUBURII		Τ	375-447						
PRATE SERVICE	PAY BY VAFFACE ALPHA SUBLIMIT	QNQ)		375-447						
PLUP SENDZ	KNA POLYMERASE ALPHA SUBUNIT		113-364	375-447						
PART SYS	RNA POLYMERASE ALPHA SUBUNIT		113-364	375-447						
PRUP STAV	RNA POLYMERASE ALPHA SUBUMIT									
PRUP VSVIO	RNA POLYMERASE ALPHA SUBUNIT		5	233-261						
PULVE VSVDA	RNA POLYNGRASE ALPHA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN Q	7						1	
PRICE VSVDA	RNA POLYMERASE ALPHA SUBUNIT		2							
FRRFF VSVIO	RNA POLYMERASE ALPIA SUBUNIT	VESICULAR STOWATITIS VIRUS (SEROTYPE NEW JEASET / STRA						1		
PRUP VSVSJ	RNA POLYNGRASE ALMIA SUBURIT	VESTOULAR STUMATION VIRUS (SERVITTE NEW SEASOT STIMATION CONTRACTOR AS STOCKATTOR VIRUS (STREET) SANDON SEASOT STANDARD							Ī	
PSPICE AMERY	ANA POLYMENASE ALPHA SUBUNII		2	301.140						
PSPD VACCV	STREET BOOTEDA SE DAMITOR		Т				-			
אינער אינער	STRING PROTEINASE INSURITOR 2		21:E6							
VACOLV	SERING PROTEDNASS DOCUMENTOR 3	S (STRAIN COPENGAGEN)		225-266						
	COLUMN TANAMAN			334,366						

		All Virgan (no becteriophages)	П	┱	Т			ABFA	AREA!	AREAG
PCGENE			J	J	1	Т	Τ	Γ	Γ	
THEFARE		LA VIRUS		27.47	1					
PSPIA_VACCC	SEATING PROTEINASE INHIBITION J	LYCTHAIN COPENHAGEN	11 - 45						İ	
TIC CAN	COCOLINS	ISI	41.15						1	
איני אינכי	MA!	AND VALIGLA VI	1 661.56	133-207						
PTAGE FOWPY		-	15.7							
PTAGS VACCV		FOWLPOX VINUS	15.							
PTAGE VARV			150							
MALA BEDV			2	164-498						
PTALA POVID		DISEASE VINUS	Τ	405-537						
VIVOU VIVOU			T	107 (0)						
	Nacional Assessment	AVIRUS	T							
777	Nacional Page 1			T						
MALA PON.Y	LAKE I ANIUCA	I YAPHOTROPIC POLYOMAVIRUS	٦	206-258	11710					
PTALA POWE	LARGE T ANTIGEN	AND ICE BOY VOMEN VARIETY (STRAIN))	\$09-544							T
PTALA POWA	LARGE T ANTIGEN	MUDSE TOT LOTTE STATE AND AND	507-542							
PTALA POVAC	LANGE T AMTIGEN	AWEDER SALAL L.P. AOUE)	\$04.539							
PTAME POVNA	LARGE T ANTIGEN	7	116.17							
PTALC BOWLI	LAMBILE T ANTIGEN	HAMSTER FOLYOMA VIAUS	T	169.432						
	LATING ET ANTIGEN	MOUSE POLYOMAVIRUS (STRAIN 3)	T							
STATE OF THE PARTY	LANDING T ANTICEN	MOUSE POLYOMAVIRUS (STRAIN AJ)	T	1						
TANG POWE		MOUSE POLYOMAYBUS (STRAIN CRAWFORD SMALL-PLAQUE)	193-326	169-401						
PTASH POVBO	MUDDLE I ANIMEN	MOVIME POLYOMAVIRUS	41-13							
PTASM POVLY	SMALL T ANTICEN	VACUATED PIC POLYOMAYTRUS	7.							
PTATA NOVAC	SMALL T ANTIGEN	CHECKEN CALIFORNICA MINTERAR POLYICEDROSIS VIRUS	408-442	017-91	489-523					
PTATE NPVBM	TICANS-ACTIVATING TICANSCILLTIONAL REGULATION	ACCOUNTS AND THE POT WIEDEROKIS VIELES	413-47	181-489	494-528					
PTATE NOVOP	THANS-ACTIVATING TRANSCRIPTIONAL REGULAL	SCHOOL MON POLICE TO THE POLY PROPERTY OF THE PROPERTY OF THE POLY PROPE	Γ	311-554						
PTAT SIVAL	THAMS ACTIVATING TRANSCRUPTIONAL REGULAT	ORGYLA PSEUDOI SUCAL A MULII CAS SUCAL INC.	Ţ							
MAT SIVAL	TAT PROTEIN	SDGAN DOMINODE ALLENCY VINOS (AUMILIO ESCANIE)								
V 14 14 1		SDAAN DAMINODER KIENLY VIKUS (ISULATE NOW VECTOR								
PTAT VILV		VISNA LENTIVORUS (STICAIN 1914)	46.74							
MAT VEV	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VISKA LENTIVICOS (SI IKAM 1314) CLORE EN 11161	15.00							
> 10	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT		111							
TIVAL STATE	TOTAL RECEPTOR BETA CHAIN PRECURSOR									
A SACTOR TOTAL	TEGLEMENT PHOSPHOPROTEDN US9	HERPES SDOLEX VIRUS (TYPE 1 / STRAIN 17)								
	MONSENSE									
TECH DAY	MONSENSE									
	TOURSE OF THE PROPERTY OF THE							-		
מונים שנים	NOW ENGE						200	1470.1516	1700-1753	1809-1867
3	The second secon	EPSTEIN-BARR VIRUS (STRAIN B95-0)	764-802		21A-012					
ATEGO HOWA	LAKOB IECOMENI PROTEST		1870-1916	26-05	100-1146					141.1900
	A STORE TO BOTTON	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	34.71	215.249	<u> </u>	2				
PTEGU HSVII	TACON LANCE LEGISLE		1237-1296	3200-22						16/0.1668
		HERPES SINGLEX VIRUS (TYPE 1 / STIALN 17)	731-765	101-443 101-443	1022-1059	120-126	1273-1309	200	177.	
PTEGU HSV80	LARGE TEGUMENI PROJEIN		1673-1714	1745-1783	1830-1854	20.20			1101.1911	1347.1400
	200	HERPES SINDLEX VIRUS (TYPE 6/ STRAIN GS)	30-71	114-161	2	27.51	8			
PTEGU HSVEB	LARGE TEGEMENT PROJECT	CAMPE LEONECATION TYPE I (CTEATH ABAP)	1860-597	(13.4E)	34-46	101-104	1100-1131	1153-1246	137-1438	1467-134
PTEGU HSVSA	LANGE TECHNENT PROTEIN	EQUIVE NEW CASH	1619-1657	1661-1695	1703-1736	(1804-184)	1947-1981			
		The Cart of the Ca	120.558	85.68	615-652	673-710	777-822	149-191	948-936	1267-1333
PTEGU VZVO	PROBABLE LARGE TECHNENT PROTEIN	HERPESVIKUS SAIMING (3 I MAIN 11)	1414-1502		_					
			707 (17	111.74	199.461	23.672	1117-1150	1415-1431	1528-1542	1572-1620
PTFRM ADE02	LANCE TEGUNENT PROTEDM	VALICELLA-ZOSTER VIRUS (STRAIN DUMAS)	1411.1705	316.13	1945.1916	137.1761				
			100					L		
PTFRM ADEOS	DNA TERMONAL PROTEIN	HUMAN ADEROVAUS 1776 3	100							
PTERM ADEB?	DNA TERMINAL PROTEIN	HUMAN ADEMOVIAUS TYPE S								
PTERM ADEI2	DNA TERMINAL PROTEIN	HUMAN ADENOVIRUS TYPE 7								

WO 96/19495 PCT/US95/16733

	**************************************	A D Vience (na hacterianhapes)				П	П	П	П	
PCCEME.	PROTEIN		AREAL	AREA 1	ABEA2	AREA	ABEA 2	AREA 6	AREA!	OBEA
PTRIN AVISI	DNA TERMINAL PROTEIN	N ADENOVIRUS TYPE 12	167-691	497-538						
PTIMAF AVISA	TRANSFORMING PROTEIN TUN		210-214							
PTOP1 SFVICA	TRANSFORMING PROTEIN MAF	ROSARCOMA VIRUS AS42	247-288	195-340						
PTOP2 ASTB?	DNA TOPOISOMERASE		137-113	269.310			┪			T
PTOP2 ASTNO	DNA TOPOISOLERASE II		146-110	41.515		T		┪		
PTSIS_SMSAV		TRUS (ISOLATE MALAWI LIL 201)	146-180	480.SE	2505	903-836	24-973	1001:1001	133:116	1
DYSY VZVD	PDGF-RELATED TRANSFORMING PROTEIN P2B-SIS		12	Ī					+	
PUBIL NOVOP	THY/COYLATE SYNTHASE	VAUCELLA-ZOSTER VIRUS (STRAIN DUNIAS)	215-260						1	
PULDI_HOLIVA	URIQUITION-LIKE PROTEIN	WEDROSIS VIRUS	2							
PULOS HSVII	HYPOTHETICAL PROTEIN UL!		169-203		·					
PULOJ HSVZH	PROTEIN U.)		R-138							
PULOJ HSVED	PROTEIN UL)	12)	93-126							
PLEA HSVII	GENE 60 PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP)	70.104							
PULOS EBV	PROTEIN ULA	HEAPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	103-136							
PULOS HCDAYA	VILLON PROTEIN BBILF I		104-145	113.347	376-410					
PLT OF HSV11	INTOTHETICAL PROTEIN ULA		216-250							
PLS OF HSVEB	VIRION PROTEIN UL6	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	36.94	103-141	294.329	171.111	41479			
PLE OF HSVSA	VIRION GENE S6 PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN AB4P)	061.68	157-413	448-503					
0V2V 90 014	VINION GENE 43 PROTEIN		091:06	131-194	303-336	364-403				
MI OR HCMVA	VIRION GENE SA PROTEIN	N DUPIAS)	10:01	150-409	704-738					
PLI DO HEVER	MYPOTHETICAL PROTEIN ULB		6-30							
PLE OF VZVD	ORIGIN OF REPLICATION BRYDING PROTEDY		174-208							
MONA II			123-163							
ME 11 MCAVA										
PIR 14 MOVA	HYPOTHETICAL PROTEIN ULIS	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	13:41	165-237						
PLE 14 HSVEB	HYPOTHETICAL PROTEIN UL!		105-343							
PIG 14 PRVND	HYPOTHETICAL GENE 49 PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP)	22.56	246-283						
PUL 14 72 VD	UL 14 PROTEIN HOMOLOG		43.95							
PLR 16 HSVED	HYPOTHETICAL GENE 46 PROTEDN		61-103							
PUR.17 HSVAU	CENTE 44 PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP)	366-300							
PUL 21 HSVEB	PROTEIN 108	ANDA-1102	219-210							
ML13 HOWA	GENE 40 PROTEIN		44.78	421-474						
PLE 24 HOLVA	DRYCHETICAL PROTEIN UL23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	213-233							
PUL24 E.TVT	HYPOTHETICAL PROTEDULL34	HEMAN CYTOMEGALOVINUS (STRAIN AD169)	9:39							
PULLS HOWA	PROTEDI UL24 HOMOLOG	RAIN THORNE VII	161-193							
PULZS HSVII	HYPOTHETICAL PROTEIN UL25		255-341	151.399						
PULJS HSVEB	VIDUON PROTEIN UL 25		38411					1	1	
PUL15 HSVSA	VINION PROTEIN UL 15	ATN AB4P)	36.43							
PLAZS ILTY	VINION GENE 19 PROTEIN	HENDESVIRUS SADAIN (STRAIN 11)	29-92	103-231	365-406				1	1
מעבע גניווע	A. I KD VILION PROTEIN	INTECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VILL) II-14	36-64	- 30 - 30				1		T
TOTAL MONTH	MODELLA PROTECTION IN 11	HIDAN CYTOMEGAL DVINIS (STRAIN AD189)	244-285	Ī						
The same	ATTO METANETRO	COUNTY HERPECUTIUS TYPE I (STRAIN ABAP)	131.117						-	
077 TO 1	COME OF BROTHER		163-197							
MALLY HOVE	MAIOS ENVELOPE CLYCOPROTEIN 300	(STRAIN AB))	342.376	Γ					-	
AND IN ALL	PROBABILE MAIOR ENVELOPE CLYCOPROTEDN 26	Γ	22.108	296-344						Γ
MAN (1914	G-PROTEDN COUPLED RECEPTOR HOMOLOG ULJ)		24-135	309-352						
PUR.N. EDV	GENE 25 PROTEIN		19-61							
PULD4 HCMVA	BENE! PROTEDY		139-200							
MEN HSVII	HYPOTHETICAL PROTEIN ULJ4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	113-147							
PULLS HONYA	VIDON PROTEIN ULJ4	HEAPES SIMPLEX VIXUS (TYPE I / STRAIN I I)	187-221							
M0 17 EBV	HYPOTHETICAL PROTEIN UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	231-168							
							i			

FULLY HSVII	MILLOR									
Π			1	10100	10000	ŀ				
	DOLFI		100 100							
			37-07	377.114	614.648	315.250	781-822			
	EN	AIN AB4P)		176.607					-	
אבא ינשא	CENE 63 PROTEIN			764.677						
Ţ										
Γ	NOTERI ULJE	HUMAN CYTOMEGALOVIRUS (STIMIN AD169)								
MEAS HEV!	2		20.00	176 166						
MILLS MEVER			24-106							
1000	3		136-172							
13000			73-109							
אנא לאטי	100.00		27-68							
MILA) VEVD			312-363							
PULAS MSVIK		S	96-137			\				
PULAS HSVIN			66.137							
PUL 47 HOWA	PROTEIN ULY		114-165	448-485	745-856					
PULAT HSVII			473-518							
PULAT HSVIF			473-518			•				
PULAT HSVBP			\$61-612			•				
PULA HSVEA		COUNTY OF STREET STREET STREET	183-246	582-620	933-828					
PULAT HSVED			319-253	171-413	817.866					
PUL 47 V2VD	97 KD ALPHA TRANS-INDUCING TRUITEIN		14-135	156.209	101-199					
PULSO HCHVA		AND CONTROL OVER 15 (CTB A DI AD169)	155.189							
POLSI HSVII	PROTEIN ULSO	TOTAL STREET,	116.169			-				
PULSI HSVE4	PROTEIN U.S.I		121-162			-				
PULSI HOVED	GENE I PROTEIN		130-161			-				
PULSI VZVD	GENE I PROTEIN	EQUINE RELUESVIRUS 1 TPC 1 (31 KAIN ADST)	122.163			 -				
7UL33 EBV		VAUCELLA-ZUSTER VIAUS (STRAIR DUFIAS)	256.001							
PUL33 HSVII	PROBABLE DNA REPLICATION PROTEIN BSLFI	EPSTEIN-BARK VIRUS (STRAIN PP)-1)								
PUL53 HSVEB	DNA REPLICATION PROTEDY ULS?	FERNES SECTEX VIRUS (TYPE 1/3 IRAIN 1/)		0,0.00						
PUL 32 HSVSA	DNA REPLICATION PROTEIN ULSS	EQUINE HEAVESVIRUS 1 TPE I (STRAIN ABOV)								
P.G. 53 VZVD	PROBABLE DNA REPLICATION GENE SA PROTEIN	FEMPES VIXUS SAMMU (STRAIN 11)	100							
PULS HOWA	PROBABLE DNA REPLICATION GENE & PROTEIN	VANCELLA ZOSTER VIRUS (STRAIN LUMIAS)						-		L
MEASH 85 MM	PROTEIN UE. SJ	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)								
PURA HOWA	PROTED ULSS	HEISPES SDOLLEX VIRUS (TYPE 27 STRAIN HUSS)		_						
PLE TO HONVA		MINAN CYTOMEGALOVIRUS (STRAIN ADISS)	2 2							
PULTS HOWA	PROBABLE DNA REPLICATION PROTEIN UL 70	MAKAN CYTOMEGALOVIRUS (STRAIN AD189)								
PULLS? HSV&U	HYPOTHETICAL PROTEIN UL74	KUMAN CYTOMEGALOVIRUS (STIATIV AD169)	4							
PULET HSVSA	HYPOTHETICAL PROTEIN SA	MENUES SDOLEX VILLS (177% 0/31 AAIN COANDA-1192)	2 2	413.616						
MALS HOWA	MYPOTHETICAL GENE 24 PROTEIN	HERPESVIRUS SADADU (STRAIN 11)								
PUL91 HSVSA	HYPOTHETICAL PROTEIN ULIS	HIMAN CYTOMEGALOVIRUS (3 INAIN ADIOV)								
MEN DV	HYPOTHETICAL GENE 10 PROTEIN	HEAVESVIRUS SATMINU (STRAIN II)								
PULTS HOWA	HYPOTAETICAL PROTEIN BOLF	EPSTEIN-BALL VIKUS (STRAIN BYS-1)	10.01			-				
PULST HSV6U	HYPOTIGETICAL PROTEIN ULM	HEMAN CYTCHEGALOVINOS (SIRAIN ADIBY)	10.10	134.316						
PULT HSVSA	HYPOTHETICAL PROTEIN PR	PERPES SECTEX VIRUS (17PE # 7 STRAIN UCARDA-1102)			. -	-				
PULS) HOAVA	HYPOTHETICAL GENE 11 PROTEIN	HERPESVRUS SABIRU (STRAIN II)		36. 36.				-		
MACH HOWA	PROTEIN ULS	HUMAN CYTOMEGALOVINUS (STRAIN AD169)								
MA.PS HSV6U	MYPOTHETICAL PROTEIN UL95	INDIAN CYTOMEGALONIAUS (STRAIN ADIM)		20.00			\downarrow	ļ		
AVACH ME RICE	INTOTHETICAL PROTEIN 13R	HERMIS SIMPLEX VIRUS (TYPI: 67 STRAIN HGANDA-1102)	- i	2:						
PAR SE IISVEU	INTOTHETICAL PROTEIN U.%	HUMAN CYTOMEGAL DVINUS (STRAIN ADIO)	5							
PLE OF 11SVSA	HYPOTHETICAL PROTEIN 148	HERPES SIMPLEX VIRUS (TYPI: 6 / STRAIN UGANDA-1102)					-			
MA CA MONY	INTOTIETICAL GENE IS PROTEIN	HENTESVIAUS SAIMING (STRAIN II)	81.5			-				
MEAN HOAVA	HYPOTHETICAL PROTEIN ULIO?	INDIAN CYTOMEGALOVIRUS (STRAIN ADIAN)	2		37, 61.	419.403	5			
4A/CII 98 918	VIRION PROTEIN ULION	HUNIAN CYTOMEGALOVIRUS (STRAIN ADIE!)	2	136-131	110-104	200.00	2			

POCENE	Allanome	All Vicuses (se betteriophages)					П	П	П	
FILE MAME	PROTEIN	YARUS	08541	AREAJ	ABEAA	1000	48542	ARIAS	AREAI	ABEA
PUND HSV11	HYPOTHETICAL PROTEIN ULIJO	HURLAN CYTOMEGALOVIRUS (STRAIN AD169)	24-13							
PUNG HSV23	URACEL-DNA GLYCOSYLASE	HERPES SOULEX YIRUS (TYPE 1/STRAIN 17)	127-264			-				
PUND HSYZH	URACIL-DNA GLYCOSYLASE	IERPES SINDLEX VIRUS (TYPE 2 / STRAIN 111)	181-229						-	-
PUNG HSVSA	URACIL-DNA GLYCOSYLASE	HEAPES SIMPLEX VIRUS (TYPE 2 / STRAIN HGS2	148-189						-	-
PUNG STVKA	URACEL-DNA GLYCOSYLASE	HELPESVINUS SAINGIN (STRAIN 11)	135-176							
PUSOZ HSVEB	URACIL-DWA GLYCOSYLASE	SHOPE FIBROMA VIRUS (STRAÍN KASZA)	=							-
PUSOT HSVEK	GENE 40 PROTEIN	EQUINE HEAPESVIAUS TYPE I (STRAIN ABAP)	20.5%							
PUSOT HCHIVA	USI PROTEIN	EQUINE HELLESVIRUS TYPE I (STILAIN KENTUCKY A)	199							
PUSII HOLIVA	HYPOTHETICAL PROTEDN HOLFS		2.36							
PUSIA HOLVA	HYPOTHETICAL PROTEIN HOLF!	HUMAN CYTOREGALOVIRUS (STRAIN AD169)								
PUSIG HOUVA	HYPOTHETICAL PROTEIN HALF4	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	1.51							
AVON KNIK	LEMOREANE PROTEIN HALFS	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	107-125			٠				
PUCA NOWA	HYPOTHETICAL PROTEIN 1941 F7	HUNGAN CYTOMEGALOVIRUS (STRAIN AD169)	294-335	\$13.518						
MISM HONA	MYPOTHETICAL PROTEIN HOLI'S	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-172			-				
MIST HONA	HYPOTHETICAL PROTEDNINGES	HIBLAN CYTONEGALOVIRUS (STRAIN AD169)	535-584							
AVACW draw	G.PROTEIN COUPLED RECEPTOR HONIOLOG US17	HIMAN CYTOMEGALOVIRUS (STRAM AD169)	9-40							
PV125 AAPME	HYPOTHETICAL PROTEIN HORFS	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	135-169	274.312		-				
PVI43 NOVAC	125 KD PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 425 / ISOLATE LEIDEN	16.52	126-367	591-649					
PVISK TRVPS	MELICASE	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	313-350	1114-1150	1139-1213					
PVIGK TRVSY	16 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN PSG)	75-117						1	
PVIA BBACV	16 KD PROTEIN	TORACCO RATTLE VIRUS (STRAIN SYNI)	18-117				٦			
PVIA BACV	IA PROTEIN	BROAD BEAN MOTTLE VIRUS	21-55	349.405	492-526	25.751	137-164	190.924		
PVIA COAV	IA PROTEIN	BROME MOSAIC VIRUS			_					
PVIA CANTH	IA PROTEIN	COYPEA CHLOROTIC MOTTLE VIRUS			346-389	487.526				
PVIACONO	IA PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	13-46	193-434	\$64-619	262.916				
PVIA CHVO	IA PROTEIN	CUÇUMBER MOSAIC VIRUS (STRAM 0)	3	393-434	584-619	868-916				
PVIA PSVI	IAPROTEIN	CUCUMBER MOSAIC VIRUS (STILAIN Q)	99-	193-434		-				
PVIA TAV	IA MOTEIN	PEANUT STUNT VIRUS (STRAIN J)	T	Т		-				
PV23K_HSVTH	IA PROTEIN	TOMATO ASPERMY VIRUS	Ī	192-411	\$57-923					
PV24K BDV	23.5 KD PROTEIN	TURKEY HEIVESVIRUS (STRAIN HZ)	117:211							
PV25K MPVAC	24 KD ANTIGEN	BODNA DISEASE VIRUS	121.69	10-17						
PV28K_PCRVI	25 KD PROTEIN	AUTOCAAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	4 -50					1		
PV31K PLRVW	18 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	16-130						1	
PV290 ASFLS	28 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	116-130							
PV39K PEBV	LIS 390 PROTEIN	AFRICAN SWINE FEVER VIXUS (STRAIN LISS?)							1	
PV79K TRVSY	29 6 KD PAOTEIN	EALT BROWNING VIKUS	100				1			
PV39K TRVTC	79 KD PROTEIN	TOBACCO BATTLE VINUS (STRAIN STRILL AND (STRAIN FOU)	107.00				Ī		T	
PVZA COAN	TA LO PROTEIN	COMPEA CHI OROTIC MOTTLE VIDILS	748.104							
IASA PENA	14 PROTEIN	CUCUMBEA MOSALC VIAUS (STRAIN PNY)	386-470							
PYZA TAV	1A PROTEDI	PEARUT STUNT VIRUS (STRAIN I)	182-816							
PVIOR TRVIC	2A PROTEIN	TOWATO ASPERACY VIRUS	723-756		-					
PVIG ASFB7	29.1 KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCA)	105-218							
PV362 ASFB?	K 140 PACITEDA	AFILICAN SWINE FEVER VIRUS (STRAIN BATIV)	13.17							
PV363 ASFB7	K162 PROFEIN	AFILICAN SWINE FEVER VIRUS (STRAIN BA71V)	24-103	161-212	190-124					
PVJA BMV	UNI PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	183-189							
PVJA CAMPA	1A PROTEIN	BROME MOSAIC VIRUS	57-11							
PVJA CATA	JA PROTEIN	CUCINGER MOSAIC VIRUS (STRAIN FIYY)	215-255							
PVJA CANO	3A PROTEIN	CUCMMBER MOSAIC VIRUS (STRAIN M)	215.23							
PVJA CONY	JA PROTEIN	CUCLINGER MOSAIC VIRUS (STRAIN O)	215-35							
PVSIK ACLSV	JA PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Y)	215-255							

							, , , ,			
PCCENE	ALLMOTIS	Al Virgini (se primitis primitis)		AREA	3					
FILE MANG	PROTEIN		٦							
PVSIK BWYV	SOLICO PROTEIN	LATE FL-1)	٦	196-233	6040					
PVSIK BWTVO	SI KD PROTEDV		113-147	18-233	5759					
PVSCK PLAVI	SI KD PROTEDI			277						
PVSCK PLAVV	14 KD PROTEIN	AGENTHGEN		438475						L
PVSEK_BSHV	SA KD PROTEDI		٦	16.68						
PV64K BWTVF	SE KO PROTECH	S (ISOLATE FL-1)								L
PV70K PLRVI	66.3 KD PROTEIN		T	214-348						
PUNCK PLAVY	69.7 KD PROTEIN		٦	109-443	345					
PV90K ANVLE	69.7 KD PROTEIN	DEM	107-141					1		
PVADE VACCC	90 KD PROTEIN			211-275						
PVADA VACCV	PROTEIN A4		33-46	311-275						
VAN VARV	PROTEIN A4	(SIRVING WAY)	33-66	210-265						1
NAME VACCO	PROTEIN A4			314-355						
7000	PROTEIN A4	ENHAUEN	Γ	20:00						
VAR. VAR.	PROTEIN AS	(STICAIN W.K.)	Γ	311-338						
אלעני אינני	PROTEIN A6		L							1
VANO VANO	PROTEIN AS	VACCINIA VIRUS (STRAIN CONGRANCES)	176-236							\downarrow
DAY OF AVAIL	PROTEIN AS	VARIOLA VIRUS	18-97					-		
7440	PROTEIN A9	VACCINIA VINUS (STIVUM CUPENHAUEN)	46.95							
מאיז האינוני	PROTEIN A9		97.134	141-173	219.20					
PVAIL VANCE	PROTEIN A!!	(STRAIN COPENITABLEN)	91.136	230-204						1
200	PROTEINAL	VARIOLA VIRUS	114-148							
200	PROTEIN A12	VACCINIA VIRUS (STRAIN COPENITALEN)	111.152							
NATE VACCO	PROTEDY A12	VARIOLA VIRUS	433-467						\downarrow	1
VACEV	16 KD ABOATIVE LATE PROTEIN	VACUALA VIANA (STAMP)	307-341	(1)-467					1	-
PVA18 VARV	54 KD ABORTIVE LATE PROTEIN	VACCINIA VIAUS (STANKE)	107-341	133-467			\downarrow			1
PVATO VACCC	36 KD ABORTIVE LATE PROTEIN	LA COMPANY VANIE ACTE A DV COPENIA GEN	1-67				\downarrow	1	1	
PVA30 VARV	PROTEIN A20	VALCINIA VINCE LE	1-67			1	\downarrow	1		
PVA22_VACCC	PROTEIN AJG	VACCINIA VIRUS (STRAIN COPENHAGEN)	\$			1	1	1		L
PVA12_VARV	PROTEIN A33	VARIOTA VIRUS	39-80				1	-		
PVA3) VACCC	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	95.143	200			-	-		
PVAJ3 VARV	PROTEIN AZ	VARIOLA VIRUS	95.143	20.62			1			_
PVA31 VARV	PROTEIN AZS	VARIOLA VIRUS	<u>*</u>		1	\downarrow	1	-		L
אינגאין	PROTEIN AJI	VACCINIA VIRUS (STRAIN WR). AND (STRAIN COPENHAGEN					1	-		
PVA33 VARV	PROTEIN A33	VARIOLA VIRUS	217-231		1	-	-	-		L
TVA33 VARV	PROTEIN AJ2	VARIOLA VIRUS	69.63		1	1	+	+	1	
PVAJ6 VACCV	PROTEIN A33	VACCINIA VIRUS (STRAIN WRI, AND (STRAIN COPENHAGEN)	26-67	109-155		1	1	+	ļ	L
PVAJ6 VARV	PROTEDY A34 PRECURSOR	VARIOLA VIRUS	19-67			1	1	-	1	-
PVAJ7 VACCC	PROTEIN AND PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	24-65			+	$\frac{1}{1}$	-		
PVAJ1 VACCV	PROTEIN AT	VACCINIA VIRUS (STRAIN WR)	3		1	1	+	-	-	_
PVA18 VACCC	PROTEIN AJ	VACCINIA VIRUS (STRAIN COPENHAGEN)	<u></u>			-	1	-		-
PVA38 VACCV	PROTEIN AU	VACCINIA VIRUS (STRAIN WR)	3		$\frac{1}{4}$	-	1	-	-	
PVA38 VARV	MOTEIN AU	VARIOLA VIRUS	44.91		1	1	1			L
PVAJ9 VACCC	PROTEIN AU	VACCINIA VIRUS (STRAIN COPENHAGEN)	-		1	+	+	-		-
PVAJ9 VACCV	PROTEIN AJV	VACCINIA VIAUS (STRAIN WR)	<u>2</u>			1	\downarrow		-	
PVA46 VACCC	PROTEIN AUP	VACCINIA VIRUS (STRAIN COPENHAGEN)	١		1	+	1		-	-
PVA46 VACEV	PROTEIN A46	VACCINIA VIXUS (STRAIN WR)	92 		1	+	1	+		-
PVA46 VARV	PROTEIN A46	VARIOLA VIRUS	2			+	+	1		L
PVA47 VACCC	Т	VACCINIA VIRUS (STIVAIN COPENHAGEN)	87.29		1	-	1			L
PVA43 VACCV	٦	VACCINIA VIRUS (STRAIN WR)	85.59			- - -				
7071	TAN WATER									

		an an annual fact bacteriashages!	٦	T	T		2000	ABFAG	AREA?	AREA
PCGENE	ALLAIOTIS]	J	7000	Т	Τ	Γ		
FILEMANIC		A VILUS		10-124						
PVA49 VACCC		AL ACENTA VIRGIE (CTRAIN COPENNAGEN)	3-40	126-160						
PVA49 VACCV		VACCINA VINOS (STRAIN VIN)	3-40	134-160					-	
PVA49 VARV	PROTEIN AAB	ACCIMIN VINOS (SILVANIA TO A)	1-40	136-160						
PYASS VACCC	PROTEIN A49	VAUULA VINUS	91-132							
PVASS VACCV	PROTEIN ASS		91.13							
PVAST VACCC		VACCINIA VINOS (SINAMA TO PENHACEN)	134-168							
PVAST VACEV		VACCINIA VINOS (SINAMI CO: COMPANIO)	134-168							
PVALI MSVK	GUANYLATE KINASE HOMOLOG	VACLIMIA VINUS (SIEMIN TEL)	230-269							
PVALI MISVN		MALE STREAM VINE CALCESTAN (COLATE)	221.262							1
PYALI MSVS	ALI PROTEIN	MALE STREAM VINOS (MOLTAL AFRICAN ISOLATE)	228-262							\downarrow
PVALI SLCV	ALI PROTEIN	IAICE SIREAN VINOS (2001)	113-151							
PV.A.1 TYUVA	ALI PROTEIN	SQUASILLEAT COAL VINOS	191-225							
PV 11.3 AUSTON	ALI PROTEIN	TOBACCO TELLOW DWANT VINOS (SILEMINA)	44-78	13-124						
PV. 11.3 BGAIV	AL) PROTEIN	BUTILON MOSAIC VIRUS (ISOLATE WEST INDIA)	Ī	83-134						
PUALS PYRAV	ALS PROTEIN	DEAN COLDEN MOSAIL VINUS		121-131						
PVAL SLCV	ALJ PROTEIN	OTATIC TELLOW MOTAR VINOS (1905)	08-99	91-125						
PVAL) TGMV	AL) PROTEIN	SQUASH LEAD CORE VINOS	44.73							1
PVAT CANVC	AL) PROTEIN	TORATO COLDEN MOSAC VINCE	22.70	84-127						\downarrow
PVAT CANVD	APHID TRANSAUSSION PROTEIN	CAULIFICHER PROPER VINES (STRAIN DAY)	22.70							
PVAT CAMVE	APHID TRANSMISSION PROTEIN	CALL IN OWER MOSAIC VIRUS (STRAIN BBC)	23.70	13:127						\downarrow
PVAT CAMVIC	APHID TRANSMISSION PROTEIN	FAST OWER MOSAIC VIRUS (STRAIN NYBIS))	22.70	93.127						-
PVAT CAMIVE	APHID TRANSAUSSION PROTEIN	CAIR IST DIVER ADSAIC VIRUS (STRAIN PVIAT)	22-70	13.133						ļ
PVAT CAMIVS	APHID TRANSAIISSION PROTEIN	CALL BLOWER MOSAIC VIRUS (STRAIN STRASBOURG)	22-70	63-130						1
PVAT COMM	APHID TRANSMISSION PROTEIN	CALT IT OWER AIDSAIC VIRUS (STRAIN W260)	¥ 20							ļ
PVAT CERV	APHID TRANSMISSION PROTEIN	CARNATION ETCHED RING VIRUS	99-138							
PVB03 VACCV	AMID TILANSMINITACIEM	VACCINIA VIBLIS (STRAIN WR)	108-142	T						L
PVBON VACCE	TROILEGE	VACCINIA VIRUS (STRAIN COPENHAGEN)	100	T	200-200					L
WEST VACE	TRUENT	VACCINIA VIRUS (STRAIN WR)	68-133	276-376	017 107					
WEGA WAR	TACIENT OF	VARIOLA VIRUS	19.134	276-377	000.744	1				
P. Bos vAcco	TAULEIN DE LIDET BANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LC 16MO)	134.798					-		L
PVB03 VACCC	PLACUES INCS TO A PACE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	154-191							
PVR05 VACCL	PLAQUE-MER / MOST BANDE PROTEIN PRECURSOR	VACCINIA YIRUS (STRAIN LISTER)	254-298							L
PVROS VACEV	A A QUESTICE / MOST MANCE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR)	254-298			-				L
PVB01 VACCV	PLAQUE: SLE / NO. 1 PO. 10 P.	VACCINIA VIAUS (STRAIN WR). AND (STRAIN COPENTIAGEN)	31.5					-		L
PVOOR VACCC	SECURE SECURIOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	89			-				L
N'TON VACE	PROTEIN BESETCH COR	VACCINIA VIRUS (STRAIN WR)	36-60						L	L
PVBIB VACE	PACIFIC TIS	VACCINIA VIRUS (STRAIN COPENHAGEN)	20.00	401-332		\downarrow				L
ANDIE ANCE	TAN TAN TAN TAN TAN TAN TAN TAN TAN TAN	VACCINIA VIRUS (STRAIN WR)	27:10	777				ļ	L	
ANA SI SA	PROTECULARIS	VALUOLA VIRUS		***************************************						
A STANCE	SIMEACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN COPENIAGEN)								L
A STATE OF THE PARTY OF THE PAR	SUBSTICE ANTIGEN S PRÉCURSOR	VACCINIA VIRUS (STRAIN DAIREN I)				-				
A SALA	LIMEACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN WR)				-				
AND AND	200 NO.	VACCINIA VIRUS (STRAIN COPENIAGEN)								
ארר.	SOLUTION DESCRIPTION OF THE PROPERTY OF THE PR	VACCINIA VIRUS (STRAIN WR)							Ŀ	
A STATE OF THE STA	ALI PROTEIN	BEAN COLDEN MOSAIC VIRUS				 	L	L	L	Ц
	at a partition	SQUASH LEAF CURL VIRUS								
		TOMATO COLDEN MOSAIC VIRUS	1			\downarrow				L
AND SOM	PEL PROPERTY	BEAN COLDEN MOSAIC VIRUS	177.70			1			_	
PVBK SULV	BRI PROTEDY	SQUASH LEAF CURL VIRUS	2				<u> </u>			Ц
THE STATE OF THE S	BRIPROTEIN	TOKATO GOLDEN MOSAIC VIRUS		363.300	191-443	1	L	_		Ц
אנפי איניני	PROTEINCE	VACCENIA VIRUS (STRAIN COPENHAGEN)								

Marif Search Ben

PCCCHE FYCH STATA FYCH STATA FYCH STATA FYCH VACCE FYCH		YIRUS		Γ	•					
1111					391-442					
111			144 991	176-408						
11	PLOTED	NKASZA)	I						-	
T			*							
			*							
Ī	PROTEIN C4		*							
1	PROTEON CA	WASING ISTRAIN KASZA)	13:13							
T	LYPOTHETICAL PROTEIN CS		2 6					-		
T	and the second s									
J		(SIMON WA)	11.70	73-121						
	PROTEIN CO		45.06							
VCB SFVKA	PROTEIN CS		100							
	HYPOTHETICAL PROTEIN CO		T	140.226	200-325	575-612				
	HYPOTHETICAL PROTEIN CO		Ţ		120.121	\$75-412				1
Ī	PROTEIN CO		91:0	100-540				L		
T			136-180						ļ.	
T			136-176							
	TAGISTIN CIT	(STAIN WA)	134-170					-		
	PROTEIN CIO		3.76							
PYC12 SFYKA	PROTEIN CIO	VIRUS (STRAIN KASZA)	144	137-182	189-240					
PICIS SFIKA	HYPOTHETICAL PROTEIN CIT		142.176							
VC16 VACCC	PROTEINCE			196.160						1
7000	PROTEINCIABLE		100-133			-	L			1
	PROTEIN C13/82)		40-VB			-				
1218 VALLE	SOLUTIONS AND ADDRESS OF THE PROPERTY OF THE P	VACCINIA VIACO (STORIN KACZA)	56-97			1				
VCIO SFVKA	THOUSEN CHARLE	SHOPE FIEROPIA VINOS (SI PONIS ESTADO)	316-252				1			L
V.CIO VACCC	PROTEIN CIV	VACCINIA VIRUS (STRAIN CUPENHALER)	130-184	670-709		-				
VCAP EBV	PROTEINCIPEL	EPSTEIN-BARR VIRUS (STRAIM BY)-1)	116-174	522-161	260-294			1		L
PICAP HCMVA	NIAJOR CAPSID PROTEIN	HUDIAN CYTONEGALOVIRUS (STRAIN AD169)	11.0	308-356						1
NCAP HSVII	MANOR CAPSID PROJEIN	HERPES SINDLEX VIRUS (TYPE 1 / STRAIN 17)		310.364	311-382	_				ļ
NYCAP HSV&U	MAJOR CAPSID PROTEIN	HERPES SIMPLEX VIRUS		100.35						1
DVY'AP HSVEB	NAJOR CAPSID PRUTEIN	FOLIDIE HERDESVIRUS TYPE I (STRAIN ADAP)		433.314	355.788	_				\downarrow
ASVSA HSVSA	MAJOR CAPSID PROTEIN	LEED PERVIEUS SAIMEN (STRAIN 11)		200					1	1
Was and	NAJOR CAPSID PROTEIN	SECUENCE ARIES VIRUS (STRAIN INDIANA S)	103:100		1	-	L			1
	NAME CAPSID PROTEIN	STEASY A POSTER VIRUS (STRAIN DOMAS)	20-12	3	\downarrow	-	-			4
200	NAME CAPSID PROTEIN	VALLELLY CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	110-248			+		_		-
NCG REVAL	ANA BROWN PROTEDY	AUTOCOCTA COLLEGE AD EP.11	145-181		1			-	L	
PVD05 FOWP	DAY-TO-STATE OF THE STATE OF TH	FOWL POX VIRUS (3) MALES (123-157				$\frac{1}{4}$	1	-	L
PVD05 VACCC	77.0 KD FRUIE	VACCINIA VIRUS (STRAIN COPENHAUEN)	131-161						-	1
PY-DOS VACCV	PROTEIN DS	VACCINIA VIRUS (STRAIN WR)				_			$\frac{1}{1}$	-
VANA VANA	PROTEIN DS	VARIOUA VIRUS				-	L			+
	PROTEIN DS	COPENIA VIBILE (STRAIN COPENIAGEM)	201		1		-			4
ALDON WALLE		VACUAL CONTRACTOR VEN	126-160					-		
PVDO VACE	207070	VACCINIA VINUS (STEEL)	124-160		1	-	-			_
PADON VARV		VANOLA VIRUS	68-69	186-122		1	+		L	_
PVDIO FOWPE	PROTEIN	FOWLPOX VIRUS (STILAIN P. 1.1)	4-52	L			1	1	-	-
PVD10 SFVKA	PROTEIN DIO	SHOPE FURNOMA VIRUS (STRAIN KASCA)	67-105	L				+		L
PYDIO VARV	PROTECTION	VARIOLA VIRUS	2	L		4	1	+		L
PVDBP CALINC	PROTECH DIO	CAULIFLOWER MOSAIC VIRUS (STRAIN CHILIN)	=		L		1	+		L
PYDDP CAMVD		CAULIFLOWER MOSANC VIRUS (STRAIN DM)						1	+	+
PVDGP CAMVE	Г	CAULIFLOWER MOSAIC VIRUS (STRAIN BBC)		-	-			1	1	+
TYTES CANY		CALD IT LOWER MOSAIC VIRUS (STRADY NYSISS)						1	+	+
PVDBP CAMVS	Г	CAULIFLOWER MOSAIC VIRUS (STRAIN STRANBOUNG)	911.116	-	-			1	-	1
SVED VACCO	DNA-BINDING PROTEIN	VACCIDIA VIRUS (STRAIN COPENHAGEN)		+				1		+
700	PROTEON E2	VACCINIA VIRUS (STIAIN WR)	200	-	-					1
VANV	PROTEINES	VARIOR A VIRUS	207	+	1		L		+	+
777	PROTEIN ET	VACCINGA VIRUS (STRAIN COPENHAGEN)	?	1	+					
	PROTEINE	CORRES (STRAIN WIL)	•	$\frac{1}{1}$	$\left\{ \right.$					
PVE03 VACTV	COMME	VACCINIA VINUS (STATEMENT)								

		All Virger (no bacterlophages)	T	Τ	1 7 30 4	A P F A A	A R EA S	AREA		
	51		1	1010	1	1000		Γ		
٦		CA VIRUS	17.							
٦		(STRAIN COPENHAGEN)	28-93							
PVE05 VACCD			38-103							
VEOS VACCV		UAPPRISE (STRAIN WR)	38-103							
PVEOS VARV			31.103							
PVEOF VACCC		S (STRAIN COPENIIAGEN)		333-266						
PVEOF VACCV				233-266						
VEOS VARV		1	105-139	367-401						
VEIL NOVAC		AT IEDENICA NIKI EAR POLYIEDROSIS VIRUS	113-163							
VEI HPVIA	EALTY IS SKD PROTEIN	т	137.171							
PVEL 11PV31		MINIAN PARLICMAVIAUS 1172 IA	8.4							
PVII 10V33	EI PROTEIN		11.67	133-167		L		1		
EVEL MPVIS			8							
VEL MOVIE			100							
1000				112-346						
VC UPVA										
rvel nove										
WEI HIVE			19-11							
PVEI HOVE			20.27							
PVE! PAPVE		7								
VEN NEVAC	STRUCTURE OF STRUCTURE	AUTOGRAPHA CALIFORNICA NINCLEAR POLYHEDROSIS VIRUS	11-11							L
WEI CIUVIK		AΤ	7			1				L
PVE2 HPV05		ADMAN PAPILLOMAVIAUS TYPE S	2.57	276-310	746.766					
PVE2 HPV08	MOBABLE EL FROIEIN		2	201-07						
PVE3 HOVIS	PROBABLE ET PROTECT		61-103	312.74						L
PVE1 HPVII	E2 PROTEIN		81.3							L
PVE3 HPVIA	EL TAUTEN			21.46						L
VET HIVIA	EZ PROJECIA	HUDGAN PAPILLOMAVIRUS TYPE 2A	2	28.183						
PVE3 HDV31	S. S. S. S. S. S. S. S. S. S. S. S. S. S	HIDAN PAPELOMAVIRUS TYPE 31	61-16							L
PVEZ PUVIS	27 20 20 20 20 20 20 20 20 20 20 20 20 20	HUBANN PAPILLOMAVIRUS TYPE 33		1000						
FVE J POV 35	ES PROTEIN	HUMAN PAPELCOMAVIRUS TYPE 35	20			-				
PVEZ PLVJV	POSTORA CA	HIDAAN PAPILLOMAVIRUS TYPE 19	21.2	1		-				
PVEZ POVA	83 PROTEIN	HUMAN PAPILICALAVIRUS TYPE 41								
PVEZ POVE	ES PROTEIN	HUBLAN PAPELOMAVIBUS TYPE 47								
200	E3 PEOTERA	HUMAN PAPELOMA VINUS TYPE SI		110.00.					L	
100 marks	ES PROTEIN	HUDLAN PAPILLOMAVIRUS TYPE 57				1	_	-		
AVES MOVED	E3 PROTEIN	HUNLAN PAPILLOMAVIRUS TYPE SB	3							
CANA SAVA	PROBABLE ET PROTEDI	HUMAN PAPELOMAVIRUS TYPE 3B	17.00							
PVE3 PAPVE	PROBABLE ES PROTEDA	DEER PAPILLOMAVIRUS	97:1							
PVE3 BCBVI	PROBABLE E3 PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS	18.36							
PVE2 BIDVI	E2 PROTEIN	PYCMY CHOO AZEE PAPILLONAVIAUS 1776	2.00	307.341						
PVETO NOVAC	EIPROTEIN	PUESUS PAPILLUMAYINGS 1478 I	200			L				
PUETO NOVOP	EARLY 19 KD PROTEIN	ANTOGRAPHA CALIFORNICA MULLEAN ANTINEGRASIS VINCES	1015							
NEA MOVIE	EARLY 19 KD PROTEIN	DAGYIA PSEUDOTSUGATA MULTICATSUD PALTITECHOSIS TING	77.0	L						4
DVEA HOVA	PROBABLE E4 PROTEIN	HERICAN PAPILLONIA YINGS 177E 14	1							\downarrow
PVES HOVED	PROBABLE E4 PROTEIN	HUBAAN PARLIOMANIUS I YPE 41	3	81.38						
MAN GVEN		=+	617.13							1
PVENV BEV	VOLAL ENGLANCING FACTOR (VEF) (104 KD GLYCOP	-	10.23							
PVENY DRYII	ENVELOPE PROTEIN	BEDG VICE (BEV)	35.45							1
PATRICK!	ENVELOPE GLYCOPROTEDY PRECURSOR		253.286			-				4
PVENY MCV3	MAJOR ENVELOPE PROTEDY (43 KD PROTEIN) (PAJK	HOLLDSCUM CONTACTORINA VINES SIGNIYOR 2 DACYII	352-336				Ц		1	1
VENY THOGY	MAJOR ENVELOPE PROTEDN (43 KD PROTEDN) (P43K)	MOLLISCUM CURI Adiosom viava sous in a cree	21.11	-		-	L			
The Marian						_				I

ALLAIDTIS LADOLES LAJOR ENVELORE PROTEIN (1) KD PROTEIN) (1) K VAC LAJOR ENVELORE PROTEIN (1) KD PROTEIN) (1) K VAC LAJOR ENVELORE PROTEIN (1) KD PROTEIN) (1) K VAC LAJOR ENVELORE PROTEIN (1) KD PROTEIN) (1) K VAC ROTEIN (1) KD LAJOR RESIDANE PROTEIN PRECURSOR VAC BE CO MAJOR MENBRANE PROTEIN PRECURSOR VAC BE CO MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN PRECURSOR VAC BE KD MAJOR MENBRANE PROTEIN VAC PROTEIN (1) FROTEIN (1) VAC PROTEIN (1) V			T	A	AL LANGE	AREA!	ARCAS	1	١
ALLANOTHE MOTEUN (1) ND PROTEIN) (P118 VAC MAJOR ENVELORE PROTEIN (1) ND PROTEIN) (P118 VAC MAJOR ENVELORE PROTEIN (1) ND PROTEIN) (P118 VAC MAJOR ENVELORE PROTEIN (1) ND PROTEIN) (P118 VAC MAJOR ENVELORE PROTEIN (1) ND PROTEIN) (P118 VAC MAJOR ENVELORE PROTEIN (1) ND PROTEIN) (P118 VAC MAJOR ENVELORE PROTEIN (1) ND PROTEIN) (P118 VAC MAJOR ENVELORE PROTEIN PRECURSOR (VAC MADOTEIN (1) ND MAJOR MEMBRANE PROTEIN PRECURSOR (VAC MADOTEIN (1) ND MAJOR MEMBRANE PROTEIN PRECURSOR (VAC MADOTEIN (1) ND MAJOR MEMBRANE PROTEIN PRECURSOR (VAC MADOTEIN (1) ND MAJOR MEMBRANE PROTEIN PRECURSOR (VAC MADOTEIN (1) ND MAJOR MEMBRANE PROTEIN PRECURSOR (VAC MADOTEIN (1) ND MAJOR MEMBRANE PROTEIN PRECURSOR (VAC MADOTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (VAC MAY PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (MAY MAY PROTEIN (1) ND MAJOR MEMBRANE PROTEIN (MAY MAY PROTEIN (1) ND MAJOR		FAREA 2			1	Ī	Ī		
MACHEN EVELORE PROTEIN (1) KD PROTEIN (1) WAG MACHEN (1) KD PROTEIN (1) WAG MACHEN (1) KD PROTEIN (1) WAG WALONE EVELORE PROTEIN (1) KD PROTEIN (1) WAG WALONE EVELORE PROTEIN (1) KD PROTEIN (1) WAG WALONE EVELORE PROTEIN (1) KD PROTEIN (1) WAG WALONE EVELORE PROTEIN (1) KD PROTEIN (1) WAG WALONE WALONE WATER (1) WAG WALONE WALONE WATER (1) WAG WALONE WATER (1) WATER		50.150	Γ		1	1			
MAJOR ENVELORE PROTECH (1) KD PROTECH (1) KY ACK MAJOR ENVELORE PROTECH (1) KD PROTECH (1) KY ACK MAJOR ENVELORE PROTECH (1) KD PROTECH (1) KY ACK MAJOR ENVELORE PROTECH (1) KD PROTECH (1) KY ACK MAJOR ENVELORE PROTECH (1) KD PROTECH (1) KY ACK MAJOR ENVELORE PROTECH (1) KY ACK MAJOR ENVELORE PROTECH PRECURSOR (1) MAJOR ENVELORE PROTECH PRECURSOR (1) MAJOR MEMBRANE PROTECH PRECURSOR (1) MAJOR MEMBRANE PROTECH PRECURSOR (1) MAJOR MEMBRANE PROTECH PRECURSOR (1) MAJOR MEMBRANE PROTECH PRECURSOR (1) MAJOR MEMBRANE PROTECH PRECURSOR (1) MAJOR MEMBRANE PROTECH (1) MAJOR MAJOR MEMBRANE PROTECH (1) MAJOR MA			-				+	1	
SULVOR ENVELORE PROTEIN (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN) (1) NO PROTEIN (1			-	-			+	†	
NAMOR ENVELORE PROTEIN (17 KD PROTEIN) (17 K VAL NAMOR ENVELORE PROTEIN (17 KD PROTEIN) (17 K VAL NAMOR ENVELORE PROTEIN (17 KD PROTEIN) (17 K VAL ROOTEIN (1 KD ALAGENT) NAMOR ENVELORE PROTEIN PRECURSOR NAMOR MENBRANE PROTEIN PRECURSOR NAMOR MENBRANE PROTEIN PRECURSOR NAMOR NAMOR MENBRANE PROTEIN PRECURSOR NAMOR NAMOR NENBRANE PROTEIN PRECURSOR NAMOR PROTEIN (11 KD NAMOR NENBRANE PROTEIN PRECURSOR NAMOR PROTEIN (11 KD NAMOR NENBRANE PROTEIN PROTEIN (11 KD FUSION PROTEIN NAMOR PROTEIN (11 KD FUSION PROTEIN NAMOR PROTEIN (11 KD FUSION PROTEIN NAMOR PROTEIN (11 KD FUSION PROTEIN (12 KD FUSION PROTEIN (13 KD FUSION PROTEIN (14 KD FUSION PROTEIN (15 KD FUSION PROTEIN (17 KD FUSION PROTEIN (18 KD FUSION PROTEIN		1	+						
MACON MACO		12.12	+	 			-	1	
ALADA ENVELORE MOTERN (1) TO PROTEIN (4) MAAAAAA ENVELORE MOTERN (1) TO PROTEIN (1) TA CAGENT) PROTEIN (1) TRACHENT) PROTEIN (1) TRACHENT) PROTEIN (1) TRACHENT) PROTEIN (1) TRACHENT) PROTEIN (1) TRACHENT) PROTEIN (1) TRACHENT (1) TRA		33.785	+	+				1	
MOTERN FI FROTEIN ETS	18-11 SURING STEPROSIS VIRUS (18-5)	-	1	1			-		
PROTEIN 1 1 1 1 1 1 1 1 1 1		15-138	_		1		-		
PROTEIN FILE AGAGEMT) PROTEIN FILE PROTEIN		124-150	=		1	1			
PROTEIN IS PROTEIN IS PROTEIN PRECURSON VAC THE DIALOR NENDRANE PROTEIN PRECURSON VAC THE DIALOR NENDRANE PROTEIN PRECURSON VAC THE DIALOR NENDRANE PROTEIN PRECURSON VAC THE DIALOR NENDRANE PROTEIN PRECURSON VAC THE DIALOR NENDRANE PROTEIN PRECURSON VAC THE DIALOR NENDRANE PROTEIN PRECURSON VAC PROTEIN IS VACANENTI VAC PROTEIN IS VACANENTI VAC PROTEIN IS PROTEIN IS VACANENTI			\vdash		7	1	+		
PROTEEN #							1	Ī	
MEDIENT PAOTEIN PAOTEIN PRECURSOR VAN BEED MAJOR MEMBANE PROTEIN PRECURSOR VAN BEED MAJOR MEMBANE PROTEIN PRECURSOR VAN BEED MAJOR MEMBANE PROTEIN PRECURSOR VAN BEED MAJOR MEMBANE PROTEIN PRECURSOR VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN FILL VAN PROTEIN GIF PACKAGENT) VAN PROTEIN GIF PACKAGENT) VAN GENE 19 PROTEIN GIF LANGEMANE PROTEIN FILL CCC PROTEIN GIF PR		211	1						
18 CO 14AOR NEADRANE PROTEIN PRECURSOR VAN 18 KD 14AOR NEADRANE PROTEIN PRECURSOR VAN 18 KD 14AOR NEADRANE PROTEIN PRECURSOR VAN 18 KD 14AOR NEADRANE PROTEIN PRECURSOR VAN 18 KD 14AOR NEADRANE PROTEIN PRECURSOR VAN 18 KD 14AOR NEADRANE PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE IN PROTEIN VAN WYPOTHETICAL GENE GENE WYPOTHETICAL GENE GENE GENE GENE GENE GENE GENE GEN		T	<u> </u>						
WED NAMES NECURSOR VAC		81-129	3	T					
W KD IALOR MEMBALNE PROTEIN PRECURSOR VAL		11.129 21.13	<u>=</u>						
14 KO MADA NEJBEANE PROTEIN PRECURSOR VAN		81-123 281-322	=						
19 KO MAJOR MEABANNE PROTEIN PROTEIN 11 VAI PROTEIN 11 VAI PROTEIN 11 VAI PROTEIN 11 VAI PROTEIN 11 VAI PROTEIN 11 VAI PROTEIN 11 VAI PROTEIN 11 VAI PROTEIN 12 VAI PROTEIN 12 VAI PROTEIN 12 VAI PROTEIN 13 VAI PROTEIN 14 VAI PROTEIN 14 VAI VAI PROTEIN 14 VAI VAI VAI PROTEIN 16 VAI VAI VAI PROTEIN 17 VAI VAI PROTEIN 17 VAI VAI VAI PROTEIN 18 VAI VAI VAI PROTEIN 18 VAI VAI VAI PROTEIN 19 VAI]							
PROTEIN 11		249-215	1						
PROTEIN !!! VA PROTEIN !! VA PRO	(STRAIN COPENIAGEN)	T							
PROTEIN !			+						
PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN GIPACALENT PROT		41.75	1	ī	110.111	\$44.503			
PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN FILE PROTEIN GIALAGEE PROTEIN PROTEIN GIALAGEE PROTEIN PROTEIN GIALAGEE PROTEIN PROTEIN GIALAGEE PROTEIN PROTEIN GIALAGEE PROTEIN GIALAGEEN FILE PROTEIN GIALAGEE PROTEIN GIALAGEEN FILE PROTEIN GIALAGEE PROTEIN GIALAGEEN FILE PROTEIN GIALAGEE PROTEIN GIALAGEEN FILE PROTEIN GIALAGEE PROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FILE PROTEIN FILE FROTEIN GIALAGEEN FROTEIN FILE PROTEIN FILE FROTEIN GIALAGEEN FROTEIN FILE PROTEIN FILE FROTEIN GIALAGEEN FROTEIN FILE PROTEIN FILE FROTEIN GIALAGEEN FROTEIN FILE PROTEIN FILE FROTEIN GIALAGEEN FROTEIN FROTEIN FILE PROTEIN FILE FROTEIN GIALAGEEN FROTEIN FILE PROTEIN FILE FROTEIN FILE PROTEIN FILE FROTEIN FILE PROTEIN FILE FROTEIN FILE PROTEIN FILE		191	7	I	T	183 779			
PROTEIN 13		101	103-143	٦	T				
PROTEIN 13		1.67	199-236	350-388	27.5				
PROTEIN FILE PROT		100					1		
PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN FIG. PROTEIN GIA. PR									
PROTEIN FISH PROTEIN FISH PROTEIN FISH PROTEIN FISH PROTEIN FISH INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION FISH INTO FUSION FISH INTO FUSION FISH INTO FUSION FISH INTO FUSION FISH FOR FUSION FISH INTO FUSION FISH INTO FUSION FISH FOR FUSION FISH INTO FUSION FISH FUSION FISH INTO FUSION FISH FOR FUSION FISH INTO FUSION FISH FOR FUSION FISH INTO FUSION FISH FUSION			T						
PROTEIN FIG. PROTEIN FIG. PROTEIN FOTOMING FOR FIG. INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN INTO FUSION PROTEIN GI P			İ						
PROTEIN FP PROTEIN FP IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN KD FUSION PROTEIN IN FROTEIN GI IN		٦	1						
PROTEIN PA PROTEIN PA PROTEIN PA IN TO FUSION PROTEIN IN TO FUSION PROTEIN IN TO FUSION PROTEIN IN TO FUSION PROTEIN IN TO FUSION PROTEIN IN TO FUSION CONTENT PROTEIN IN TO FUSION CONTENT PROTEIN PROTEIN GI PROTEIN FI (RADIEIN CO) PROTEIN FI (RA		135-173	2007						
FALET PROTEIN (FACAKENT) FALET PROTEIN (FACAKENT) FALET PROTEIN (FACAKENT) FAC PUSION PROTEIN FACTERIO (FACAKENT) FROTEIN G) FROTEIN		13-57							
PAOTED (FACENET) FOOTED (FACENET) FOOTED (FACENET) V V V V V V V V V		73.111							
THEFT PROTEIN UTAGES. INTO THE TROTEIN UTAGES. INTO THE TROTEIN UTAGES. INTO THE TROTEIN UTAGES. PROTEIN GI CENT J PROTEIN GI CENT J PROTEIN GI MATORIN GI PROTEIN GI		70							
14 KD FUSION PROTEIN 11 FOURSON PROTEIN 11 FOURENCI 12 FROTEIN GIP 13 FROTEIN GIP 14 FROTEIN GIP 15 FROTEIN GIP 16 GENE 1 PROTEIN (OM L.) 17 FROTEIN GIP 18 FROTEIN G		100							
INTOTRETIES IN PROTEIN ROTERN GI PROTEIN GI	(A) (A) (A)	Ī,	12-563	591-647	130.764				
INTOTNETICAL GENE I PROTEIN V PROTEIN GI PROTEIN GI CENE I PROTEIN GI CENE I PROTEIN GI CENE I PROTEIN GI CENE I PROTEIN GI CENE I PROTEIN GI PROTEIN GI PROTEIN GI PROTEIN GI PROTEIN GI CHYPOTHETICAL GENE I MEMBANE PROTEIN INTOTNETICAL GENE I MEMBANE PROTEIN V V PROTEIN GI	TPISH VIRUS) (CCV)	T							
PROTEIN GI PROTEIN GI PROTEIN GI GENE 1 PROTEIN PROTEIN GI PROTEIN		ATT-IR							
PROTEIN GI (PAGAIENT) MOTEIN GI GENE I PROTEIN (OM L.) PROTEIN GI PROTEIN G	STATE AND WRITE	240.2	1						
CENT 1 PROTEIN CO. CENT 1 PROTEIN CO. CENT 1 PROTEIN CO. CENT 1 PROTEIN CO. PRO	(in the control of th	301-339	1						
CENE I MOTERN GENE I PROTEIN PROTEIN GIA P	US	141-177							
CEAR 3 MODEIN (G. L.) CEAR 3 MODEIN (G. L.) FROTEIN G. PROTEIN (G. L.) PROTEIN G. PROTEIN (G. L. M. M. M. M. M. M. M. M. M. M. M. M. M.	ESVIRUS TYPE I (STEATE AND THE PARTY AND AND THE PARTY AND	141.171							
CENE 1 MOTEIN (OM L.) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN FI (PROTEIN CO) P	ESVIRUS TYPE I (STRAIN REMIUCAT A) LETTER	2.2							
PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI (PROTEIN G) PROTEIN FI PROTEIN	103	١.	344.780	155-309	L				
PROTENG) WOTENG) WYOTHERAL GENE I MEMBRANE PROTEIN IN PROTEIN G) PROTEIN G) PROTEIN G) PROTEIN I (PROTEIN GP) PROTEIN I (PROTEIN GP) WROTEN I (PROTEIN GP) HYOTHERICAL GENE IO MEMBRANE PROTEIN WYPOTHERICAL GENE IO PROTEIN KYPOTHERICAL GENE IO PROTEIN	RITS (STRAIN COPENHAGEN)	T	T	315.319					
THOTHERICAL CENE & MENGRANE PROTEIN IN HYPOTHERICAL CENE ! MENGRANG PROTEIN IN HADTEN GT PROTEIN GENE 13 PROTEIN HYPOTHETICAL CENE 18 PROTEIN HY		1	Ţ			L			
HYPOTHETICAL GENE & NEUGRANE PROTEIN IN THYPOTHETICAL GENE TO MELABRANE PROTEIN IN THOUSEN GO PRACEMENT) PROTEIN FI (PROTEIN GO) PROTEIN FI (PROTEIN GO) PROTEIN FI (PROTEIN GO) PROTEIN FI (PROTEIN GO) R WITTOTHETICAL GENE IS PROTEIN R WITTOTHETICAL GENE IS PROTEIN NYTOTHETICAL GENE IS PROTEIN NYTOTHETICAL GENE IS PROTEIN	ERPECULLIS I (CHANNEL CATFISH VIRUS) (CCV)	6							
C PROTEINCAL CENE 1 NEMBRANG PROTEIN IN TROTHE INCOME. TO PROTEIN GO. THOTEIN IT (PROTEIN GO) THOTEIN IT (PROTEIN GO) THYPOTHETICAL GENE 10 NEMBRANE PROTEIN THYPOTHETICAL GENE TO THYPOTHETICAL GENE TO THYPOTHETICAL GENE TO THYPOTHETICAL GENE TO THYPOTHETICAL GENE TO THYPOTHETICAL G	PERFECTION OF THE CATFISH VIRUS) (CCV)	٦					L		
PROTEIN GO PROTEIN II (PROTEIN CO) PROTEIN II (PROTEIN CO) (PRACHEMI) PROTEIN II (PROTEIN CO) (PRACHEMI) HYPOTHETICAL GENE IO MENGRANE PROTEIN KYPOTHETICAL GENE IO PROTEIN	THE CONTRACTORY		324-358		1				
V PROTEIN OF PROTEIN CO. PROTEIN CO. PROTEIN OF PROTEIN OF PROTEIN CO. PROTEIN OF PROTEIN CO. PROTEIN CO. PROTEIN CO. CENBLANE PROTEIN C. CENBLANE PROTEIN C. CENBLANE PROTEIN CO. CENBLANE PROTEIN CO. CENBLANE PROTEIN CO. CENBLANE PROTEIN CO. CENBLANE CO. CENBLANE PROTEIN CO. CENBLANE CO. CE	AUS (STEAM COTTO	114-175	114-158						
PROTEIN OF PROTEIN GO) PROTEIN FI (PROTEIN GO) (PACCHENT) PROTEIN FI (PROTEIN GO) HYPOTHETICAL GENE 10 MENBALME PROTEIN GENE 12 PROTEIN KYPOTHETICAL GENE 10 PROTEIN	105	104-318				\downarrow	-		_
PROTEIN FI (PROTEIN CO) PROTEIN FI (PROTEIN CO) PROTEIN FI (PROTEIN CO) PROTEIN FI (PROTEIN CO) PROTEIN FI (PROTEIN CO) GENE 13 PROTEIN KYPOTHETICAL GENE 10 PROTEIN KYPOTHETICAL GENE 10 PROTEIN	INUS (STRAIN COPENIAGEN)	104.116					-		
PROTERN FI (PROTEIN ON (PAGEMEN) PROTEIN FI (PROTEIN ON (PAGEMENT) HEYOTHETICAL GENE 10 MEMBRANE PROTEIN KYPOTHETICAL GENE 10 PROTEIN	INUS (STRAIN WR)								-
HATTOTHETICAL GENE 10 MEMBAJNE PROTEIN HYPOTHETICAL GENE 10 MEMBAJNE PROTEIN GENE 12 PROTEIN KYPOTHETICAL GENE 10 PROTEIN	103								
HYPOTHETICAL GENE 10 MENBANE PROTEIN GENE 12 PROTEIN KYPOTHETICAL GENE 10 PROTEIN	TATION HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	6:0							1
GENE 13 PROTEIN KYPOTHETICAL GENE 16 PROTEIN	A MRIN COVI. REAZ B	2			1	-	-		
KYPOTHETICAL GENE IS PROTEIN	IS CADAIN (STRAIN !!)				+	-			
THE PERSON NAMED IN COLUMN 1 IS NOT THE PERSON NAMED IN COLUMN 1 I	PENERS VIEWS SAMELY (CHANNEL CATFISH VIRUS) (CCV)	٦	=		-	-	-		
THE PROPERTY OF THE PROPERTY	MENTES VIALOS (CITATORIS CATE ISH VIALUS) (CCV)	174-208	22.22			-			
HYPOTHETICAL CENT IS PROTED	KCTALUNID MEMPS VIRUS I COMPANIE CAMPPO	197-441							
KITOTHE ILLAL CETE	MODRE! ENTONOTON VINOS (MILES								
PVGI SPVIR GIL PROTEON									

The property of the property The property of the property	PCGUNE	ALL:SHORIS		1	П	ABEA L	4854	ABEAL	AREAS	ABEAI	ANTAL
Comparison of the comparison				<u> </u>		120-157					
The control of the	١			i							
	1		Ť	Ī	117.670	660-893	149-1055			-	
	11211		ī	2	4.108						
The control of the	112.11		_	64.119							
	6.4 HSV:1	HYDRIG IN AL CENE JUTEOISTI	ř	55.300							
GIN 16011P 1990	CIR ANEPV	INTOINE IN ALL CENE TO THOUGHT	ī	9	104.218						
TOTAL TOTAL	# A A	IN POTICAL CON PROPERTY	PRINCIPAL ACRIA VIBILS SPVILBIALD	25.53	105.336						İ
	3.5	GENE 2 PROTEIN	The Coll Action County of College	55-310							
	11.7511 (6.5)	GENE 2 PROTEIN	MINUTA SELECTION OF LOT VALUE CONTINUES OF SELECTIONS OF S	10.00							
	CM USVII	HYPOTHETICAL GENE 33 PROTEIN	7	11.5							
	C15 115VII	INPOTHETICAL GENE 34 PROTEIN	7								
	C17 115VII	HYPOTHETICAL GENE 19 PROTEIN	Ī	2							
The proof is a proof in the p	127510	HYPOTHE FICAL GENE 37 PROTEIN	-i	25.41							
THE PROPRESS THE		INPOLIE BYAL GENE DE PROTEÎN		=					1		
GENT PROTECT GENT PROTECT GENT PROTECT GENT PROTECT INTODITE INCLUDE SPRINGLY FOR THE STATE SPRINGLY FOR TH		7,900 de el 2720 1 v 00 al 10 de 21		134-158	166-100						
GINT PROTEIN PROPERTY PRO	1 A		MROPLASMA VIRUS SPVI-RBAZID		961-791	201-144					
INTOTITE ILLA GINE A PROTEIN	2	UENE J'FROIEIR	China China Colonia A Contra		11:131						
INTOTITE ILEAL GINE SI PRODIEN IEAPENING SAMBIA INTOTITE ILEAN CONTROLLED INTOTITE ILEAL GINE SI PRODIEN IEAPENING SAMBIA ISTANIA IN	Cet HSVII	GENT 9 PROTEIN	STRUCTASTAN VIKOS (ST. 4)	Ī	367.796	124.361	119:178				
INTODIESTICAL GINE S PROTEIN	COS HISVSA	INPUTITE TICAL GENE 43 PROTEIN	CI ALURIO REPUBBILICA I CLIMACE CANTON TO CONTRACT	1							
INTODITE ICAL GINE A PROTECH ICTALINDO IRRAFENDRIS I CITANNEL CATESI VIRISTICCY 144-157 111-157	C46 IISVII	HYPOTHETICAL GENE 45 PROTEIN	ELLESVIRUS SAIMING (STRAIN 11)		200	100					
INTRODITE INCL. GENE APPOTEN INTRODUCENCY AND STANDAY CONTINUENCY 150-11 150	C48 115VII	PROB 4BLE MAJOR GLYCOPROTEIN	CTALUND ICAPESVIRUS (CHANNEL CATFISH VIRUSITLY)								
INTOILE ITCAL GENE APPOTEEN INTERVENUES SALABILISTANIN 11) 4101 4102 4103	Ges HSVSA	HYPOTHETICAL GENE 48 PROTEIN	CTALURID HERPESVIRUS I (CHANNEL CATTISH VIRUS) (CCV)	١							
INTERPRETATE GLAG GANG STATE OF THE SECOND GLAG STATES OF THE STATES O	45/251 000	HAYPOTHE FICAL GENE 48 PROTEIN		j	900	737.767					
CHEST IN CHECKED CHEST A MODALE LA TORNICE CATTISIS VIRUS) (CHEST A MODALE LA TITISIS VIRUS) (CHEST A MODALE LA TITISIS VIRUS) (CHEST A MODALE LA TITISIS VIRUS) (CHEST A MODALE LA TITISIS VIRUS) (CHEST A MODERNER LA TITISIS VIRUS) (CHEST A MO	CAR ANGERV	HYPOTHU TICAL GENE 49 PROTEIN		103			Ĭ				
GENE 4 PROTEIN STRONGEN STRONGEN STRONGEN CATEGORY STATES STRONGEN STATES STA	CA COVA	CAR PROTEIN		=							
ITTOTICE ICAL GINE 13 NICKOBANE PROTEIN CTALUND SERVESVINUS (CLANNEL CATTISM VAUS)(CCV) 11-13 102-196 17-131 102-196 17-131 102-196 17-131 102-196 17-131 102-196 17-131 102-196 17-131 17-	100	CENE + PROTEIN	-	9							
GENE 11 GLACOPROTERS	GII HSVSA	HYPOTHETICAL GENE SI MENBRANE PROTEIN	ICLALUMD KERPESVIRUS I (CHANNEL CATTISH VIRUS) ICCVI	=	2						
INTODITE LICAL GINE 1) PROTEIN CTALUND GENESYNUS CHANNEL CATTEST VIRUS) CCV 15.75	Ci lisvii	GENE SI GLY COPROTEIN		2	2	162-176					
INTODITETICAL GENE SI PROTEIN	CIO IISVII	HYPOTHETICAL GENE 33 PROTEIN	Т								
INTODITE INCL. GENE 3 FROTEIN INTADIA GENES VIRGINIS I CHANNEL CATTISII VIRUSICCY 111-135 111-137	GIS HSVII	HYPOTHETICAL GENE SA PROTEIN	- 7	2							
INTOTICE ICAL GENE SPROTEIN	G11 IISVSA	HYPOTHETICAL GENE 35 PROTEIN	ICTALUMIO HE IPESVIRUS I (CHANNEL CATHISH VIRUS) (CCV)	661.03							
INYOTIGETICAL GENE SA PROTEIN ICTALUMD IGANES VINUS ICTANNEL CATTSSI VRUSSICCY 151-179 151-174 1	CS6 HSVII	HYPOTIETICAL GENE 19 PROTEIN	T	Ī							
INTROTTEE TOLL GENE SO MEMBERS HEADEN INTROTTEE TOLL GENE SO MEMBERS HEADEN INTROTTEE TOLL GENE SO MEMBERS HEADEN INTROTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTROTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTROTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTROTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTROTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN INTOTTEE TOLL GENE SO PROTEIN	GSP HSVII	HYPOTHETICAL GENE 14 PROTEIN	ī	Ī	7	944-918					
GENE 19 POOLEN HERESONIUS SADRIM (STAIN 1) 15-107	GS9 HSVSA	SENE 19 MENIDRANE PROTEI	CTALUND ICHESVIRUS I (CIIAMEL CATFISII VIRUS) (CCV)		(7)						
INTOINE II.CAL GENE 61 PROTEIN CTALUND IEDVESVIRUS CCIANMEL CATISIS VIRUS) (CCV) 14-184 111-1134 1	/G) SPVIR	GENE S9 PROTEIN									
INTOTICE LICAL GENE OF PROTEIN CTALUND IERRESVIRUS CTIANMEL CATISH VARUSICCY 143-144 111-134 1	CGI LISVII	GENE SPROTEIN		100							
ITYOTHETICAL GENE 64 PROTEIN ICTALUND IEDZESVINUS I CITIAMEL CATISH VIRUS) (CCV) 194-194 1111-1144 1111-	V(6) 115V11	HYPOTHE HICAL GENE 61 PROTEIN	CTALURID HERPESVIRUS I (CHARMEL CATHISH VIRUS) (LCV)								
INTOTILE TICAL GENE APPOTEIN ICTALUMD HERNESVIRUS ICTIANNEL CATTISH VARUS 111-1134 111-11	VG65 HSVII	HYPOHEHCAL GENE 61 PROTEIN	7	100							
	COS HSVII	INPOTITETICAL GENE 65 PROTETN	1.								
ITYO IEE ICAL GENE 6 PROTEIN ICTALUMD IEANESVINUS ICTIANNEL CATISIS VARUSICCY 21-218 121-219 111-219	VCSO HISVII	HYPOTHETICAL GENE 64 PROTEIN	_	ī	201		1416 1141				
INTOTIETICAL GENE 37 PROTEIN CTALLUND IELNES YNUS I CCIANNEL CATRISH VRUSSICCY 413-454 113-1319 114-1319 115-	VG48 HSVII	HYPOTIGETICAL GENE 67 PROTEIN	┰	Ī	301-348	4071.1771					
INTODITETICAL GENE 12 PROTEIN ICTALUMD TERRESTMUS ICHANGE CATTRIN VARDILICAT 111-105 181-115 111-115 1	VCT2 ISSVII	HYPOTHE TICAL GENE 66 PROTEIN	ICTALUNID ICENTESVIRUS I (CITANNEL CATTISM VIRUS) (CCV)								
INTOCHIETICAL CENE 31 PROTEIN ICTALUMD IRROESVRUS ICHANNEL CATTAIL VRUSIFICATOR 111-139 111-130	COS HISVII	HYPOTHETICAL GENE 73 PROTEIN	1		10.00	40.7					
GENE & PROTEIN SPIROPLASMA VRIUS SEVILARA BEAUDE ITEIN 1331-1387 1119-2158 1319-1387 1319-3158 1319-	VGB SPVIR	HYPOTHETICAL GENE 75 PROTEIN	1	£ :							
A VALAN PRECINSOR A VA	VGF1 IBVB	GENE 1 PROTEIN	SPIROPLASMA VIRUS SPVI-REAZ D	100					7711	1741,1104	
GLYCOPROTEIN HISTORICASOR (JATELY GLYCOP PORCINE RESPIRATORY COROMAVRIUS (STRAIN MUT) 7004 FBE 111.315 CONTROL OF THE PRINCIPLE RESPIRATORY COROMAVRIUS (STRAIN MUT) 7004 FBE 11.315 CONTROL OF THE PRINCIPLE RESPIRATORY (STRAIN FILE) CONTROL OF THE PRINCIPLE RESPIRATORY (STRAIN FILE) CONTROL OF THE PRINCIPLE RESPIRATORY (STRAIN FILE) CONTROL OF THE PRINCIPLE RESPIRATORY (STRAIN LY) CONTROL OF THE PRINCIPLE RESPIRATORY (STRAIN LY) CONTROL OF THE PRINCIPLE RESPIRATORY (STRAIN LY) CONTROL OF THE PRINCIPLE RESPIRATORY (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS CORONAVIRUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS CORONAVIRUS CORONAVIRUS CORONAVIRUS CORONAVIRUS (STRAIN RESUS CORONAVIRUS CORO	VGII) HCMVA	FIPROTEIN	AVIAN INTECTIOUS BRONCIUIIS VIRUS (SIRAIM BEAUDE) IEJ (I	21.13	1971-1171	9617-4119	7386-9866		Т		
E G Y Y CORLOTEN PRECINSOR (MATRIX CLYCOP) PORCINE REPRESENTATIVE CURDINAVIRUS (STRAIN ESTIMATION CLASS CONTROLLING) 441-414 110-415 110-1105	VGLI CVPRI		HUMAN CYTOMEGALDVINUS (STRAIM ADIM)								
E3 GLYCOMODE IN PRECUSOR (SPIKE GLYCOPRO BOVING COROMAVILUS (STRAIN L.)) E3 GLYCOMODE IN PRECUSOR (SPIKE GLYCOPRO BOVING COROMAVILUS (STRAIN L.)) E3 GLYCOPRODE IN PRECUSOR (SPIKE GLYCOPRO BOVING COROMAVILUS (STRAIN L.))) E3 GLYCOPRODE IN PRECUSOR (SPIKE GLYCOPRO BOVING COROMAVILUS (STRAIN L.))) E3 GLYCOPRODE IN PRECUSOR (SPIKE GLYCOPRO BOVING COROMAVILUS (STRAIN L.))) E4 GLYCOPRODE IN PRECUSOR (SPIKE GLYCOPRO BOVING COROMAVILUS (STRAIN L.))) E4 GLYCOPRODE IN PRECUSOR (SPIKE GLYCOPRO BOVING COROMAVILUS (STRAIN L.)))	VGL1 CVBF	EI GLYCOFROTEIN PRECURSOR (MATRIX GLYCOP			910.010	961.100	1041.1304				
ES CLYCOROTERN PRECISSOR (STRE CLYCORNO BOVINE COMONYULUS (STRAINLY) ES CLYCOROTERN PRECISSOR (STRE CLYCORNO BOVINE COMONYULUS (STRAINLY) ES CLYCOROTERN PRECISSOR (STRE CLYCORNO BOVINE COMONYULUS (STRAINLY)) ES CLYCOROTERN PRECISSOR (STRE CLYCORNO BOVINE COMONYULUS (STRAIN MEBUS FOLLOWING COMONYULUS (STREET)	VCA.1 CVBL9	E2 GLYCUPROTEIN PRECURSOR (SPINE GLYCOPRO				1141					
ES GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO BOOTHE COMMANDUS (STIAM MEBUS)	VCL1 CVBLY	ET GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO		1		100	1011.1361				
IS TO ACCORDITE TO PRECIDE SOURCE SELECTION OF THE PROPERTY OF	VCL 1 CVBM	ET GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPRO				1100	1361.1305				L
LA UNIVERSITY AND THE PROPERTY AND THE P	PVGL1 CVBQ	ET CLYCOPAOTEIN PRECIASOA (SPIKE GLYCOPAO		74.7		2017	100.100				

		AR VITURE INC COLUMN TO THE PROPERTY OF THE PR	AHEAI		ALLA	1	į			
CCINE			Γ	\$87-068	993-1109	1263-1309				
וויר בסבור		1361	230.016	055-1112						
Via y CVIII		ī	Ï	901-1117	1379-1315				-	
1		TALE OF LOCAL	Ī	040-1070	1310-1263					
VG. 1 CVAIA3	STATE OF VODE OF THE STATE OF VCOPEO	Ī.	ī	111110	1170-0111					
VAIR.		A AMPLIA	Ī	140.076	1129-1174					
			Ī	40.02	663-333	119.011	1040-1186	1352-1369		
CVFFS	12	21	Ī		107	66.63	1040-1186	1353-1389		
CVaria			i			11.02	1038-1184	135-1317		
CVPPR	1	_	i	22-420			10101	1350-1317		
CVPU			69.110	146-480	680-731					
CVE			124-158	161.509	665-679	10-95				
CVPRIM			374.331	464-500	165.670	116-963				
	ET CLYCOPROFEIN PRECURSOR (SPINE GLYCOPRO	12	69.610	146.480	166.049	187-921	1038-1184	28-287		
			18.102							
	PROPERTY OF MEMBERS OF YCOPROTEIN	Ī	100.341	\$1715	695.736	863.636	1043-1189	135-1303		
1	TO SELECTION OF THE COMMENT OF THE C			1007						j
200	E. G. T. Company of the Company of t	ī			0001					
	E3 CLYCOTROILERY PRECUESOR									
	E1 GLYCOPROTEIN PRICE VARIOR	7	60.5	1037-1031						L
VGL3 IBVK	ES CL VCOPROSEIN PRECURSOR	=	417-478	2	201.00					
20.00	ET CLYCOPROTEIN PRECURSOR		437-478	132-904	000					
3	ET CLYCOPROTED PRECURSOR	AND AND AND AND AND AND AND AND AND AND	13:00	139-162				-		
l	CLYCOPROTEIN B PRECURSOR			130.162	417.470	631.483	20.5			
1	GLYCOPROTEIN B PRECURSOR		120.000							
1.	CA VIOLEGIE IN B PAECUASOR		27.000							
1.	CL VOODOTETN B PRECURSOR		917.000							
	CONTRACTOR OF THE CONTRACTOR O	HEADES SINDLEX VIRUS (TYPE 1/STRAIN ROS)	8							
١	COSTON PRECIENCE	IOM)								
PVCLB IISV	CONTRACTOR DESCRIPTION OF PRECINE SOR		2							
١	C. VOORDOTEIN R PRECUASOR									
	CL VIOLED IN THE PARCUNSON	JERPES SINDLEX VIRUS (TVPE 27 STRAIN SAU)								
	CI VOOROTEN B	HERPES SINGLEX VIRUS (TYPE 6 / STRAIN UCANDA-1101)								
	CL VCOPROTEIN I PRECURSOR	BOVING HERPESVIRUS IVPE		100 070						
1000	CL VOOROTEIN B. I PRECURSOR	BOVINE IERPESTAUS TYPE 2 (STRAIN BNIV)						_		
	CI VIDENCE IN I PRECURSOR	BOVINE HERPESTAUS TYPE I (STRAIN COOPER)		1		-				
	CL VCOSED18 DA B PRÉCUBSOR	EQUINE HERVESVIAL'S TYPE I (ISOLATE HVST)A)				-				
	CLYCOMOTEON BPACCURSON	EQUINE HEAPE SVIRUS TYPE 4 (STRAIN (441)								
	CLYCOPOLENA PRECURSOR	EQUINE HEAPES VIAUS TYPE I (STRAIN ADI)								
	CLYCOPEDIED B PRECURSOR	EQUINE HERPESYING TYPE I ISTRAIN ABAP)								
	CLYCOPROLETY B PRECUTSOR	EQUINE HELDESVIAUS TOPE I (STRAIN KENTUCKY D)		1	187.845					
	CLACOPROTEIN B PRECURSOR	PLAKEN'S DISEASE ICEAPES INUS (STRAIN NO.10)				-				
	Ţ	HERPESVIAUS SABILITIESTRAIN II)			100	110.330	160-014			
	T	ANDINE CYTOMEGALOVIRUS (STRAIN SAUTH)							L	L
	ī	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKIJAUSER / DECKE						-		_
200	COLUMN TO THE PROPERTY OF THE	VALICELLA ZOSTER VIRUS (STRAÍN DUNIAS)	-	2			 			
15.C.C. 115.11	١	ILEAPES SINDLEX VIAUS (TVPE I / STRAIN IT)	55.50			-				
	ī	IERPES SLIDTEX VIAUS (TYPE I / STRAIN KOS)	66.5		-					
V.C.C. 115V.	GLY CORDIEIN C PRECIATION	IERDES SUCLEX VIRUS (TYPE 1)	2		_	<u> </u>	1	-	1	L
VCLC IISVI)	GLYCOPHOLEIN C PACK URSON	HEAPES SOULEX VIAUS (TYPE 27 STRAIN 333)	17.5					-		
PYCIC HISMBC	GL VCOPROTEIN C PALCURSON	MOVING HE RESVINUS TYPE I (STRAIN COOPER)								1
PYCAC HSYEB	١	FOLIDGE HERPESVIRUS TYPE I (STRAIN ABIP) AND (STRAIN KEN	1183-210			1	-			1
MUTCH SWIB	١	-	61-67						_	1
PVCLC HISMED	SECRETORY GLYCOPROTEIN GEST SE PRES	-	43.03					+		1
		_								

		-		A BFA 2	AREA	AREA	AREAS	AREA 6	. Y M C Y A	֝֝֝֝֟֝֝֝֝֝֝֝֝֡֝֝֝֡֝
	CONTRACTOR OF THE PROPERTY OF			NAME OF THE PERSON NAME OF THE P	-	Г	Г	Π		
1111111		KIIAUSER / DECKE	10.33							
	VCOPROTECT	VAUCELLA-20SIFA VIRUS (STRAIN DUALVS)	280-331						1	
	YCOPHOTEIN GPV	VAUCELLA. 20STER VIRUS ISTRAIN SCOTT)	160-131							
	YCOPACIEIN D PRECURSOR									
	GLYCUPROTEIN D PRECURSOR	RUN KEN	=:							
	VCHPAGIEIN D PRECERSOR	EQUINE MEMPESVIRUS TIPE I ISTRAIN KENTURKY A)								
	CH VCUPACIEIN E PRECURSOR	HERPES SINDLEX VIRUS (TVPL 11 STRAIN 17)								
	YCOPHOIEIN E PRECURSOR	SERVES SINDLEN VIRUS (TVPE 1)								
DATE BERNE	PUSION OF YCOPACIEIN PRECURSOR	BOVINE RESPIRATORY SYNCY HAL VIRUS (STRAIN ASSIGN)	146.702	304-343						
112VI	ILSKIN GLYCOPROTEIN PRECURSUR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGE	Ī	100	200					
2000 17:4	SHIN GLYCOPROJEIN PRECUASOR	POLINE ALSPIRATORY SYNCYTIAL VIAUS (STRAIN ABEA)	٦	267-302	20.50					
IGNSVI	IUSIUN GLYCOPROTEIN PRECURSIIR	_		160.181	364-603					
I IIASVA	SKIN GL YCOPHOTEIN PRECURSOR		_	261.102	506-549					
MSVL	DUSION CLYCOPHOTEIN PRECURSON			161.101	506-549					
13.00	SION CLYCOPADIEIN PAFFUMSOA		116.302	261.302	306-547					
NE ASS	TO ACCURATE VALUE OF THE CORPORATION OF THE CORPORA			267.303	506-349					
NE ASI	CONTRACTOR OF A CONTRACTOR CONTRA	9	11-11	328-268	432.500					
	CONTRACT VOORDOLESA PRECUESOR	ī	Ī	271-172	455.501					
, a you	SOL CE YCOPROLETY PRECESSOR	A[A-1]	11-11-	336-369	453.500					
MINDA	CONTRACT VEOPEDICIN PRECUBSOR	MUNIPS VIRUS (STRAIN SOL. 1)	20.50	101-179	105.272	447.502				
-	#05#00Je4 75#10#40U \ 10 700	MINUS VINUS (STRAIN MITTALIARA VACCINE)	20.54	101-179	115.77	447.502				
PROUS	CSON CLYCOPROTEIN PRECURSOR	AICHTS VIRUS (STRAIN AW)	20.54	103.179	115-272	447.502				
7.02	USION GLYCOPROTEIN PRECURSOR	AND DE VIRUS (STRAIN SOL)	10.54	101-170	335.332	447.503				
9,02	USION GLYCOPROTEIN PRECURSON	S (STRAIN AUSTRALIA VICTORIANT	13.113	211.372	436-513					
201702	USION GLYCOPROTEIN PRECURSOR	ETTE CAS)	133.163	111.171	436-517					
KDVIK			111.111	111.111	116-319					
2			-	111.111	426.919					
וימני אסער		NEWCASTLE DISEASE VIAUS (STRAIN ITALIENVS)		116.372	136-517					
_			٦	201-172	476-517					
PYCELF MOVO PL	USION CLYCOPROTEIN PRECURSOR			111.172	426-512					
	ISION GLYCOPROTE IN PRECUASOR	LANDW6)	1	100	225					
	FUSION GLYCOPROTEIN PRECURSOR		1	21:12	626-919					
	PUSION CLYCOPROTEIN PRECURSOR	NEWCASTI E DISEASE VILUS (STRAIN TEXAS G B AL)								
Vicin Miloso	DION GLYCOPROTEIN PRECURSOR		Τ	27.60	91. 44.					
Ī	TOSION CLYCUPACIEIN PRECURSON	VIRUS (STRAIN CIO)	Ţ,	103.343	199.70					
	PROPERTY OF THE PRESTY OF THE		T	477.528						
Ī	EURION CLYCOPACIEN PRECINSOR	(STRAIN GREER)		27.338						
Ī	FUSION GLYCOPROTEIN PRECURSOR	(STRAIN TOSHIBA)	9.15	111.538						
PVGLF PILIFE	USION CLYCOPROTEIN PRECURSOR		117.113	107-241	656-518					
_	USION CLYCOPROTEIN PRECURSOR	(STRAIN NIII (7115)		207.241	41.533					
Ī	USION GL YCOPROTEIN PRECURSOR	(DETE O)		114-165	(47-11)					
SENDS	USION CLYCOPROTEIN PRECURSOR		113-110	234.265	448-506					
SENDI	USION GLYCOPROTERN PRECURSOR	AUTANTS)	П	111-111	463-533					
	USION GLYCOPROTEIN PRECURSOR		П	111.331	463-533					
2	USION GLYCOPROTEIN PRECURSOR	USP		219-271	463-533				1	
PY CH I SEND?	USION GLYCOPROFERN PRECURSOR	9		Ĩ.	61-311					
Svei	USION GLYCOPROIETN PRECURSOR	IRAIN 2)		111:33	463-519					
SVS	USION CLYCOPROTEIN PRECUASUR			£4.50						
TREV	FUSION CLYCOPROTEIN PRECURSOR	SDITAN YAUS S (STRAIN W.)		2.33	431-487					
Pren G age v	FUSION CLYCOPROTEIN PRECURSOR		103-161	PE-374	457.442]	

	3,000	All Vieures (na bacteriaphoges)	ARCAI	ARCAI	ANTAL	OREA!	48542	ARTAS	744	1
PCG1.NE			ì	Γ						
117.24.11	THE PARTY OF THE P	E EPHENERAL FEVER VIRUS	Ī	104.13						
		VIRUS ISTRAIN CONTINUE	Ì						-	
- 1		_								
1001	NAME AND STREET OF THE STREET									
	MAJOR SURFACE OF TOTAL OF THE CO.	Ī								
	MAIOR SURFACE CLYCOROLLING	_	20.00			-				
PICIO IUSVS	MINIOR SURFACE GLYCOPROLEIM C		10.15							
:	MINIOR SIMPACE CLYCOPROTEING	CONTACT STATES OF THE STATES O	200		İ					
100	NIANOE SURFACE GLYCOPROTEIN G	ICAIAN RESPIRATORY STATE THAT THE STATE OF T	19.6							
	STATE OF YOUR OF BING	ICAIAN RESPIRATORY SYNCYTIAL VIRUS ISTACIN RECOVER								
	THE STATE OF THE S	HIBIAN BESPIRATORY SYNCYTIAL VIRUS (SUBGROUP BY STRAIN								
1	MANOR SURFACE CATTLE ACTION OF	THE AND SPRING TOWN STANCY THAL VIRUS (STRAIN A2)	20.00							
2	MIAKUR SLIRE ACE CL VCHPROTEIN G	A CALLED A COLOR OF THE PARTY AND INC. SCHOOL OF THE PARTY AND A CALLED	39.63		į					
	CONTRACT CH VOUTBOILING	IUNIAN RESPIRATORY STALTINE VINOS L'OUCON								
	THE PERSON NAMED IN COLUMN TO SERVICE AND ADDRESS OF THE PERSON NAMED IN COLUMN TO SE	CULINE HERFESVIRUS TYPE 4 ISTRAIN 1942)			1					
PYTH C SIGNA	CLYCUPROILING PALCONSON	34 TATA		100.00						
PYCE C SYNV	SPIKE GLYCOPROTEIN PRECURSOR		(11.53)	!						
973157	COLLE CLYCOPROJEIN PRECURSOR	SONCIALS TELLOW ME! SINGS	141.103							
	105 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VIRAL HENIORAHAGIC SEPTICENHA VIRUS (STRAIM PILLI)								
PICE C VSVIC	SPIKE GLYCUTHOLEIA PALCOTTO	STELLIN AR STONIATITIS VIRUS (SEROTVIE INDIANA / STRAIN C	476-310							
PVCI H EBV	SPIKE GLYCOPROTEIN PRELUASOR	PACATAL BARB CIBIN CATE AIN BOS.E.	33-67	160.301	136.360	20.100				
PVZ:141 DCMVA	GLYCOPROTEIN GPIS PRECURSOR	LIVELY BAND VINCE LOUIS AND ADDRESS OF A PARTY.	200	370-311	693.741					
ı	CI VIDER DIETA II PRECURSOR	ICHIAN CYTOMEGALOVINOS (STRAIN ACTOR)	Ī	203.300						
Ų	- CONT. 100 - 100	ILIPIAN CYTONIEGALOVIRUS (STRAIN TOWNE)							_	_
	G. YCOTROILE HI PACCUMSON	HERRE CAMPIER VIRUS (TYPE I / STRAIN 19)	447.481							
i	GLYCOPROTEIN H PRECURSOR	15 AC C 3 STOR C C	447.481							
1	CLYCOPROTEIN II PRECUASOR	HERVES SIMILLER VIAUS IN THE LAST COMME	143.404							
١	SON STATE OF	IEINES SINDLEX VIRUS (TYPE 6/ STICKIN CS)						L		
- 1		BOVINE HERPESVIRUS TYPE I (STRAIN COOPER)								
PICE II IISVE	GLYCOPROTEIN II PRECURSOR	COLUMN TISEDESYMBUS TYPE 4 (STRAIN 1942)	134.379	414.455		-				
PVCLT HISVED	CLYCOPROTEIN H PRECURSOR	COUNTY IN THE TANK I AT A ABAPI AND ISOLATE NV	117-111	407-448						
1	GLYCOPAOTEIN II PRECURSOR	EQUINE DERVESTANCE IN C. 1 (2)	79.5	334-453	664.912					
1	CI YCOPROTEIN IS PRECURSOR	IERPESYTRUS SATALIST (STRAIM 11)	***							
	CI VOORDIEIN IS PRECURSOR	ALUMINE CYTOMEGALOVIRUS (STRAIM SAILLII								
	CLASSOCIETY WINE CURSOR	PSEUDORABIES VIRUS (STRAEN RAPLAN)							L	
PVG. II PRVP		PSEUDORABIES VIRUS (SIRAIN MIA-3)	236-280							
PVG.H PRVII	CL TLUFAU EM IL TRELIDADO	SCELEVORANIES VIRIS (STRAIN BUCE)	236-360							
שיכון יצים	GLYCOPROTEIN H PRECURSOR	SCOOL STATE OF THE AND DIALES	455.306						_	
PVGL I ICNIVA		VAUCELLA-2031ER VINOS (311001) DOMINOS	1111	133.339						
100	INDIEDIATE EARLY GLYCOPROTEIN PRECURSOR	HAMAN CYTONE GALOVIRUS (STRAIN AUTO)		1	1736.1367					
NO.	CAPA CONDITION OF CHIEFOR	BUNYAVIRUS GERMISTON								
VCLN	ī	BINYAVIAUS LA CROSSE (150CATE L'14)	641-471	060-016						
PVGLM BUMSH	N POLYTROIEIN PACCOASON	DINY A VABILE SHOWSHOP HARE	£3.63							
PVCIN BUNDA	_	STATE OF THE PARTY	140.174	504-543	905-939					
PVCL NI DUCEV	M POLYPROTEIN PRECURSOR	BUPI ANIMERA VINCE	111.010	139-1300						
PUCLM HANTB	N POLYPROTEIN PRECURSOR	DUCE VIKUS	401.737							
HINAIL MICA	IN POLYPROTEIN PRECURSOR	HANTAAN VIRUS (STRAIN B.1)	200							
ILANII I	IN POLYPROTEIN PRECURSOR	HANTAAN VIRUS (STRAIN HOLD)						L		
1	Contraction to the Contraction t	HANTAAN VIRUS (STRAIN LEE)	51-22							
ACC PER PARTY	M TOLITAGE THE CONTROL	HANTAAN VIRUS (STRAIN 16-118)	2.10							
PVCI NI INSV	NI POL YPROIEIN PRECONSOR	INDEATIENT MECADING SPOT VIRUS	1047-1101							
PVGLM PHV	M POL YPROTEIN PRECURSOR	APPENDIX NITT VINITE	11:1							
PVGLM PTPV	M POLYPROTEIN PRECURSOR	TROSTEL TIME THOSE	149.231							1
PVGI M SEOUR	M POLYPROTEIN PRECURSOR	MINIA 10KU MEEUOVIKUS	1							
E ICEO	N POLYPROTEIN PRECURSOR	SEOLA VIRUS (STRAIM BUTY)	300			_				
STORY OF THE	N. POLYPROTEIN PRECUNSOR	SECUL VIRUS (STRAIN ICZ?)						<u> </u>		
2	MONETH INTITION OF YCOPROTEIN GNS PAECURSO	BOVINE EPIERIERAL FEVER VIRUS				1122.1334				
100	BERT ONER GLYCOPROJEDY PRECURSOR	BERNE VIAUS					-			
WOLK PRVD	SCHOOL VONDOTENCY	PSEUDORABIES VIRUS (STRAIN FUCE)	100 P					-		
VCL V JOHN	SECRETED OF TOURSDIEN PRECURSOR	ALNIN ALENAVIRUS	301.349							
PVGLY LASSG	1									

170000	XI MOTIS	Att Vieners (no batteriaphoges)					1000	, , ,	ABFA?	ARFAE
THE PARTY.	7.5.C.		P.V.	7070	7	9	Τ	Τ		
130000	GLYCOPROTEIN POLYPROTEIN PRECURSOR	VIRUS (STRAIN GA191)	27.760							
	CLACOPROTEIN POLYPROTEIN PRECURSOR		316.361	119.411						
1000	C. COSSOCIATION PROCESSOR	STRON	333-363	195.412					-	
	CI VOOPBOTEIN POI VPBOTEIN PRI CURSOR	_	134-156	111.367	303-412					
VICE V BIARV	CLI VCOPROTETH POL YPROTETH PRECURSOR		36-38							
2041	CI YCOPROTETN POL YPROTETN PRECURSOR	PICIUNDE AREMAVIRUS	334-375							
PVCI V TACVA	CI VODEDTEIN POLYPROTEIN PRECURSOR		115-363							
1000	CL YCOPROFEIN POLYPROFEIN PRECURSOR	TACANDE VIRUS (STRAIN VS)	303-331	277						
	CONTROL POR VAROTETA PRECITA SOL	TACALIDE VIRUS (STRAIN V?)	101-150	311-415						
מרג וארגו	CONTRACTOR AND VALUE OF COLUMN SECURIOR	FACARIBE VIRUS (STRAIN TRVL 11591)	303-151	111-116						
A LINE CANA	OF TOTAL STATE OF THE STATE OF		135-649							
LINE CANA	GENOME TOLITICAL IN	TOWNER A MANCAIT VIRING	160-301							
PYCHAI CPShiv	GENORIE POLYTROIEIN M	COWPEA SEVERE ADDIAGOUST STRAIN DG	10.20	150.702	114.918					
PVC,NAI ACAIV	CILINONIE PULTINIONINI		11.671	913-016						
אכיהו בסא	GENORIE POLYPROTEIN MI	70.007	94-149							
C EBOV	PROBABLE PLENBRANE APPLICEN OFF		260.321	334.368	469.503					
PVGP BIABVAI	STRUCTURAL GLYCOPROTEIN PRECURSOR	124001111111111111111111111111111111111	41. CO.							
PVGP MABVP	STRUCTURAL GLYCOPROTEIN PRECURSOR	MACCING VINOS (STANIN PIOSONE)	70.00							
PVIND VACCC	STRUCTURAL GLYCOPROTEIN PRECURSOR	MALBURG VIRUS (STRAIN PUPP)	200							
PVIIO3 VACCV	LAIE PROTEIN HI	VACCINIA VIRUS (STRAIN COPENITAGEN)	74-17							
PVIIO2 VARV	LATE PROTEIN 112	VACCINIA VIRUS (STRAIN WR)	10.00							
PVIDS VACCC	LATE PROTEIN HT	VARIOLA VIRUS	76-97							
PVIDS VACCV	PROTEINIS	VACCINIA VIRUS (STRAIN COPENTIAGEN)	19:13							
PULIDS VARV	PROFEINIS	VACCINIA VIRUS (STRAIN WR)	110.105							
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PROTEINE	VARIOLA VIRUS	136-203							
A VACCO	PROBABLE HELICASE	LILY SYAPTOAR ESS VIRUS	136-160							
VACCV	HOST BANGE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	216-279							
AVIOLA VACCO	TOST BANCE PROTEIN	VACCINIA VIRUS (STRAIN WR.)	216-179							
AUG AVE	PROTECTION	VACCINIA VIRUS (STRAIN COPENHAGEN)	26.193	210-244						
PVIOI VARV	PROJECT	VACCINIA VIDUS (STRAIN WR)	150-193	210-244						
PVIDE VACCV	PROJEINI	VALIDLA VIRUS	18 19 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	210.246						
PVIOS VARV	PROTEINIS	VACCINIA VIRUS (STRAIN WR)	20.03							
PVIOT VARV	PROTEIN	VARIOLA VIRUS	2							
PVIDS VACCC	PROTEIN I)	VALIOLA VIRUS	113-407							
PVIDE VACCV	PUTATIVE RNA IELICASE ID	VACCINIA VIRUS (STRAIN COPEMIAGEN)	2							
PVIOL VARV	PUTATIVE RNA IELICASE II	VACCINIA VIRUS (STRAIN WA)	944-519							
PVIET RCMVA	PUTATIVE RNA IELICASE IS	VARIOLA VIRUS	¥.50							
PVIET BICKLYT	SEKD DOCEDIATE EARLY PROTERVI	INDIAN CYTONEGALOVINUS (STRAIN AD169)	2	20.70	200	Q Y				
PVIET MCMVS	55 KD INDIEDIATE-EARLY PROTEIN I	HURIAN CYTOMEGALOVIRUS (STRAIN TOWNE)	2	6		476-4X0				
PVIET NIVOP	INDLEDIATE EARLY PROTEIN I		14.20							
PVIEW MPVAC		7		20.00						
PVIF CAEVC	U.D.(EDIATE.EARLY REGULATORY PROTEIN IE-N	3	100-110							
PVIF FIVE	VINION INTECTIVITY FACTOR	CATANE ATTOUTS ENCEPHALITIS VAUS (STRAIT CORK)								
PVIF FIVSD	VINION INTECTIVITY FACTOR	PELINE INSCRIPTION OF THE STANDARD OF THE STANDARD	K							
PVIF IIVIAZ	VINION ING ECTIVITY FACTOR	FLINE WAIGHOUTHERLY VIACS (ISOLATE SAN DECO)								
PVIF IIVIBI	VINION INTECTIVITY FACTOR	HUNKA INDICATE FICENCY VINUS 1 TPE 1 (ANY DST 1304.A TE								
PVIF IIVIDS	VINION INFECTIVITY FACTOR	THE PROPERTY OF THE PARTY OF TH		7						
PVIF IIVIEL	VILLON INTECTIVITY FACTOR	MORAN INDICATE THE TANK I TOTAL (1973 INC. ATE.)		2 3						
PVIF IIVIN	VIATOR INFECTIVITY PACION	MARKA MANAGERICENCY VIRISTYDE I INCEPTOR ATE	1 3							
PVIF HVIRIA	VIRION INTECTIVITY PACION	THE ALANDON FILENCY VINIS 17FE 1 (MAL. 150LA 1E)								
All divi	VINCENTY FACTOR	L	7	2.5						
CHAIL HALL	VINDOW DATECTIVITY FACTOR	ğ	7	2						
PVIP IIV	VINUA INTECTION I COSTO									

FCGENE	IALLMOTIS	ses for berterlegheger)	NATA I	AREAT	AREAJ	AREA	ABEA?	ABKAS	OREAL	1858
!	CROICIN	Mary Alexander	ī	(Γ	Γ			
ONIAI IIA	VIBION INTECTIVITY FACTOR	ı	Ī	3						
	VIRION IN ECTIVITY FACTOR	Ì	1	10.00					-	
l	VINION IN ECTIVITY FACTOR			1	-					
İ	VIRION IN ECTIVITY FACTOR	_								
ĺ	VIRION IN ECTIVITY LACTOR	HINIAM INVITINDDEFICIENCY VIRUS TYPE I ISTRAIN DUANNAME								
	VIRION IMPECTIVITY FACTOR	HANNA BARILMODEFICIENCY VIRUS TYPE 1 (21CTIC-2) JISOCK								
1000	CHICATOL PARTY OF TOTAL		Ī							
	TOTAL SALES CONTRACTOR OF THE PROPERTY OF THE	1	103.195							
IIV IIV		IRNIAH INBRANDESICIENCY VIRUS TYPE 3 (150LATE NSILZ)	183-193							
PVII 11V2RO	VINION IN ECCUPATION	THE ALL PACHETER OF VIEWS TYPE 3 (SOLATE ADD)	161-191							
PAIR DAIVYS	VIRION INTECTIVITY FACTOR		-							
PVIE SIVAI	VIBIGIN INTECTIVITY FACTOR	OVINE LEWINING (STRAIN SALONING CO. 175)	Ī	140.707						
PVII SIVAG	VINION IN ECTIVITY FACTOR	SINITAN INDICHODE FIETENCY VIRUS (ACHIES) ISCLATE!	Ī							
STATE SIVE	VISION DA ECTIVITY FACTOR	-	Ì							
	COLUMN CONTRACTOR AND TO BE SEEN THE PROPERTY OF SECURITY OF SECUR	CLONE CA	.16	5-13						
NA PARA		STATIAN TANDAMORFICIENCY VIRUS (TYO.) ISOLATE)	10-11	50.103						
23.00	VIETON IN THE LINE OF THE PROPERTY OF THE PROP	CHAIR AND GE INTRIBUDES ICTENCY VIRIS	7							
PVIS SIVEB	VINION IN ECTIVITY FAL TOR	CHIEF STATE CONTROLL CONTROLL AND CANAL	=							
PULL HISVII	VINDON INFECTIVITY FACTOR	SIMILAN INCHIDENCE THE CONTROL OF TH								
PVIND HISVED	PROBABLE INTEGRAL MENDRANE PROTEIN	HEAPES SINDLEX VIXUS (TYTE 1/51ILALIV 17)	T.	***						
PVIND HSVSA	PROBABLE INTECRAL NENDRANE PROTEIN	AIN ABAP)								
500	INTELLIAL MENDRANE PROTEIN		٦							
7	PRODUCE PATECOAL LICENSEANS PROTEIN	4 DUNIAS)		13710	147.301					
LAIK! SSA!	Trought With the		13.130	21:12						
PVIDI VACCC	PRUBABLE INTENANCE	VACCINIA VIBILE (CTBAIN COPENCIACEN)	2.2							
PVIDI VACCV	FROIEIVI	TOTAL VIOLET CLEAN WELL	35.50							
- 1	PROTEIN	VALCINIA VINOS (STINATIVA PA)	25.50							
PVK03 VACCC	PROTEIN	WANDLE VIEW AND COREMINACEM	19.63							
١	PROTEINKI	VACCINIA VIAUS (STANIA COTEMINALIA)								
Ì	PROJEINKI	VACCINIA VIADS (STANIA WA) AND ACTEAN COPENIACEN	13.140							
PVL03 VACCC	PROTEINKY	Ī	11.0							
PVL03 VACCV	PROTEIN L1									
PVL03 VARV	PROJETY L2	(STRAIN WR)								
PVLI CRPVK	PROTEINLY	VARIOLA VIRUS	T							
	PROBABLE LI PROTEIN	APILLONDAVIRUS (STILLIN KANS								
PVLI 10 VOS	PROBABLE LI PROTEIN	AVIAN PAPELLOMAVIRUS 19V-L	R							
	PROBABLE LI PROTEIN	HIMAN PAPILLONA VIRUS TYPE S	135-383							
	PROBABLE LI PROTETN	HIDNAN PAPILLOMAVIRUS TYPE I	74.70							
1	PRODABLE LI PROTEIN	INDIAN PAPILLONIAVIRUS TYPE IA	345-170							
l	PROBABLE LI PROTEIN	US TYPE 47	157.191							
PVI. REOVO	PROBABLE LI PROTEIN		1							
PVL2 IUPVOS	NIAJOR CORE PROTEIN LANGEDA I	REDVIAUS (TYPE 3 / SIRAIN DEARING)	٦	117.6						
	PROBABLE LI PROTEIN	HUNIAN PAPILLOMAVIRUS TYPE	141.333							
	PAOBABLE L3 PROJEIN	HIBIAH PAPILLOMAVIRUS TYPE I	154-343							
	PROBABLE L2 PROTEIN	INDIAN PAPILI GMAVIAUS TYPE 16	145.333							
	PROMABLE LI PROJEIN	HUNIAN PAPILL CIMIA VIRUS TYPE IA	345-379							
	PROBABLE LY PROTEIN	HUBIAH PAPILLOMAVIRUS TYPE 11	166-326							
	PROBABLE L3 PROTEIN	INDIAN PAPILLOMAVIRUS TYPE 35	183-333							
1001	PROBABLE LI PROTEIN	HIDIAN PAPILLONIA VIRUS TYPE 47	341-375							
PV 1 HPVSB	PROBABLE LY PROTEIN	HIDAAN PAPILLONIAVIRUS TYPE SI	763-327							
0,01	PROBABLE L3 PROTEIN	HUMAN PAPILLOMANTRUS TYPE SB	141.175							
PVI 3 REOV3	MINOR CORE PROJEIN LANGEDA 1	REDVIRUS (TYPE 3 / STRAIN DE ARING)	107-146	2						
PAL REOVE	NINOR CORE PROTEIN LANGEDA 3	REOVIRUS (TYPE 2 / STRAIN DIJIONES)	-1							
PVL W LAVI	MINOR CORE PROTEIN LANGON)	REDVINUS (TYPE I / STRAPH LANG)	٦	20.163	2113-6113					
PANOL VACCC	LA PROTEIN	TIPURA INDESCENT VIRUS	146-180	141.374						

.:

7676	ALCAIOTIS	All Viveus in Beriefing and 11	Ì	Ī					I	
P.C. PARIE	PROTEIN		ABEAL	ABEAL	7578	SEAS	252	4854	245	ALLA
II REDVL	PROTEIN ALI	AGEN	2							
PUNIT REOVU	MINOR VIRION STRUCTURAL PROTEIN MU.3		Ī							
111 REOVD	ALAIDA VIRION STRUCTURAL PROTEIN NO. 1/AIU-10			619.619						
PUNI REDVI	MAJOR VIRION STRUCTURAL PROTEIN MU. 1A(U-1C		416-450	011.662						
PUNI REOVE	AIAIOR VIRION STRUCTURAL PROTEIN MID-IMID-IC	REOVERUS (TYPE 2/STRAIN DEJONES)	019-910	616-642						
PVN1 REOVD	MAJOR VIRION STRUCTURAL PROTEIN MIU. IMIU-IC	REOVIRUS (TYPE I / STRAIN LANG)		611-662						
PVAIAT BRSVA	ALAIDA NONSTRUCTURAL PROTEIN AIU.NS	REOVINUS (TYPE) / STRAIN DEALING)	13.190	107.00	\$13.538	618-490				
PUNIAT HRSVA	MATRIX GLYCOPROTEIN M2	BOVINE RESPIRATORY SYNCYTIAL MRUS (STRAIN ASINO)	8.2							
VAIA2 TRTV	MATRIX GLYCOPROJEIN MI	HURIAH RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	04:07							
WHAT COVO	MATRIX GLYCOPROTEIN NIZ	TURKEY MIINDTRACIEITIS VIRUS	16.70							
1000	750000000000000000000000000000000000000	CANINE DICTEMBER VIRISACTBAIN ONDER CIEPODRIA	101.114							
	PIA INIA TRUITIN	CANANT COLUMN AND COLUMN COLUM								
AND AND A	MAINTE (NI) PROTEIN	INTELEGIZAC STRUM CIMIN		207.10						
VALAT NOVD	PIAIRIX PROIEIN	NEW CASTLE DISEASE VIRUS (SIRAIM AUSTRALIA, VICTORIA, DI	200				-			
VALAT PIJB	MATRIX PROJEIN	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	124-158							
PYSIAT PUM	MATRIX PROTEIN	BOUNE PARAMILLENZA I VIRUS	M-113	104-152						
VAIAT RABVA	NIATRIX PROTEIN	HUNTAM PARAINTLUENZA I VIRUS (STRAFY NIH 47815)	1111	101-153						
PUNAT BABVE	MATRIX PROTEIN	i i	101.01							
AT BABVE	NIATER PROTECT		10.10)							
AND DE			10.04							
			101.03							
******			101							
5										
NAT PANA					-					
NIAI VSVIC		_								
MEI CVBM		FL INDIANA VSTRAIN								
CARL CARS			Ī							
		_		111.111						
L. CLARK	EL C. T. OFROIEIN PRECURSOR	PORCINE TRANSMIDLE GASTROCATICATIS CORONALIRUS (S)	66.2							
VAIL CVINE		INDS (STRAIN ENIS)								
110				35.30						
	EL CLIVENIEN PRICLASOR									
7.(6) (9)		Ť	Ī	177.218						
PARE BAR			٦	77.318						
E BVE		161	٦	17.211						
7 XII XI EBY		US (STRAIN KBBSB)								
אוא נאוננ	E PROTEIN		٦							
PAND CANNO		CALL IT LOW ER ANDSAIC VIRUS (STRAIN CNI-1041)	٦	120.02						
CAME				170.134						
CAIS	MOVEMENT PROTEIN			170.314						
PI VIP CANIVS		CAULIFLOWER MOSAIC VIRUS (STRAIM NYBISS)		170.134						
PIND CANIVA				270-324						
PLYED CERV		IRAIN W260)	_	130.134						
PINIP PAIVO		CARMATION ETCHED RING VIRUS	313-346							
PUND SOCKIV	MON ENIENT PROTEIN		187:181							
PLAISA IPBDB	MONEAGNI PROTEIN		16-110							
VAISA IDEDC		DUCK IEPATITIS B VIRUS (BROWN SITANGITAL DUCK ISOLATE S	11:11	136.361						
VAISA IDBOU		_	111.111	33).360					İ	
NORTH TOTAL	PIANON SUMFACE ANTIGEN PRECURSOR	-	316-375	110.323						
NISA IDBGS	MAJOR SURFACE AMINGEN PRECURSOR	UNGITAL DUCK ISOLATE ST	111:44	134.341		Ī			İ	
VAISA POBILE	MAJOR SURFACE ANTIGEN PRECURSOR	IIIS VIAUS	210-244							
SA WITVE	MAJOR SURFACE ANTIGEN PRECURSOR		294-328							
THEA WHIVE	MAJOR SURFACE ANTIGEN PRECURSOR		106-343							
TICA WITY	MANOR CITY ACE ANTICEN PRECITATOR	ACCORDING MEDITAL VIBILS OF						Ì		

12000	141.1310719		Ì							
1	PRODUCING THE PROPERTY OF THE		02:01							
THE WHY I	MAJOR SUTFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATHIS SINGS	1 25:11							
TAIN DIVIN	PROBABLE NIAJOR SURFACE ANTIGEN PRECURSOR		50.10				Ì		-	
NAME OF STREET	MATRIX PROICIN !	S (STRAIN INDIAN/1317-61)	!	111						
PANEL LANA	NATIONAL INTERPRETATION		ī	11.11						
PVNIII IACAO	MINIMINI PROFEIN	NE UENZA A VIEGO (SIEGO A AZ ANTI A BONGOLIATO)							1	
VOID 100%	VIAIRIX (NEI) PROILIN		11.13	14.22						
	II (NII) PROIDIN		971.50	111.111						
Will tark	VIATRIX (NII) PROTITION	NI CUITA A VINOS CARACTORIO PI ACUE VINUSANIO P	ĺ	14.211						
	MAIRIN (MI) PROTLIN		92:20	114-111						
12.1	NATELY (NIL) PROTEIN	533	93.136	114-223						
NI NY I	NA JAIN (NII) PROJEIN	13018	!	14.333						
1	MAIRIX (MII) PROTEIN	Ť	3:136	3.5						
İ	NATRIX (SII) PROTEIN		93.126	14-311						
00.141	MATRIX (BIL) PROTEIN	ATOMIC MODEL	I	74-222						
TWEE TANK	MAINIX (NI) PROTEIN		Ī	34.333						
	ALBERTALI) PROTEIN		Ī	74.222						
	NIATEN IND PROTEIN	-								
200	N. T. S. S. S. S. S. S. S. S. S. S. S. S. S.	-								
OVER LINE	National State of the State of	_	\$ 1							
1190	National Property of the Party	INTLUENZA B VIRUS (STRAIN BAED40)	3							
12021 12021		7	1			-				
LYES ENGL	MAINING THE PROPERTY OF THE PR	ωŤ	*			-				
DANIE INDA	PROBABILE MALENA (PROPERTY)	INTLUENZA B VIRUS (STRAÍN BJANN AUBONJING (WILD-TYPE))	2			-				L
PVIII INBLE	PROBABLE MAINA (PLI) PROTEIN	THE LIENZA D VINUS (STRAIN BLEDA)	2							L
PANT INBSI	PROBABLE MATEUX (PLA) PROTEIN	ORE/211/19)	اء							
PWILL MYXVI.	PROBABLE MAININ INITI THOISEN		Ī	165.107						<u> </u>
N. S. B. VACCO	N. 10 FROIEIG	EN)	=							
PVK01 VACCV	TACITOR IN THE PROPERTY OF THE									
FV. 14 RO185	TAULE IN THE SECOND LANGEST AND ACTUAL TO SEC	/ STRAIN SHINTOKU)	1							
PVX14 ROTPC	NOW STRUCTURED THE PROPERTY AND ADDRESS OF THE PROPERTY AN	C / STRAIN COWDEN)		\$:-						
PUNCA AAVI	NONSTRUCTURAL PROTEIN		Ī	3.3						
PINCA RSV	DNA M. PLICATION PROTEIN	INCE STUPE VIRUS	130-163							
PLYCH PAVEO	MACON PACIFICACION PROTECTIVA	BOVINE PARVOVIRUS	<u>.</u>							
N.K.S. ADVG	TACOMORE POST OF THE PAST OF T	ALEUTIAN MINK DISEASE PAR VOVIRUS (STRAIN G)	Ī	20.00		95.	979.01			
PVNCS AEDEV	NOTE OF THE PARTY	AEDES DENSONUCLEOSIS VIRUS (STRAIN GKV 002 002)	276-319	11.57	363.040	2				
ANCS IDAIA	NOW AND PROJECT AN	FELINE PANLEUKOPENIA VIRUS (STRAIM 193)	33.00							L
VKCS MEVA	SACRET SECTION AS .	MINK ENTERINS VINUS (STRAIN ABASHIRI)	3.5							
PVKC PRICERIA	MONTANCE DEDICE NAS-	ANJRINE MINUTE VIRUS (STRAIM MIVALI)	19.61	2		1				
VAC S BILDERIN	MONTAPED PROTEIN NS.1	ATUMUNE MINUTE VIRUS	13.00	138-161						L
NIA STAN	PROBABLE NONCAPSID PROTEIN NSI	BOVINE PALVOVIRUS	777					L		
MILY A SURVE	NOW APSID PROTEIN MS.1	CANINE PARVOVIRUS (STRAIN M)								
PVACS PAVILLE	NONCAPSID PROTEIN NS.1	HUBIAN PARYOVIRUS BIR		160.307						
PVKCS PAVPN	NONC APSID PROTEIN NS.1	HANISTER PARVOVIRUS TO		140.310	104.146					
NAME OF A	NONCAPSID PROTEIN MS-1	PORCINE PARVOVIRUS (STRATIN MADIC-1)								
PVINSI BIVIT	MONSTRUCTURAL PROTEIN HS!	BLUETONGUE VIRUS (SEROTYPE 197150L 41E USA)								
PVKSI BIVIA	MONS IRUCTURAL PROTEIN MS!	DICETONGUE VIRUS (SEROITYE 17/150LATE USA)	103.14			-				
PVNS: BIVES	NONSIAUCTURAL PROTEIN MS	BLUE IGNGUE VIRUS (SEROI TYE I / 1804 ATE COLITH ABBICAL	103.141							
PVNSI BIV20	MONSTRUCTURAL PROTEIN NS!	BLUE I GRACE VIRUS (SERVIT ITE VI ISOLATE SCOTTE SELECTION OF SELECTION AT SELECTIO	101-141							
PVNSI EIDV?	HONSINUCTURAL PROTEIN WSI	REUE TOWARD VIRUS (SEND) 17 E EST SEROS YPE 3 STRAI	~							
PVNSI IAAM	MONSTRUCTURAL PROTEIN NS	PART (FRAZA A VIRIIS (STRAD) AANNI ARBORANO)	-							1
PYNSI JACAO	MONSTRUCTURAL PROTEIN MS1	DOLUGEZA A VIDIR ISTRADI ACAMELA: DAGOLIANI	15.16							4
PWNSI IACKG	HOMSTRUCTURAL PROTEIN NSI	בארסניאלא א ייייביי								

	ALLAKO 119	All Virutes (no betteriopheges)	Ī		ABEAS	1000	Aura	ABY 3	ARFAG
HE KANK	CROIFIC	CONTRACTOR AND AND AND AND AND AND AND AND AND AND		Ī					
PVKSI IACKI	NOWSTRUCTURAL PROTEIN MS	Ì	3						
	MONTH AND TOWN TO SEE THE PROPERTY AND T	3	1						
TO THE PERSON NAMED IN COLUMN 1	MONETHER AT BROTEIN ME		9						
PVNSI IAFOAI	NONSTRUCTURAL PROTEIN NS		46.20						
VNSI IAFOW	HONSTRUCTURAL PROTEIN HS!		19.00						
VANSI TATPA	NONSTRUCTURAL PROTEIN NSI		10.01						
PVMSI IALEI	HONSTRUCTURAL PROTEIN NS!	ISA OS TOCK	19:01						
PVNSI IALEM	HONSTRUCTURAL PROTEIN HS!	7)	11.13						
WEST TANIAL	MONSTRUCTURAL PROTEIN MSI		10.01						
PVIVSI TARLAN	HONSTRUCTURAL PROTEIN NSI	TANENS	10.11						
PVS:SI PANAO	NONSTRUCTURAL PROTEIN NST		19:01						
2	NONSTRUCTURAL PROTETY MST	INFLUENZA A VIRUS (STRAIN AMIALLARDINE IN YORKMSTATE	69-13						
PVNSI JAPIO	NONSTRUCTURAL PROTESY NSI	Г	66.10						
PWSI LAPII	MONSTRINCTURAL PROTEIN NS!		19.67						
	NONSTRUCTURAL PROTEIN NS!		10.07						
PVS LOS	NONSTRUCTURAL PROTEIN NS		10.11						
2	HONSIAUCTURAL PROTEIN NSI	158/78)	10 67						
PVNS1 IATKO	NOWSTRUCTURAL PROTEIN NS!		(1.1)						
PVNS INTRC	MONSIAUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN ACTURKEYMETICLEHENI-GLILITMA	10.01						
PASS INTER	NONSTRUCTURAL PROTEIN WS!		11.11						
PASS IAIRS	PONSIAUCTURAL PROTEIN NSI		19:00						
IATRI	NONSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS ISTRAIN ACTERIASOUTH AFRICASI	16.10						
PVNSI IAZII	NONSTRUCTURAL PROTEIN NS	(LIVE)	(8-8)						
VNSI MBAC	MONSTRUCTURAL PROTEIN MS1	INTLUENZA A VIRUS (STRAIN ASWINEAOWA/19/19)	(8.6)						
PUNSI INBGA	NONSTRUCTURAL PROTEIN MSI		143-133						
×	MONSTRUCTURAL PROTETIFINST	INTLUENZA B VIRUS (STRAIN BIGATA)	143.133						
VNSI_INBIET	HONSIRUCTURAL PROTEIN HSI		=						
ORNI ISBNO	HONSTRUCTURAL PROTEIN HS	B VIRUS (STRAIN BATTRA)	10:11						
VNSI DOLE	HONSTRUCTURAL PROTEIN HS!	B VIRUS (STRAIN BADA6)	13.13						
PVKSI INGADO	MONSTRUCTURAL PROTEIN NS!	D VIRUS (STRAIN DA EE/40)							
PVNSI DABPA	MONSIAUCTURAL PROTEIN MSI	GALCENZA B VIRUS (STRAIN BAICATLANGYS)	Ī						
PANSI INDICO	MONSTAGE DAYS PROTEIN NS								
200	MONCHE LITTER AT PROCESS MAC	POREMINE							
PVNS1 DON'S	MONSTRUCTURAL PROTEIN NS			Ī					
PVNSI DIBYA	MONSTRUCTURAL PROTEIN WS!		100						
PVNS1 AJISV9	MONSTRUCTURAL PROTEIN NSI	(2)	10:111						
VINS2 BIVI?	MONSTRUCTURAL PROTEIN NS	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 9)	67.103						
PVNS1 BTV1X	NONSTRUCTURAL PROTEIN NS3	ISOLATE USA)	201-137						
PVNS1 CVIAIN	HONSTRUCTURAL PROTETH MS3	BLUETONGUE VIRUS (SEROTYPE 10)	103-237						
PVNS1_EIDDV1	HOMSTRUCTURAL PROTEIN HS2		71.105						
PVNSI JAALA	HONSTRUCTURAL PROTEIN MS2		104-172	276-311					
PVHS1_IAANA	NONSTRUCTURAL PROTECN NS2		14.93						
VNS1 IAANN	NONSTRUCTURAL PROTEIN NS2		14-93						
VVS3_IACHI	NOMSTRUCTURAL PROTEIN NS2	INTLUENZA A VIRUS (STRAIN AVANN AUBONÓVO), AND (STRAIN I	16.93						
VNS1 IACKG	HONSIAUCTURAL PROTEININS		16.93						
PVNS1 IACKI	NONSTRUCTURAL PROTEIN MS2	Uneel	14.30						
PVNS1 IADA3	HONSTRUCTURAL PROTEIN MS2		9						
VNS2 (ADE)	HOMSTRUCTURAL PROTEIN MS2		2.2						
PVNS2 LADUS	HONSTRUCTURAL PROTEIN NS3		8						
14694 14694	INCINCIPLE TO A SECOND LANCE	DATUENZA A VIRUS ISTRAĽS ANDICKARRANEJIAN							

MALES MALE			The state of the s	Ī	Т		7.00	4864.5	AREAS	AREAI	AREAJ
ADDITIONAL MODERNAL		ALLAIOTIS		Ī	Ī	1	Τ	Г	П		
MODEL MODE	2115	ZB1087	NZA A VIRUS (STRAIN AFORT MONMOUTIVIAT)		1	i					
ADDITIONAL PROTEINS ADDITIONAL PROTEINS ADDITIONAL PROTEINS ADDITIONAL PROTEINS		MONSTRUCTURAL PROTEIN NST		-		-				-	
PROFITE CHALL FROITE WITH WILLIAGE A VILLE (TALKA ALERGACADEW) 127	i	NOWSIRUCTURAL PROTEIN NS		=							
MODITION OF HOLES WITH MILESTAL A VILLE STATEMENAL PROPERTY 11.75	١.	NONSTRIKCTURAL PROTEIN NST	_	3							
NOST SECTIONAL POOLINES NOST LUCKOLAN POOLINES NOST SECTION	VINST IALEN	NONSTRUCTURAL PROTEIN NS		<u> </u>							
MOST INCULUAL FOOLER'S MOST INCULUAL FOOLE	VNS7 IAMIA6	HOWSTRUCTURAL PROTEIN NS	ا	=							
NOWS INCULUAL FOOLIN NO.	WHST IAMAI	HONSTRUCTURAL PROTEIN NS		1 2							
NOOSISTECTIONAL POOLINE NO.	NAIS IANIAN	NONSTRUCTURAL PROTEIN NS	=			į					
NOORS INCULOUS, PROTEIN NO. PRILINGS A. VILLOS STEAM ALLESSE VAILED	VYS1 IANIAO	NONSTRUCTURAL PROTEIN NS	⋍	(6)	-						
NOOST INCULTAL POLICIES NOT	WALLAND LAND	NOWSTRUCTURAL PROTEIN NS2	INTEREST A TIME OF THE PARTICIPANT DATE OF THE PARTICIPANT OF THE PART	2							
MONST INCUITAL POLICIES	VANCE LAPIG	MONSTRUCTURAL PROTEIN MSZ	Ī	-							
MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE LATER) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MOTLEREA A VIRUS (STAND AVERALALISE) 151 MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTUOAL PROTEIN STATEMENT MONSTRUCTU	THE CONTRACT	MONSTRUCTIONAL PROTEIN NS2	Ī	2							
The control of the	TO SENA	CONTRACTOR AL PROPERIN NS2	Ī								
MORNING TO ALL POOLINES MORNING THE MAY A WING STAND A VALUE STAND A	VNSZ IAPIZ	STATE OF STA						L			
MOST INCULAL PROTEIN	PVNS1 IAPUE	NONS INC. LOWAL THOUSAND	_	-	Ì						
PROPERTING TUALAR PROTERNING PROPERTING TO A PROPERTING TO A PROPERTING TUALAR PROTEIN NAT.	PVNS2 IATE	NOWSTRUCTURAL PROTEIN 755		2	i						
MONSTRUCTUAL PROTEIN NS. PROTEIN NS. PROTEIN NS. PROTEIN NS. PROTEIN NS.	PVNS1 IATER	HOWSTRUCTURAL PROTEIN MS.	DATE OF A VIRUS ISTRAIN ATURKEYORE CONTI	1.3	1						
MONES INCTITUAL FOOTEN WEST MOTERATE A VIRES STEAM ACASSEMPT! 14.10 19.119	PVNS2 IATRS	HOMSTRUCTURAL PROTEIN NSS	CONTRACTOR OF THE PROPERTY AND CAME!	22	-						-
MONST STACE TO ALL POSTERN HAS MONST STACK TO ALL POSTERN HAS	VNS2 IAUSS	HOMSTRUCTURAL PROTEIN MS3	DOLUGIA A VIDOS (SER A PA A A RICE AND 3)	1.0							
MONSTRINCTIONAL PROTEIN MAY MONTENANCALAMINI) 1-41 19-119	PANS DABLE	NONSTRUCTURAL PROTEIN MS2	INCLUENCY A VIRUS LATER AND AND AND AND AND AND AND AND AND AND		•						-
MONSTRUCTULAL PROTEIN NST MOSTERA C VARUES STRAND COLORA NEEDS MOSTER NST	AVEC :0344	HONSTRUCTURAL PROTEIN MST	INCLUENZA B VIRUS (STRAIN PACEDO)		110						
MONSTRUCTURAL PROTEIN 151 MONSTRUCTURAL PROTEIN 151		MONETHICITAL PROTEIN NS	DOLLENZA B VINUS ISTRAIN OF TANAON IN 19	10.1							
MONSTRUCTURAL PROTEIN NYREARONA VIRUS OF MACE MONSTRUCTURAL PROTEIN MACE MACA HOUSE STCRESS VIRUS (SEROTYPE 5) MACA HOUSE START STCRESS VIRUS (SEROTYPE 5) MACA HOUSE START STCRESS VIRUS (SEROT		MONG BLICTICAL PROTECT NS3	INGLUENZA C VIRUS (STRAIN CUIVO)	100							
NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 17.10 15.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTURAL PROTEIN A JULICAN HORSE SICKNESS VIRUS SEROUTES 1.11 NONSTRUCTU	100 CM	SOCIETY BY PROTEIN	PINEUNIONIA VIRUS OF MICE	Ī	1						
NONSTRUCTURAL PROTEIN WS) AFRICAN HORSE SIGNESS VAUS SEROTYPE 9) 14-19 102-147	VNS) Alisvi	POTENTIAL PROTECTION	AFRICAN HORSE SICKNESS VIRUS (SEROFYPE 3)	Ī	Ī	41.315					
MONSTRUCTURAL PROTEIN MONSTRUCTURAL PROTEIN 1 1 1 1 1 1 1 1 1	PVRS) AHSVV	TOTAL STATE OF THE PROPERTY AND THE PROP	AFRICAN HORSE SICKNESS VIRUS (SEROTVPE 9)	Ī	T.						
MONSTRUCTURAL PROTEIN 3	PVHS3 BRD	TOTAL TOTAL PROPERTY IN	BROADHAVEN VIRUS	1							
MUNISTRUCTURAL PROTEIN MAINAM CORONAVMUS (STRAIN KT)19 11-47	PVNS) CVPFS	ACM INC. LOS AND BELLEVILLE IN THE PROPERTY OF	PORCINE TRANSMISSIBLE GASTROEMTERJTIS CORONAVIRUS IS	-	İ						
MONSTRUCTURAL PROTEIN NST ALCE STARTE CARGNAVRUS (STALIN K.191) 1-4	PV-SS CVH33	202 14 C 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HUNIAM CORONAVINUS (STRAIN 139E)								
MONSTRUCTURAL PROTEIN CANING ENTERIC CORONAVRUSISTIAN R-1441 143	P. N.S. BSV	AND AND AND AND AND AND AND AND AND AND	ALCE STAIPE VIAUS	-	İ						
MONSTRUCTURAL PROTEIN	NAS CACAL	MISTORY IN THE PROPERTY OF	CANINE ENTERIC CORONAVIRUS (STRAIN KIND)	1	İ						
NONSTRUCTURAL PROTEIN	200	TOUR THE PROPERTY OF	FELINE ENTERIC CORONAVIRUS (STRAIN 76-1643)		İ						
MONSTRUCTURAL PROTEIN C	11 A SA	N. S. C. S.	FELINE INTECTIOUS PERSTONITIS VIRUS (STRAIN 79-11-4)								
MONSTRUCTURAL POTEIN C NEASTES VIRUS (STANIN FOLO) 1514	PVNSC CDVO	CALL CONTRACTOR OF THE PARTY OF	CANINE DISTEMBER VIRUS (STRAIN ONDERSTEPOORT)			ŀ					
NONSTRUCTURAL PROTEIN	PUNSC MEASE	TOUR THE PROPERTY OF THE PROPE	LIEASLES VIRUS (STRAIN EDATONSTON)	-	Ì						
NOWS INCLUDAL PROTEIN	PVWSC MEASI	MONSTAC LONG TO THE PROPERTY OF THE PROPERTY O	LEASLES VIRUS (STRAIN IP.) CA)								
	PUNSC MEASY	NONSTRUCTURAL PROPERTY	MEASLES VIRUS (STRAIN YANIAGATA.I)		Ì						-
MONSTRUCTURAL FROITENC	SUNSC MIEB	NOTICE STATE OF THE PROPERTY O	INDIAN PARAINTLUENZA I VIRUS (STRAIM CTS)		Ì						
	NASC FILLS	ON STORE IN COLUMN STORE	HILDIAH PARAMALUENZA I VIRUS (STRAIM C19)		Ī						
	ANC LINE	SON STATE OF THE PROPERTY OF T	HILDIAN PARAINFLUENZA I VINUS (STRAIN CI. 973)	1							
MONSTRUCTURAL PROTEIN C MURIAN PARAINA LIENZA A VIRUS (STRAIN MILE 2019) 117-157	NAX.	CONCIDENTIFIED PROTEIN C	HUNIAN PARAINS LUENZA I VIRUS (STRAIN CI-LAUS)	Ī							
SONS BLUCTURAL PROTEIN C SERVA VRIUS STANN & A STANN &	200	MONGING LINAL PROTEIN C	MUNICIAN PARAINFLUENZA I VIRUS (STRAIN MILL 0183)	T							
SONS BUCTURAL PROTEIN C SERDAL VIRUS (STANIN LANDIS) 131-167	THE WAY	KONSTRUCTURAL PROTEIN C	SENDAL VIRUS (STRAÍN 474)				ļ				
KONSTRUCTURAL PROTEIN C SENDAL VIRUS STRAIN 2) 44-102 KONSTRUCTURAL PROTEIN NS. N. BAPATENS GERANSTON 11-15 KONSTRUCTURAL PROTEIN NS. S BAPATAVRUS GERANSTON 11-15 KONSTRUCTURAL PROTEIN NS. S BAPATAVRUS LA CROSSE (ISOLATE L'11) 1-19 KONSTRUCTURAL PROTEIN NS. S BAPATAVRUS LA CROSSE (ISOLATE L'11) 1-19 KONSTRUCTURAL PROTEIN NS. S BAPATAVRUS LA CROSSE (ISOLATE L'11) 1-19 KONSTRUCTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL PROTEIN NS. S KONSTRUCTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL RAPITARIA RAPLANQUAN (DATA) (DATA) KONSTRUCTURAL PROTEIN NS. S BAPATAVRUS CONTACTURAL RAPLANQUAN (DATA) (200	KONSTRUCTURAL PROJECTO	SENDAL VIRUS (STRAIN HARRIS)								Ц
HONSTRUCTURAL PROTEIN NEATH LUCATURAL PROTEIN NEATH	STATE SECTION	KONSTRUCTURAL PROTEIN C	SENDAI VIRUS (STRAIN Z)	Ī	75.						
NONS FLUCTURAL PROTEIN NS 5 SUNYAVIRUS GENATS ON	Series Series	MONSTRUCTURAL PROTEIN MS.A.	INDATIENS MECROTIC SPOT VIRUS (INSV)	Ī					L		
MONS INICTURAL PROTEIN NS 5 BUNY AVRIUS LA CROSSE (ISOLATE L'19) MONS INICTURAL PROTEIN NS 5 INCOLAN VIBUS MONS INICTURAL PROTEIN NS 5 INCOLAN VIBUS (ISOLATE L'19) MONS INICTURAL PROTEIN NS 5 INCOLAN VIBUS (ISOLATE L'10) MONS INICTURAL PROTEIN NS 5 INCOLAN VIBUS (ISOLATE L'10) MONS INICTURAL PROTEIN NS 5 INCOLAN VIBUS (ISOLATE L'10) MONS INICTURAL ANTICEN DIPON VIBUS (ISOLAND RAPLAN) (PRA) MONS INICTURAL ANTICEN DIPON VIBUS (ISOLAND PONAVIEN) (PRA)		KONSTRUCTURAL PROTEIN NS-S	BUNYAVIAUS GERMISTON								
MONS FILECTURAL PROTEIN NS S NACOLAL VIRUS LA CROSSE MONS FILECTURAL PROTEIN NS S NACOLAL VIRUS (103) MONS FILECTURAL PROTEIN NS S NACOLAL VIRUS (103) MONS FILECTURAL PROTEIN NS S NEGOCIAN VIRUS (103) MONS FILECTURAL PROTEIN NS S PREGODALBES VIRUS (STRAIN DODIAN) (DAV) MATERIAL PROTEIN ANTICEN DIRON VIRUS (STRAIN DODIAN) (DAV)		Ī	BUNYAVIBUS LA CROSSE (ISOLATE L74)								
NOSS INCTINAL PROTEIN NS 1 INCOLAN VRUS NOSS INCTINAL PROTEIN NS 1 INCOLAN VRUS (105) NOSS INCTINAL PROTEIN NS 1 UNKINEM VRUS (UK) NOSS INCTINAL PROTEIN NS 1 PREUMORAN VRUS (STRAIN KAPLAN) (PRV) NATI FORDER NACIALAR ANTIGEN DIRON VRUS (STRAIN PROJAWI) (1940)		Ī	BUNYAVIRUS LA CROSSE								
HOWSTRUCTURAL PROTEIN IS: 10SCAMA VIRUS (TUX) A MONSTRUCTURAL PROTEIN IS: 10SCAMA VIRUS (TUX) II PRODABLE HOCLEAR ANTIGEN BY PROPAGE HOCLEAR ANTIGEN BY PROPAGE TO BY PROPAGE HOCLEAR ANTIGEN BY PROPAGE HOCH ANTIGEN BY PROPAGE HOCLEAR ANTIGEN BY PRO	200	Ī	NAGUAD VIBUS								
MONSTRUCTURAL PROTEIN MS S UNICIDATEM VIRUS (STRAIN KAPLAN) (PRV) PROGRAFIE MUCLEAR ANTIGEM PRODUCTURE (STRAIN BOLIANI) (IMI) (DHO) MANTE DERIOTETH	100	NONSTRUCTURAL PROTEIN MS S	TOSCAMA VIRUS (105)								
PROBABLE MUCLEAR ACTICEN PREUDOALBES VRUS (STEALN BOTANI) (DHO) MACT FOR DEFENDE THE	200	T	UURUNIEMI VIRUS (UUR)								
MAKE FORDTEN		Ī	PSEUDORABIES VIXUS (STRAIM KAPLAM) (PRV)								
	3	Notice of the stat	DHORL VIRUS (STRAIN BADIANUSINAI) (DHO)	1							

PCGCKC	ALLAIDTIS	All Viruses (ne bacterisphages)	Ī	П	T	100	1000	7127	48649	78741
HENNE	ZROJEIN		Ī	Ī		Т	ī	Т	Т	
PVNUC IAANA	NUCLEOPROTEIN	EDOLA VIRUS		Ī	-	Ì	T			
PUNITE INANA		INFLUENZA A VIAUS (STRAIN WANAS ACUTAPRINIORIE 49571)		*	137.406		Ī			
PVNIC IABLA	NICT EDPROTEIN	INFLUENZA A VIRUS (STRAIN AVANN ANDONAMO)		27-408		j			-	
PANIE IABLID	MICHEOFROTEIN	MILUENZA A VIBUS (STRAIN ABRAZILLIMI)		27.406		İ	Ī			
PVNIC IACAL	MUCLEOPROTEIN	INTUENZA A VIRUS (STRAIN ABUDGERUGARAIOKKAIDOVIAT)	-62	96-134	157-408	1				
PVNUC IACKG	MUCIEOFROTEIN	INTLUENZA A VIRUS (STRAIN ACALIFORMANOTI)	1	276		1	1			
PANIK IACKP	MUCI EDPROFEIN	_		١	37.406	1	1			Ī
PACIFIC IADALI	KIKL TOPROTEIN	((1))		M-154	357-406					
PANIE IADAS	MACL ECPROTEIN	_	1-42	96-156	357-408					
1400	NOTICE CONTRACTOR OF THE PROPERTY OF THE PROPE	Γ	1-03	151-96	357-408					
Tool True	MACH EQUALITY AND A STATE OF THE STATE OF TH	/AK12/96)		P6-130	360-408					
1000	National Contraction	DITLIENZA A VIRUS (STRAIN ADUCK/ENGLAND/1/34)	1.43	151-94	357-406					
STATE TO SE		DOLLIENZA A VIRUS ISTRAIN ADUCK/ENGLANDVIAS)	7	20.00	157-408					
200	7310403	INTELENZA A VIRUS (STRAIN ADUCKAIONG KONG/771)	27-1	\$6-130	353.401					
THE PERSON	2310303	POLUENZA A VIRUS (STRAIN ADUCKAIEADHIS 97474	7	20.00	337-408					
2000	713-04803-047	PIELLEMEN A VIRUS (STRAIN ADUCKALANITOBATIS))	2	134	357-408					
PACIFICATION	Marci Foed of File	DOLUENZA A VIRUS (STRAIN ADUCKARW ZEALAND/11/76)	3	96-154	357-401					
AND MAN	WINT CORPOTEIN	Ť	251.98	157.406						
PACTE IATOR	TO THE POST OF THE		Ī	153.400						
PUNIT INDO	NICLEORDIEM	INFLUENZA A VIRUS (STRAIN AFORT MONAIOUTH/141)	7	33.40						
THE LABOR		INTLUENZA A VIRUS (STRAIN AFORT WARREWING)	337-408							
	2000	THE LIFTHER A VIRUS ISTRAIN AFOWL PLAGUE VIRUS/DOBSON	7	20.50	197-408					
		REFLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSROSTOCK		96-150	80-090					
TO THE PARTY OF TH	THE POST OF THE PARTY OF THE PA	NET TRUTA A VIBILE (STRAIN ACREY TEAL/AUSTRALIA/1/19)	 ?	Ī	157-404					
TANK TANK	Wild Cost of the C	NET HENZA A VIRUS ISTRAIN ANCIR L'AIARYLANDYSTI	Ī	21-60	_					
TOO VICE	Ni Coepos Line	١	251.28	27.408		-				
Sour Lagran	Marci Foreout IN	DALUENZA A VIRUS (STRADY ACCULLADARYLAND/102078)	9	151-31	357-409					
PUNIT IAGUA	Marci Forestien	DIFLUENZA A VIRUS (STRAPY ACULLALARYLANDVIOLS779)	Ī	2	357-409					
PURIC INGUN	MUCLEOPROTEIN				157-409					
PVINIC IAGON	MUCLEOPROTEIN	É	-	151-96	157-409					
PYNIC IAIIC	MUCIEOPROTEIN	DIFLUENZA A VIRUS (STRAIN A/GULLA/INMESOTA/MS/10)	1-43	K-154	157-400					
PYNUC INJU	NUCLEOPROTEIN	POLLENZA A VIRUS (STRAIN AAUCKOXX40)		11-409						
PYMUC IAIRO	MUCLEOPROTEIN				357-408					Ì
PVNUC JAIDA	MUCLEOPROTEIN	(()			157-408					
PVAUC IAIDI	NUCLEOPROTER	6		¥:134						
PVNUC IAIRO	NUCLEOPROTEIN		Ī	127409						
PVNUC_IAIDE	MUCLEOPROIEIN			37.400		T				
PVMUC IAHTE	MUCLEOPROTEIN	(STICAIN A/EQUINE/FIXAGOE/179)		1			1			
PVAUC IAKIE	MUCL EOPROTE IN	INT UEWAA A VIRUS				1	Ť			
NAUC IN EN	MUCLEOMOLEIM	DOBLIENZA A VIRUS (STRAIN ANTENNA)		37.400	-					
VNUC INMA	MOLECULOR STATE OF THE PARTY OF	INTLIERZA A VIDUS	Ī	Τ	157-408		Ī			
PLYST TANGE	MAIN SOPROTEIN	STRATH APLALL ARDINEW YORKS 15073)	Ī	Ī	357-404					
PUNCTION TANGE	NO SCI BORBOTE DA			251-26	357-408					
PVAIC IANTA	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAM APREW JERSEYATA)	7	25.2	357.408					
PVAUC IAOIU	MUCLEOPROTEIN	MILLIENZA A VIDUS (STRAIN ANTINOM)		157-409						
PANC IAPAR	NUCI EOPROTEIN	DOLUENZA A YDUS (STRAPI AORIOVAS)	1.41	157-406						
PVNC APUE	PUCLEOPROTEIN	NGLUENZA A VIRUS (STRAIN APARROTAL STERM)	7	П	157-404					
PVNUC IARUD	NUCLEOPROTEIN		7							
PVNUC IASEO	MUCLEOPROTEIN	ШΤ	7	٦	197-404					
PYNUC IASHU	MUCLEOPROTEIN	INFLUENZA A VIAUS (STRAIN ASEALMASSACKUSETTS/IMO)		I	157-409	1				Ì
PVNIK IASIN	MIKLEOPROTEIN	¬	•	151-408		1	1]		

				П			Ī	7 . 4	6.04.0	714
PCGENE	ALLMOTIS		ALIAL		ABEAL	1854	2000	1		
- 1	KROJIK	THE LIENZA A VIRUS (STRAIN ASTNOADURE/1951)	?	Ī						
- 1	NUCL EGROLE IN	THE LIENZA A VIRUS (STRAIM ATEAL/ICEL AMD/19/19)		1	37-406					
PUNIC INTEN	NIXT EOFTOILE	INFLUENZA A VIRUS (STRAIN ATURKEYAINNESOTA/1461/1)		Ī			T			
VYOC IAIRO	NUCLEO CROSSING	DIFFUENZA A VIRUS (STRAIN ATURKEYONTALIOM11244)		1	237-40					
PVNC IAIRS	NIK EUTON IN	INTLUENZA A VIRUS (STRAIN AMERINSOUTH AFRICAMI)	T							
PVROC IAIRI	March sometimes	INFLUENZA A VIRUS (STRAIN ATERNATURIA EMIALIATI)	3		131.40					
200	NI STORAGE STATE	INTLUENZA A VIRUS (STRAIN AVTEXAS/1/71)								
LANGE MANY	See Of the Control of	INIT. UENZA A VIRIIS (STRAIN ACDORAVIONI)	7							
VINCE AUS	201000000000000000000000000000000000000	INTLUENZA A VIRUS (STRAIN AUSSIMOTT)	7	337400						
PVMJC IAVIO	ACCEPTANCE IN	INFLUENZA A VIAUS (STRAIN AVVICTORIA/SAB)	157-408							
PVRUC IAWIN	NUCLEUROIEN	INTI LENZA A VIRUS ISTRAIN AWHALEAIAINE/JIMA)	1.43	2 2	137.409					
PUNIC IAMID	MIXTEUROISIN	MATI IS NO A VIRIUS ISTRAIN ANTIAL EPACIFIC OCEANISMS	1-42	25-32	157.408					
PURIC A WIL	MICHEOPROTEIN	NATI (FAZA A VIRLIS (STRAIN ANVILSON-SAILTW))	1.43	157.400						
PUNIC JAWIS	NIKCLEOPROTEIN	CHILLIANZA A LIBIS (STRADA AAVISCONSDA) 52/091)	77	94-154	337-408					
PVWUC IA239	MUCLEOPROTEIN	CONTRACTOR OF THE CONTRACTOR O	=	25-25	153-406					
PUNUC IAZAI	MUCLEOPROTEIN	THE COURT A CORP. AND AND AND AND AND AND AND AND AND AND	7	24-124	307-151					
PYNUC IAZCA	MUCLEOPROTEIN	INCORPORATION OF THE PROPERTY	3	337-409						
PYNUC JAZDA	NUCLEOPROTEIN	DOLUENZA A VINUS (STRAIM ASMINECAMBRICADO)		167-400						
PVNUC JAZGE	MUCLEOFROTEIN	POLUENZA A VIAUS (STEAM ADWINEDUARUONOPUS)		94.154	157-408					
PVNUC IAZHI	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ASWINEAGEMAINTINE)		20.00						
PUNDE 147113	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/SWINEARONG ROMOWY)			117.400					
200	MAICH EDPEOLEIN	DELUENZA A VIRUS (STRAIN ASWINEAKONG KONG/126/12)	-							
2	NEO FORCE	INFLUENZA A VIRUS (STRAIN A/SWINEAICNG KONG/11/01)		2	100					
7 100	AND COMPONENT	INFLUENZA A VIRUS (STRAIN A/SWINE/TOWA/1970)	7-7-3	26	207.76					
YMUL, IAZII	TOTAL STATE OF THE	INFLUENZA A VIRUS (STRAIM ASWINEADWAII97471)	143	25.2	337-468					
PVNUC IAZII	NOTE OF THE PARTY	DIFLUENZA A VIRUS (STRAIN ASWINEMOWAM)	~	96-154 10-154	357-408					
PVRUC 1AZII	MUCLEURICIEM	DELIENZA A VIRUS (STRADA ASWINEATAL VIASSINA)	173	96-154	157.406					
PVRDC 1AZII	MUCLEOFIGH	DELIENZA A VIRUS (STRAIN ASWINEATAL VIZITE)	7	P\$1-96	357-408					
PVRUC IAZII	MCLEORGIEIN	INCLUENZA A VIRUS (SIRAIN A/SWINEATAL Y/141/81)	1.43	96-154	157-404					
PVRUC IAZIS	MULEURDIEN	DIELENZA A VIRUS (STRAIN ASWINEATAL YASHAR)	1-13	26-154	357-408					
PVRUC IAZIA	MOLEUTANIEM	NELLENZA A VIRUS (STRAIN A/SWING/JALESBURGAZ)	73	94-154	357-408					
PVMUC IAZBIA	ACCEPTANCE IN	INFLUENZA A VRIUS (STRAIN A/SWINEASAY/A4)	1-13	96-154	357-406					
WAC IAZNE	MACLEOFAUTE IN	DELIENZA A VIBUS (STRAIN ASWINENETIERILANDS/1245)	143	¥-1%	357-408					
VNUC. IACUI	AND TOPOCHET	INFLUENZA A VIRUS (STRAIN ASWINE/CHROTUTS)	1-13	26-154	157-408					
PLACE IAZON	MOLEUTROILIN	INTEREST A VIRUS (STRAIN ASWING/ONTALIONAL)	1-13	¥-1%	33.406					
1000	NI CEST CONTRACT CONT	INCLUENZA A VIRUS (STRAIN ASWING/TENNESSEE/24/7)	3	3.5	27.40					
PANIE AZES	NICI EOPROTEIN	INGLUENZA A VIRUS (STRAIN A/SWINE/WISCONSIBVI/S))	=	2						
PVNIE DIBAA	MUCHEOPROTEIN	INTLUENZA A VIRUS (STRAIN ASWINEANISCONSINVINI)	7	20.00	137-408					
PVAUC INBAC	MUCLEOPROTEIN	INTLUENZA B VIRUS (STRAIN BVANN ARBORVINS)								
PV:NUC DNBAD	MUCLEOPROTEIN	INGLIENZA B VIRUS (STRAIN B/AINN AUBORVING (COLD-AUANTE								
PVYOU INBLE	MUCLEOPROTEIN	INTUENZA B VIRUS (STRAIN BANNA ARBONING (WILD-ITTE))								
PVNUC INBSI	MUCLEOFAOTEIN	DELUENZA B VIRUS (STRAIN BALEDAD)								
PVNUC INCCA	NUCLEOPROTEIN	INTLIENZA B VIRUS (STRAIN B/SDKGA/ORE/212/7)								
PVNUC MABVM	MUCLEOPROTEIN	INTLUENZA C VIRUS (STRAIN CRALIFOUNIAVIE)	2							
PVNUC MABVP	MUCLEOPROTEIN	MARBIRG VIRUS (STRAIN MUSORE)								
PVOOI VACCC	MUCLEOFROTEIN	MANBURG VIRUS (STRAIN POPP)	2							
PVOO! VARV	PROTECNOI	VACCINIA VILUS (STRAIN COPENHAGEN)		107-11						
VACE FROM	PROTEINO	VARIOLA VIRUS	103-145	103-238	7117					
A 100	153 KD PROTED	FOXTAL MOSAIC VIRUS	2							
274	ILL KD PROTEIN	HARCISSUS MOSAUC VIRUS (PAIV)	1519-1575							
PVOR! PVACE	176 KD PROTEIN	PAPAYA MOSAIC POTEXYIRUS (PMV)	2		1474-1532					
PVOR1 PVX	223 KD PROTED	POTATO VIRUS M (STRAIN RUSSIAN) (PVA)		A						
PVOR! PVXCP	165 KD PROTEIN	POTATO VIRUS X (PVX)	1516-530							

	PROTEIN	VIRUS	1367	ABEAJ	OHES.	2854	AREA 5	18541	AREAT	AHEAS
NOT SAYEN	I SE KO PROTEIN	POTATO VINUS X (STRAIN CP) (PVX)	\$10.947							
PLORI WCMIN	110 KD PROTEIN	STAAWBEARY AILD YELLOW EDGE-ASSOCIATED VIAUS (SNIVE		931.945						
PLURI WCMVO	IATED PROTEIN	WINTE CLOVER MOSAIC VIRUS (STRAIM M) (WCMV)	1360-1219							
PLP10 NPVAC	147 KD PROTEIN	WILLE CLOVER MOSAIC VIRUS (STRATM O) (WCMV)	1240-1369							
P1 P10 NP10P	PIO PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS (=							
P. PIG BASOV	PIOPROIEN	DRGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	3							
PV P10 RCDV	PRUIEIN SIG	RICE BLACK STREAKED DWARF VIRUS (RBSDV)	19-312	25.43	506-556					
71.W 014.4	NONSTRUCTURAL PROTEIN PASIO	NCE GALL DWANT VIRUS (RGDV)	2							
PAPIT RDV	NONSTRUCTURAL PROTEIN PUSIO	WOUND TUSIOR VIRUS (WTV)								
MIN HAV	NONSTRUCTURAL PROTEIN PUSIT	RICE DWARF VIRUS (RDV)	25-80	273-314						
PVPI3 RDV	MONSTRUCTURAL PROTEIN PHSTI	WOUND TURIOR VIRUS (WIV)	2.3							
1111	SOSSIBICTURAL PROTEIN PIL	RICE DWARF VIRUS (RDV))	100							
PILL WINE	HONSIN UCTURAL PROTEIN PASIS	WOUND TUNIOR VIRUS (WIV)	101.03							
PLF10 JISVEB	NONSTRUCTURAL PROTEIN PUSIS	WOUND TUNIOR VIRUS (STRAIN MI) (WTV)	68.108							
PLP1 HCNVA	CAPSID ASSEMBLY AND DNA MATUR VIION PROTE	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP) (EHV-I)	169-231							
Dev211 (1.7 ve)	PROBABLE CAPSID PROTEIN VP21	HISTAN CYTONEGALOVIRUS (STRAIN ADIES)	41-02	146-180						
Pi F. 1 F110V	PRUMABILE CAPSID PROTEIN (P2)	HERDES SIXIMEN VIRUS (TYPE & / STRAIN UGANDA-1103)	11.61							
7. F. S. 115. EB	NITABIRANE ASSOCIATED STRUCTURAL PROTEIN V	EBOLA VIRUS	166.200							
PY PYS HSVSA	CAPSID PROTEIN VP26	EQUINE HERPESVIAUS TYPE 1 (STALIN ABAP) (CHV-1)	16.11							
PLE'S HP'OF	CATSID PROTEIN VP26	HERVESVIAUS SAINITU (STRAIN 11)	1.10							
0127 3:479	PIG PROSEEN	ORGYIA PSEUDOTSUGATA KRILTICAPSID POLYTIEDROSIS VIRUS	111-159							
PV FT AIISVA	CAPSID PROTEIN VP36	VARICELLA.20STER VIRUS (STRAIN DUNIAS) (VZV)	11.11							
P. F. B. IVIO	OUTER CAPSID PROTEIN VP2	ATRICAN HORSE SICKNESS VIRUS (SEROTYPE 47 STRAIN VACCI	136-163	70.304	410.465	014-662	684-720	976-1056		
P. P. BIVII	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEROTYTE 10/150LATE USA)	161-725							
PVP2 BIVIT	QUIER CAPSID PROTEIN VP3	BLUE TONGUE VIRUS (SEROTYPE 11/150LATE USA)		159-593						
P. P. BTVIS	OUTER CAPSID PROTEIN VP2	_		161.709						
NTI EMDVI	OUTER CAPSID PROTEIN VP2	-		37-610	101.09					
P. P. ROTER	OUTER CAPSID PROTEIN VP2	ISE VIRUS ISENOTYPE IJ (EHDV	×	147.301	405-459	61-43	620-668			
7.73 20180	ANA BINDING PROTEIN VP3	BOVINE ROTAVIRUS (STRAIN RF)		91.316	3	П	3			
PAPE ROLLA	MAN-BINDING PROTEIN VP2	BOVINE ROTAVIRUS (STRAIN UK)	1	11.31	526-558	1	676-755			
N P. ROIPC	ANA BISBING PROTEIN VT	INDIAN ROTANTAUS (SEROTYPE I / STRAIN WA)		403-536	23.563	T	685.764		1	
N N KOLSI	ICAA BINDING PROJEIN VY	PURCER ROLLANTRUS (CROUP C.) SIRAIN CONDEN	Ī	33.00	27.5	117.71	199	703-746	1	
PVP10 ASFE	RAA-BINDING PROTEIN VY3		2		24.63	200		1		
1000	TROSTIOTACIEIN TO								1	
P. P.S. EBOV	PHUSPHOPROTEIN P12	VER VIRUS (STRAIN DATIVITAS) VI	=							
PVP15 NPVAC	POLYMERASE CONDLEX PROTEIN VP11		= 9							
PVP15 NPVBA	EARLY 15 KD PROTEIN	AUTOCRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	14.103							
PVP13 VACCC	EAALY 15 KD PROTEIN	BOAIBYX MORI NICLEAR POLYHEDROSIS VIRUS (BNS-TV)	6-102	334-338						
PLP15 VACCP	INDIANODOLINANT ENVELOPE PROTEIN P11	JINGENI	5							
PVP35 VACCV	INCHINODOLITMANT ENVELOPE PROTEIN PIS		=							
AY	THE STANDARD WIND HE SAVEL OF PROTEIN PER	VALCINIA VIAUS ISTRAIN WRI								
	USE CORE DEDICATE LA LLOY CALLES AND LA CALL	SUNT PLANT SECTION STATES STATES							Ī	
OLA LANG	VATIONE PROJECT		Ī		20.10					
VIA ULA	Val Cong Photein		T					Ī	Ī	
PYPE BITOVE	VOI COLE PROTEIN	4114	T					Ī		
PVP1 EIDVA	VPI CORE PROTEIN	é	T		20.15			İ		Ī
VPI GILV	VPI CORE PROIEIN	VIRUS	Ī	13.370	741.813	11.10				
PVP1 RDV	P) PROTEIN	US (GFLV)	П							
PVP) ROTPC	AIAJOR 114 KD STRUCTURAL PROTEIN			117-672		П				
PVP1 ROTSI	INVER CORE PROTEIN VP)	POACINE ROTA VIRUS (GROUP C / STRAIN COWDEN)	2.3	139-163	110.105	917-905	117-071			

in the state of th	ALLN0115		ANTAL	7997	AREA?	4554	45.5	ABEAS	SEC.	
LEANE	CED JETS	STATE OF STRAIN SAIL		344.238	11.16	431.402	200			
7. F40 EBV	INNER CORE PROTEIN 173	HEINIAN HERPESY IRUS 4	133.467							
11.20 1137.11	CAPSID PROTEIN P40		100.30	199.633						
PYP40 115VEB	CAPSID PROTEIN P40	VEHV.11	10.103							
PVP40 B.TVT	CAPSID PROTEIN P40	HORNE VER	15	\$09.537						
PVP-10 SCMVC	CAPSID PROTEIN P46		157.400							
PV P40 VZVD	CAPSID PROTEIN P40	5	167.746	110 523						
PLP11 NPVAC	CAPSID PROTEIN P40	SIS VIRUS (31:16							
PY PAI ROIS!	STRUCTURAL CLYCOPROTEIN GF1	_	=	81:518	528-630					
PVP+2 ROTS!	OUTER CAPSID PROTERS VP4	SINDAN IN MOINT IN CALL	=	117-510	331-446					
PAA VACCC	OUTER CAPSID PROTEIN VP4		55.139	35.35	744-626	167-161				
PAA VACCV	NIAJOR CORE PROTEIN PAR PRECURSOR	VACCINIA VILUS (S IRAIM CONC. VILVOC. V	27.78	35.38	316.363	794-426	167-168			
PLPIA VARV	NIAJOR CORE PROTEIN PAA PRECURSOR	VACCINIA VIKUS (SIRAIM "A)	3.10	19.75	205.030	150.892				
PLP48 FOWPV	MAJOR CORE PROTEIN PIA PRECURSOR		1	20.35						
THIS VACCC	MAIOR CORE PROTEIN PAR PRECURSOR		1	135.163	149-103					
PVP IB VACCV	MAJOR CORE PROTEIN PAD PRECURSUR	VACCINIA VIRUS (STIANIA LUTENIAUEA)	=	33:16	105-201					
PUPUR VARV	MAJOR CORE PROTEIN PAR PRECURSOR	VACCINIA VIAUS ISTRAIN WAY	=	133.163	149-10)	L				
PV.F4 BTV10	MAJOR CORE PROTEIN PAD PRECUISOR	VARIOLA VIRUS	119.61	119-613						
PVP1 BTV11	VP4 CORE PROTEIN	ELUETOMOUR VICES (SERVITED IN 1800 AND 1800)	149.607	179-609						
eves nevel	VP4 COME PROTEIN		109-695	17903						
PVP4 DIVIA	VPA COME PROTEIN		169.607	179:609						
PUP NCDV	VPA CORE PROTEIN	I INCOLM	117.11	20.430						
PVP4 RDV	OUTER CAPSID PROTEIN VP4	REMAINS CALL MANAGES VINCES OF THE SECOND	10.01	64.03	637-679					
PVP4 R0104	MONSTRUCTURAL PROTEIN PAST	SOUNT BOTAVIETE (SEROTYPE &/ STRAIN B&41)	=	10.10	316.374	494-518	128-65)			
FVF4 ROIBC	OUTER CAPSID PROTEIN VP4	SOUTH BOTAVIETE CARACTERS	=	150	578-430		·			
PVP4 ROTBU	OUIER CAPSID PROTEIN V74	POWER BOTAVIBLE SELECTION	=	20.00	136-379	484-518	138-453			
PVP4 ROTEH	OUIER CAPSID PROTEIN VP	FORTINE BOTA VIRUS (STRAIN II-2)	===	113-146	111.114	145.370	<u>2</u>	SM-453		
PVP4 #01G	OUTER CAPID FROIDING	(E)	117.131	416-519			-			
TO TO THE	CALTER CAPACIDADIEIN VP4	ILBIAN ROTAVIRUS (SEROTYPE I / SIRAIN 1016)	=	2	17.71	6	2			
91100 743	CALLER CAPSID PROTEIN VP4	INDIAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-S)	2	2	11:31	10:31		777		
DITOR POTE	OLITER CAPSID PROTEIN VP4	INDIAN ROTAVIRUS (SEROTYPE I / STRABI 694)	2	3	317-316	20-300		2000		
VP4 1011U	OUTER CAPSID PROTEDN VP4	IUMIAN ROTAVIRUS (SEROTYPE 1/STRAIN DSI)	2		10.10					
VP4 ROTIO	OUTER CAPSID PROTEIN VP4	HUNIAN ROTAVIRUS (STRATIV KO)								
PVP4 ROTIG	OUTER CAPSID PROTEIN VP4	HASIAN ROTAVIRUS (STRAIN RU)				10.10	13:63			
PVP4 ROTIDA	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN LZO)			11.11	23043				
VP4 ROTIEN	OUTER CAPSID PROTEIN VP4	INDELAN ROLAVIROS (SENO) TVE I 7 STAVIT PUT		11.11	10.00	404-310	2143			
PVP4 ROTED	OUTER CAPSID PROTEIN VP4	TOTAL AND A VINCE (SEROT VE STEAM PE		1	10.15	63.53	357-111			
VP4 ROTIG	OUTER CAPSID PROTEIN VP4	INDEAN BOTAVIBLE (SEROTYPE) STRAIN RAV)	=	91:18	11.11					
PAPE ROTHT	OUTER CASED FROILIN VIA	MINIAW BOTAVIBUS (SEROTYPE 4 / STRAIN ST THOMAS 3)	3	136.373	337.338	403-113	170 001			
PVP4 ROTILY	OUTER CASH MOTERN VA	HIDAN ROTAVIRUS (SEROTVPE 4/ STRAIN VATO	1.35	111.111	144-176	443.513	22.53			
VP4 ROINW	COLER CATALOGRAPHY	HAIAN ROTAVIAUS (SEROTYPE I / STRAIN WA)	1.35	111.111	344.338	41.517	30.53			
NA ROLLS	COLER CASIO ROLL WAS	POLCINE ROTAVIRUS (SEROTYPE 5 / STRAIN 05U)	112.146	464-516	\$20.039					
VP ROIN	Contract Care of the Care of t	PORCINE ROTAVIRUS (GROUP C.I STRAIN COWDEN)	9	33.16	341-378	101.134	205			
VE ROING	CITER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN GOTT) RUED)	=	26.33	2	3	300	200		
HUJOU VENE	OUTER CAPSID PROTEIN VPA	PORCINE ROTAVIRUS ISTRAIN YN!)	=	3	*		1	777.111		
PVPA BOTTS	OUTER CAPSID PROTEIN VP4	NICE SUS ROTAVIRUS	=	=		2				
PVP+ BOISS	OUI ER CASID PROTEIN VP4	SIMIAM II ROTAVIRUS (STRAIM SATE FEN)	=				100			
VIW MIV	DE OUTER CAPSUD PROTEIN VP4	SIMILAN II ROTAVIRUS (STRAIM SAIT-SENT)	2							
PVPS AHSVO	NONSTRUCTURAL PROTEIN PHS	WOUND TUNIOR VIRUS (WIY)				-				
ONE SAVA	OUTER CAPSID PROTEIN VPS	AFRICAN HORSE SECRESS VIAUS (NEROLIVE: 47 STRAIN CALL								
PVP1 BIVIO	OUTER CAPSID PROTEIM VP1	BROADHAVE'S VIRES (BRID)								

		All Vieunes (no hacteriophoges)	П						ABFAT	AREAG
CCCNE	ALLMOTIS		1	3	3	4	Т	Τ	Γ	
TL AND THE		TONGUE VIRUS (SEROTYPE 10/150LATE USA)	2.0	05-26	X-211					
1 O VII	UDIER CAPSID FROIEIN VI		14-58	92-130	22.45				Ī	
VYS BIVID	GOTER CAPSID PROTEIN VIS		2.5	137.55	5				1	
VIA BIVIA	COLER CATSID PROTEIN VP	ī	=	2						
	Service Charge Page 18 VPS	╗	2.5	82-163						
TVP3 CIVEA	COLER CAPGO PROTEIN VPS		2	77.76		16.	16.6			
200	CATTER CARCIN PROTEIN VPS	श्र	14.31	97:176						
100	OUT TO THE PROPERTY OF		99.0	2						
			434-503	347.588	131.708					
PVF61 BIVIO	COLEA COM TAGES	PE 10/1SOLATE USA)	163-215							
PUP61 AIRDV	VP6 PROTEIN		128-202							
PVP61 NPVAC	PROBABLE MONSTAULTORAL TO AND THE	A POL YIJEDROSIS VIRUS (29.96	351-366						
PVP43 BTV10	61 KD PROTEIN	BELLETONICHE VIELTS (SEROTYPE ID/ ISOLATE USA)	11-11	159-207	214-251					
BUTTLE NOVOP	VPS PROTEIN	ROSIS VIRUS	30-341	47170						
PVP61 NPVAC	MAJOR ENVELOPE GLYCOPROTEIN PALCURSOR	DECEMBER 11 TO STATE OF THE POST OF THE DECEMBER 11 TO STATE OF THE ST	15.35	760.764	441-411					
PVP67 NPVGM	AIA JOH ENVELOPE GLYCOPROTEIN PRECURSOR	A DESCRIPTION OF THE PROPERTY OF THE PROPERTY IS A COLUMN TO THE PROPERTY OF T	206-281							İ
PVP6 01V11	NIAIOR ENVELOPE GLYCOPROTEIN	CALLERIA MELLUALLA MULLIAN FOLITA	116.911							
PVP4 BTV13	VP6 PROTEIN									
P. P. DIVII	VP4 PAOTEIN			110.001						
PLPA BIVIS	176 PROTEIN	BLUE TONGUE VIRUS (SEROITYPE I / 1) SOLLATE USA)								
51.P6 01V2A	V P6 PROJECT	BLUETONGUE VIRUS (SEROTVPE I / ISOLATE SUCTIFIATION)								
700	L'PA PROTEIN	BLUE TONGUE VIRUS (SEROTVPE 7/1501 ATE USA)			107 071					
	CTRICTURAL PROTEIN PO	AICE DWALL VIAUS (ADV)								
	CONTINUE AT PROTECT PA	WOUND TUNIOR VIBUS (WTV)								
٠.:	44 X 310 44 14 14 14 14 14 14 14 14 14 14 14 14	WOUND TUNIOR VIRUS (STRAFN NI) (WTV.)	20.75	716-334						
1	STAN ICHARACTER	AUTOGRAPHIA CALIBORNICA MICLE AR FOLVIE HRIDSIS VIRUS I	20.12							
	10000	CHORISTONEURA FUNITERANA NUCLUAR FOLVIII, DROSIS VIRU	115-453							
N 711 115%5A	NINGS AND AND AND AND AND AND AND AND AND AND	HERPESYTHUS SAINING (STRAIN 11)	20.05	163-211	230-110					
N N NAVA	THURSDAY THE THE THE THE THE THE THE THE THE THE		84.78	363.387	106-440					
01/10	WALCON THE STATE OF THE STATE O	BITETONGUE VIRUS (SEROTYPE 10/15OLATI, USAL (SCROTYPE	184-138							
110141	VA COME VACITIES	BILLETONGER VIRUS (SEROTYPE 11/15/12 ATE USA)	301-335							
	VA) CORE PROJECT	IN THE TOWNER VIRES (SEROTYPE 17 / ISOLATE USA)	114-220							
P. P. BIVIA	VP COR PROTEIN	NI HETONGLE VIRUS (SEROLYPE 17 ISOLATE AUSTRALIA)	16-33							
7. P. BIVIS	NATIONE PROTEIN	STATE SOUTH ALTERNATION OF THE SOUTH AFRICAL	104-236							
PAPP BTV2A	VP. CONE PROJEIN	ALCELOSOR VIEW (SEROT VPE 27/150LATE USA)	15.21							
PAPT EIEDVI	VP CORE PROTEIN	VPE 1) (CHOV	16.50	134-178						
VO. 177	VP / CORE PROTEIN	Contract States	\$4.0	133.355						
AIM (AIA	CONSTRUCTURAL PROTEIN PKS	THE DA AND VINES INC.	2.5	19:30	167-151					
PLPED NOVAC	NOVSTRUCTURAL PROTEIN PKS?	WOUND TOWNER WITH SAM PIN VIII DROSS VIRUS		20.00	156.304	321.78				
PLPET MPVOP	CAPSID PROTEIN PIO	AUTOCACATION TO ANIMATICA PRINTED POLITICIDAD SIS VIRUS	791-01	10.431						
P. P. BTV10	CAPSID PROTEIN P47	CACCION TO COMPANY OF THE PARK TO SECOND A SECURITY OF THE PARK TO SECOND A SECOND A SECURITY OF THE PARK TO SECOND A SE	24-103	165-219						
N.PI BIVII	SONSTRUCTURAL PROTEIN PE	ALCETOMORE VALIDATED TYPE 11 / 1501 ATE USA)	¥-102	113.319						
P.70 BTV11	MONSTRUCTURAL PROFESS PE	PLUCIONCIE VIDIO (SEROITYPE II / ISOLATE USA)	24-102	103:319						
P. P. BTV17	NONSTRUCTURAL PROTEIN PE	BLUE TOWNING VIEW AND THE USAL	54.102	165-219						
PVF6 BTVIA	KOASTRUCTURAL PROTEIN PE	ALIFTONIZIE VIRUS (SEROTYPE I / ISOLATE AUSTRALIA)	26.102	103-210						
PVTG BTVIS	NONSTRUCTURAL PROJECT VA	ALLIE TONGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	24-103	103-219						
PAPE BTV3A	MONSTRUCTURAL PROTEIN 78	AL INTOMORE VIRUS (SEROTYPE 2/150LATE USA)	34-102	115-219						
P. PS FOWPV	MONSTRUCTURAL PROJEIN PS	FOWN POX VIRUS	197-145							
7 P	STRUCTURAL PROJEIN PREFICE CONSUM	BICE DWARF VIRUS (RDV)	13-43	186-226						
>1%	MONSTRUCTURAL PROTECTION TO	WOUND TURIOR VIRUS (WTV)	100-313				_			
PLPS WINE	STRUCTURAL PROJECT TO	WOLIND TUNIOR VIRUS (STRAIN NI) (WTV)	140-212							
TYPC BYDY!	STRUCTURAL PROTEIN PROTEIN PRECUES		13-39							
PLPILE MOVAC	POINTIVE GENCHELLINGE OF PROTEIN	ALTIOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS (144-22)	(144-22)							
PVPIE NOVOP	19 KD POLYIR DRAL ENVELUE FACTOR							•		

11.07 PROTEIN ONCO 11.00 PRECURSOR P		46.2.2.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	1010	oug		
THE FOLICIAN TH	1.1.781 100-185 1.1.781 1.1.781 1.1.78 1					
10	10-116 10-118 1					
VEW PROTECTION 190	1.31 4.32 4.39 4.30 4.40					
TYP FROTEN TYP FR	6.19 6.19 6.10				1	
VEV ROLLEN VEV PROLEN VEV	5-12 5-13 5-10					
VEU PROTEIN INC. INC. INC.	1.19 1.10 1.10 1.10 1.10 1.10 1.10 1.10					
VEW PROTEIN VEW PROTEIN	6.59 6.40 6.40 6.40 6.40 6.40 6.40 6.40 6.40					
VEU PROTEIN 1910	1.19 1.40 1.40 1.40 1.40 1.40 1.40 1.40 1.40					
VEO PROTEIN ITAL VEO PROTEIN VEO PROTEIN VEO PROTEIN	1-40 6-40 6-40 6-47 6-47 6-47 6-47 6-47 6-47 6-47 6-47		-			
VEOPTOTES INC. VEOPTOTES	6.40 5.72 6.40 6.40 6.40 6.40 6.40 6.40 6.40 6.40		1	+		
VEV PROTEIN III	5.70 5.90 6.10 6.72 6.40 6.72 6.40 6.40 11.71 6.40 11.71 6.40 11.71 6.41 11.71 6.41 11.71 6.41 11.71 6.41 11.71 6.41 11.71 6.41 11.71 6.41 11.71 11.71 6.41 11.71					
VEV PROTEIN INC. VEV PROTEIN VEV PRO	5.50 5.47 5.49 5.40 5.41					
VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU VEW PROTEIN INU IN	1.50 4.40 4.40 4.40 4.40 4.40 4.41					
VEU PROTEIN ITEL	2.19 2.19 2.19 2.19 2.19 2.19 2.19 2.19					
TUP PROTEIN TUP TUP	6.56 4.40 4.40 4.40 4.40 4.40 4.40 4.40 4.4					
VEU PROTEIN VEU PROTEIN	6-17 6-18 6-19 1-19	.				
VEW PROTEIN III	6.17 6.19 6.19 6.14 11.13 10.14 10.14 10.14 10.15 10.10					
VEU PROTEIN ITEM	6-72 6-39 6-40 6-10 6-14 6-14 6-13 10			_		
VYD PROTEIN INC. VYD PROTEIN INC. VYD PROTEIN INC. VYD PROTEIN INC. VYD PROTEIN INC. VYD PROTEIN INC. VYD PROTEIN VYD PROTEIN INC. VYD PROTEIN VYD PRO	(4.59 (4.59 (4.50 (4.10) (4.10) (4.10) (4.11) (
VEV PROTEIN III	6-40 6-40 6-10 11-20 6-14 12-13 14-131 14-131 14-13 14-131					
VPU PROTEIN HI VPU PROTEIN VPU PROTEIN	(4-40 (4-11) (4-					
VPU PROTEIN III	21.70 20.74 20					
VYU PROTEIN VYU PROTEIN	11-16 11-1	-				į
VPV PROTEIN	0.74 (1.187 (1.189 (1.1					L
VPY PROTEIN VPY PROTEIN	241-247 241-247 24-14 24-15					
Ver Routen Ver	241.107 14.10			-		
ALPHAA PROTEIN ALPHAA PROTEIN THE PROTEIN	244.249 90.144 10.144 10.144 10.144 10.144 10.144 10.146 10.144 10.146 10.14					
CONSTRUCTURAL PROTEIN NCVP NO	0-144 30-31	+	-	 - -		
Y16 PROTEIN W	14.51					L
VAP FACIENT VAP FACIENT VAP FACIENT VAP FACIENT VAP FACIENT VAP FACIENT CLYCOPOTENT V7 CLY	16-13 16-43 16-43 16-43 16-13 16				1	
VY6 PROTEIN W 6 PROTEIN W 6 PROTEIN W 6 PROTEIN W 6 PROTEIN W 6 PROTEIN W 7 PROTEIN	1.0					
VAP PROTEIN WAS PROTEIN WAS PROTEIN	INTERPRETATION 1-4 11-10 1-10					_
VAP PROTEIN VAP PROTEIN VAP PROTEIN VAP PROTEIN VAP PROTEIN VAP VAP PROTEIN VAP VAP PROTEIN VAP VAP PROTEIN VAP VAP PROTEIN VAP VAP PROTEIN VAP VAP PROTEIN VAP VAP PROTEIN VAP VAP PROTEIN VAP PROT	11. 19. 19. 19. 214 11. 19. 19. 214 11. 19. 214 11. 19. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 11. 29. 214 12			_	_	
CAY CORNOTED W PAGE CAY CORNOTED W	23.0 22.130 10.131 10.135 10.136					
CAYCOROTEN VP) NOWSTRACTIONAL PROJECT HCV7] NOWSTRACTIONAL PROJECT HCV7] NOWSTRACTIONAL PROJECT HCV7] NOWSTRACTIONAL PROJECT HCV7] NOWSTRACTIONAL PROJECT HCV7] NOWSTRACTIONAL PROJECT HCV7] CAYCOROTEN VP) CAYCO	1 10 10 10 10 10 10 10					
MONSTRUCTURAL PROTEIN HCV71 MONSTRUCTURAL PROTEIN HCV71 MONSTRUCTURAL PROTEIN HCV71 MONSTRUCTURAL PROTEIN HCV71 GAYCOPOTEIN V71 GAYCOPOTEIN V71 GAYCOPOTEIN V71 GAYCOPOTEIN V71 GAYCOPRO	1 STACH OSU) 10-136 11-13 11-14 11-15			\ 		
MONSTRUCTURAL PROTEIN HCVP1 MONSTRUCTURAL PROTEIN HCVP1 MONSTRUCTURAL PROTEIN HCVP1 MONSTRUCTURAL PROTEIN HCVP1 MONSTRUCTURAL PROTEIN HCVP1 MANUAL CUTAL PROTEIN HCVP1 GLYCOPROTEIN VP1 G	146 1111 106-114 11-10 1					
MONSTRUCTURAL PROTEIN PACY MONSTRUCTURAL PROTEIN PACY MONSTRUCTURAL PROTEIN PACY MONSTRUCTURAL PROTEIN PACY GAYCOPROTEIN V? GAYCOPROTEIN V. GAYCOPROTEIN V? GAYCOPROTEIN V. GAYC	1.00 11-110 1-40 11-110 1-40 11-130 1-41					1
MONSTRUCTURAL PROTEIN REVYY MONSTRUCTURAL PROTEIN REVYY GLYCOPROTEIN V?	ALIN DATI) 1-10	1				
HONSTRUCTURAL PROTECN NAVATA HONSTRUCTURAL PROTECN NEVATA GLYCOPROTEN VP GLYCOP	1-46 14-12 14-13				-	
MONSTRUCTURAL PROTEIN MEVY: GLYCOPROTEIN V? GLYCOPROTEI	AAIN B641) 1-45 AAIN 641) 1-45 1-45 1-45 1-46 1					L
GLYCOPOTER V71 GLYCOP	140) 154) 154 154 154 154 154 154 154 154 154 154				 	
GAYCOPROTEIN VP1 GAYCOP	(1
GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1	1) 2.54 1) 1.54 1) 1.54 1) 1.54 1) 1.54 1) 1.54 1, 1.5				-	1
GLYCOPOTEN V7 GLYCOPOTEN V7	1) 2.54 1.51 1.51 1.51 1.51 1.51 1.51 1.51 1					
GLYCOPROTEN VP 1 GLYCOP	51 51 51 51 51 51 51 51				L	L
CLYCOPROTEIN VP 1 CLYCOPROTEIN	134 13 134 13 134 13 134 13 134 13 134 13 134 13 134 13 134 13 134 13 134 13 134 134					L
GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1 GLYCOROTER VP1	1514. 1514. 1514. 1515					-
GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1 GLYCOROTEM VP1	1-45 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)					
GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V? GLYCOPROTEIN V?	15.44 12 12 12 12 12 12 12 12 12 12 12 12 12					1
GLYCOPOLEN Y7 GLYCOP	10-116 10-116 10-116 10-116 110-116 110-116 110-116 110-116					
GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1 GLYCOPROTEIN VP1	19518 100EA ROTA 41-78 41-78 18519 18519 18519 18519					
GLYCOPROTED VP? GLYCOPROTED VP? GLYCOPROTED VP? GLYCOPROTED VP? GLYCOPROTED VP?	181-170 181-171 181-171 181-170 181-170 181-170		1			L
GAYCOPROTEIN VP 1 PLECURSOR GLYCOPROTEIN VP 1 PLECURSOR GLYCOPROTEIN VP 1 PLECURSOR GLYCOPROTEIN VP 1	STAIN RV-1 STAIN RV-1 STAIN RV-1 STAIN RV-1 STAIN RV-1 183-139 183-130 183-130 183-130 183-130					L
GLYCOPAGIEN V77 PAECUASOR GLYCOPAGIEN V77 PAECUASOR GLYCOPAGIEN V77 GLYCOPAGIEN V77	15.79 24.3 213.330 24.330	Ţ			-	
GLYCOPROTEIN VP? PRECURSOR GLYCOPROTEIN VP? GLYCOPROTEIN VP?	TALIN RV-4) 2-43 TEAIN RV9, 181-320 TEAIN RU9) 141-320			1	-	L
GLYCOPROTEIN VP?	103-330			+		-
GLYCOPROTEGY VP?	212-330			1	+	1
	7			1	1	+
CI ACCEPTOR DE VP.						+
C. SCORD SERVICE	201.130			1	+	+
C. C. C. C. C. C. C. C. C. C. C. C. C. C						4
PYSO ROTION GLYCUTRUIED TO THE MAILS MILETAN ROTANTRUS (SEROTTOE 2/5 ITANIN MAILS)						

WO 96/19495 PCT/US95/16733

18000	41 30719	All Viruses (no batteriophoges)	Ţ	Т	7	ARTA	AREAS	ARKAS	ABEAL	AREAS
1	PROTEIN		1	100	Γ	T	Γ			
ı	GLYCOPROTEIN VF?		T	41.	İ					
G1108 W3 14	CI YCOPROTEIN VP)	-			Ī					
20100	CL VCOPROTE IN VP 3	O AND STRAIN DO	T							
100 BOTTO	GLYCOPROTEIN VP)	HUMIAN BOTAVIRUS (SENOTYPE 1/STRAÍN P)	27.710							
PUSCO BOTHS	GLYCOPROTEIN VP)	5	186.300	T		Ī				
PV C00 BOTH!	CLYCOPROTEIN (P)	٦		Ť	1 2					
	(A) 21810 EQUIV (C)	INDIAN ROTAVIRUS (SEROTYPE 4/ STRAIN ST THOMAS))	1	T	2/12	1				
10101	CONTRACTOR OF THE PROPERTY OF	INDIAN BOTAVIRUS (SEROTYPE 47 STRAIN VATO)	2.2		267-120					
				287-170						
7 50 ROIF?	CLICAROLEIPAN	POPULOS BOTAVIBUS (SEROTYPE 3/SIRALY AT/16)	017:10							
P. 500 ROTP)	GLYCOPROTEIN VP	POBLINE BOTAVIBLE (SEROTYPE 1/STRAIN CRW-9)	312.330							
P1 500 ROTP4	CLYCUPROTEIN VP)	CONTRACTOR STATE OF THE PROPERTY OF THE PROPER	Ī	108-242	282.330					
PV509 ROTP5	CLYCOPROTEIN VP)	CALCING BOTA AMBIE (SEPOTVBE CAST AND OSE)	383.330	İ						
P1 509 ROTP6	GLYCOPROTEIN VP?	PORCEAS ROLLANDS (SENOTING 1) 4 PROSECUTION (SENOTING SEN	92,330	T						
PY 509 A0178	GL YCOPHOTEDN VP?	CALLAG ACIA VIACO COMPANIA COM	T	200.262	077.710					
PY SOO ROIPK	GLYCOPROTEIN VP7	MUNICIPE FOLIANTOS (SERVINES AV STRAIN BLANTA)	T	Ì						
PI SOP ROTPAI	GLYCOPROTEIN VP!	PORCENE BOTAVIRUS (STRAIN R.)	Ī	Ī	911					
V4109 603 14	GLYCOPROTEIN VP?	PORCINE ROTAVIRUS (SEROTYPE 4/STRASS BAIL-1)		Τ						
114100 005.14	GLYCOPROTEIN VP?	PORCINE ROTAVIRUS (STRAIN YM)	Т	211.120						
13100	CLYCOPROTEON VP	AMESUS ROTAVIRUS	20.53	Ì						
	C. COSSOCIETA CO.	SINIAN II RUTAVIRUS (STRAIN SAII)	242-330							
FO EC	OF TOTAL STATE OF THE PARTY OF	BOVINE BOTAVIRUS (STRAIN MCDV)	13.161							
PV-510 RO185	MONSTRUCTURAL OF TOTAL SECTION	ROVING ROTAVIRUS (GROUP C./ STRAIN SIBNTOKU)	13.50							
PVS10 R018U	MINOR DUTER CAPSID PROTEIN	BOWNE BOTAVIBLE (CIBADALIK)	19:42							
PVS10 #01112	MONSTRUCTURAL CLYCOPROJEIN NO. 17	BOVING BOLLACION OF ANY AND AND ANY AND ANY AND ANY AND AND AND AND AND AND AND AND AND AND	21:0							
P1 \$10_ROTH?	MONSTRUCTURAL GLYCOPROTEIN NCVPS	HUNDAR BUILDING (STRAIN ARE)	13-162	İ						
PVS10 BOTH	MONSTRUCTURAL GLYCOPHOTEIN NCVPS	HUNIAGE ROLLA (1919-1919-1919-1919-1919-1919-1919-191	13-163	İ						
PVS 10_ROTHC	HONSTRUCTURAL GLYCOPROTEIN NCVPS	SCRIM ROLAVINOS (SIRAIN AMA CLOSE OF	10.00							
PVS10 ROTHW	MINOR OUTER CAPSID PROTEIN	SCHAN HOLAVIROS (CACOUT C.) STANIA ENSTOCA		İ						
PVS10 ROTS1	NONSTRUCTURAL GLYCOPROTEIN NCVPS	MINIAN ROTAWAUS (SERVITE IT STANDAY)		Ť						
PVSII ROTGA	NONSTRUCTURAL GLYCOPROTEIN NCVPS	SDITAN 11 ROTAVIRUS (STRAIN SATI)	Ţ	9,7	Ī					
PVSII ROTG	MONSTRUCTURAL PROTEIN	HADOLI DIARRILLA ROI	T							
PVS11 ROTHS	NONSTRUCTURAL PROTEIN	ROTAVIRUS (GROUP B / STRAIM IDIR)		İ	1					
PVSII ROTIN	AUNOR CUTER CAPSID PROTEIN	HUMIAN ROTAVIRUS (SEROLYPE 27 STRAIN RV-3)								
PVSII ROTHO	MINOR OUTER CAPSID PROTEIN	HIDAN ROTAVIRUS (SEROI TPE I / SIRAIN SMI)	1	T						
PVSII ROTID	MINOR OUTER CAPSID PROTEIN	HOLAN KOTA WAS (SENDING OF STRAIN OF)		Ì						
PVSII ROTIIW	ATIMOR OUTER CAPSID PROTEIN	HUNGAN MOLAVINOS (SENOT PER LA CITATION DE LA CITAT		Ī						
PVSII ROTSI	MUNOR OUTER CAPSID PROTEIN	IDIALAM ACTAVIROS (SENOTITE 17 SINAIR WA)	100	Ì						
PVS48 TBRVC	NANON OUTER CAPSID PROTEIN	SINIAR II KOLATIKO SINIARIO SALI	21.741	İ						
PVSH MURDI	SATELLITE RNA 48 KD PROTEIN	TONATO BLAKE BANG VINOS 13 TAKIN CHILIS ASTRAIN SEL	97.0	Ī						
TYSH MUNITS	SMALL HYDROPHOBIC PROTEUS	AND THE VISITE OF THE PRINCIPLE OF AND ISTRAIN EDINGS	7							
PVSII MUNDA	SAALL HYDROPHOBIC PROTEIN	MARGE VIEWS (STRACK EDINGBURGH 4)	17.							
PVSH MUMBA	SMALL HYDRUPHOPPIC PROTEIN	AND THE CARDS (STRAIN MATSUYANA)	15:51							
PVSH ARMAIP	SHALL HYDROTHORIC FROIEN	LAILAIPS VIRUS (STRAIN BELFAST)	13.52							
PVSII NUMBER	WINDER DESCRIPTION OF THE PROPERTY OF THE PROP	LIGARS VIRUS (STRAIN ENDERS)	70							İ
Carrie Market	CALL IN CORPORATION OF THE PROPERTY AND THE PROPERTY OF THE PR	MARDS VIAUS (STRAIN JERYL-LYNN)	97.6							
PVSII PICEUR	STATE STATE OF STATE	MURR'S VIRUS (STRAIN KILHAN)	16-0							
	CLAIL RYDECHOBIC PROTEON	MUNDS VIRUS (STRAIN DRUSTOL 1)	13.53							
TO SECUL	SMALL HYDROPHOBIC PROTEIN	MIRES VIRUS (STRAIN MIT ANAMA VACCIME)	13-21							
1000	SMALL HYDROPHOBIC PROTEIN	ARBOS VIRUS (STRAID) TAXAHASHI)	170							
OVOTA INCOME	SMALL INDROPIOBIC PROTEIN	NUMBES VIRUS (STRAIN URABE VACCINE AMIS)	1	٦						
PVSII DEOVI	SIGMA I PROTEIN PRECURSOR	REDVIRUS (TYPE 1 / STRAIN DEARING)	T	(3):-(1)	M:-104					
PV411 REOVE	SIGMA I PROTEIN PAECURSOR	REDVIRUS (TYPE 1/STRAIN DYJONES)		1						

ACCOUNT OF THE ACCO	İ		All Virgier (no bacteriofitages)	Τ.	1	AREAJ	AREAS	AREA! AB	ABEAS	ABEA1	1230
A				Ι	113,191						
			AUS ITYPE 1 / STRAIM LANG)	T,							
		PROTEIN PRECURSOR	S	2	j	+					
SIGNAL 13 BODGEN	PEON			20.32				1	Ì		
	Ī			1				1			
	Ī	1		1	-						
SIGNATIONAL PROTEEN PRECURSOR PREVISES PRESIDENCE PRECURE	VSIS REOV										
STRECTOLAL PROTECT PRECADON SEPATHISE VAND STRAND PARTICLES 1111.11	VST1 ICE VBU		ÆV)	7							
STRECTURAL PROTEIN TRECTATION SEPATITIE UNINS STREAM PAGES AND HEAT STREET TREETS	VS12 IEVAE			13:13		İ					
STRUCTURAL PROTERS PECCUSION HEAVITIES VARIS STRAND PALES 1919	PUSTS HEWAIT			10.33			1	+			
STRUCTIONAL PROTESS PRECURSION REA ATTEM MARKATALINES 110-159 110-				18-352				 			
STATECTORAL PROTEIN CAPADONIUS STRAM ENTING WITH STATE AND STATES WITH STA	V.217 HEALY							_			
11 11 12 12 13 14 15 15 15 15 15 15 15	PVS13 HEVRM			27.5	İ						
1.14001EN 13. CAMBONNESS TERMS 1.150	VIIA CAPVI			20.58		İ		-	Ī		
1 1 1 1 1 1 1 1 1 1	174			0:130	_			1			
1				2	<u> </u>						
1	PV14 CAPVK			T							
10 PROGRAGE BOA PACKAGING PROTEIN INDIAN PARABOLISTICALIN GUADALISTIC 11-41	PVIER EDV		B93-1) (HUNIAN HERPESVIRUS 4)	٦		Ì	Ì				
PRODABLE BUA PACKAGING PROTEIN HIGHWAY IT TRACAS UT THE ATTICLES STATEM STA	BVIER SICHVA	PROBABLE DNA PACKAGING PROTEIN			617-438	Ì					
	NAMES AND VALUE	PROBABLE DNA PACKAGING PROTEIN		161.502					Ī		
PROBABLE DAY PACKAGING PROTEIN FEMANSIALLA VOIR STRAINS ALS STRAIN		PACK ACING PROTEIN	Ī								
PRODABLE DAY PACKACING PROTEIN HEAVY PALINE LIGHANEL CATESIN'N HUSTICAL	PVIET HISVED	KIDDE OF THE PARTY OF THE PROPERTY OF THE PROP	Т	T	344						
PROBABLE DNA PACKAGINO PROTEIN NEMESVIRUS SABRINI (STRAIN DURASIYEV) 114-11	P. ICR IISVII	THOSE CAN THE STATE OF THE STAT	╗	1	İ						
PRODABLE DAY PACKAGNO PROTEIN	PUTER HISVSA	PROBABLE DAY PACKACING TOTAL	SEPRECYMING CANADA (STRAIN 11)	130-101		1		-			
VAROTHETICAL 19 TO PROTEIN VALUE AND STRAIN WAS STR	PVTER VZVD	PRODABLE DNA PACKAGDIO PROTEIN	STATES A STATE OF THE STATE OF	316-421					I		
V PROTEIN	417.18	PROBABLE DNA PACKAGING PROTEIN	DALIPIY-4AL	=======================================							
		700000		1							
VIPOTIERIE VIP	PL'YI SENDA	VINDICIN	ENDAI VIRUS (STRAIN 6/4)								
INTOTICE TICAL 10 10 PROJECT INTOTICE TICAL 10 10 PROJECT INTOTICE TICAL 10 10 PROJECT INTOTICE TICAL 10 10 PROJECT INTOTICE TICAL 10 10 PROJECT INTOTICE TICAL 11 10 PROJECT	PY101_SSVI	YI PROTEIN	CIT FOL OBUS VIRUS-LIKE PARTICLE SSVI	2							
	PY 101 SSVI	HYPUTHETICAL 19 I KD PROTEIN	THE PARTIE AND THE PARTIES SAVI	4.45	İ						
INTOTIGETICAL	1000	HYPOTIGETICAL 10 B KD PROTEIN	SULP CLOSUS VINCOLINA PARTICLE COVI	55.50		1					
	100	HYPOTHETICAL II O KD PROTEIN	IN FOLORUS VINUS-LINE PARTIES & ST.	30.00							
INPOTIETICAL 13 KD PROTEIN COAT PROTEIN LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS STRAND FIRM LELNE CALEVINIUS LEL		WYDOTHETICAL II 9 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE 33.								
INTODIEGICAL 13 NO PROTEIN IN COAT PROTEIN FILING CALEVINUAS STRAIN CIVE TRUST HILDS INTODIGGICAL 13 NO PROTEIN IN COAT PROTEIN LETTER CALEVINUAGE DISEASE VIRUS STRAIN FILICUS INTODIGGICAL 13 NO PROTEIN IN COAT PROTEIN LABORALISCE DISEASE VIRUS STRAIN FILICUS INTODIGGICAL 13 NO PROTEIN IN COAT PROTEIN LABORALISCE DISEASE VIRUS STRAIN FILICUS INTODIGGICAL 13 NO PROTEIN IN COAT PROTEIN LABORALISCE DISEASE VIRUS STRAIN FILICUS INTODIGGICAL 13 NO PROTEIN IN COAT PROTEIN CAREFORD WEST REVENUE TO A STRAIN FILICUS STRAIN	PYIIK TYDYA	ATT COOK AND AND AND AND AND AND AND AND AND AND	TOBACCO VELLOW DWARF VIRUS (SFRAIN ALSTINALIA)		Ì						
INTOTICE HEAL 11 NO PROTEIN NO COLT PROTEIN ELLINE CALENVINUS ISTRANN FRAICES	PY11K FCVC	100	FLINE CALICIVIANS ISTRAIN CPUST PIVICION								
	PYIX fCVF9		BELLING CALIFORNIAUS (STRACK FOLCEN)				1				L
	PYIN NOV		STATE OF THE PROPERTY OF THE STATE OF THE ST	9. -	ļ			1			
	PV12K RIDV		CADILLE MONTH OF THE PARTY OF T	3.5				1			
HYPOTHETICAL 13 TKO PROTTEN CASSAVA LATEN'Y VEDS STATEN'S DEALY NICE ALASY HYPOTHETICAL 13 TKO PROTTEN HYPOTHETICAL 13	200	HYPOTHETICAL 12 1 KD PROTEIN IN COAT PROTEIN	PASSIT IENOMOINGE CINESANT LINES	100							
		AVENTIFICAL IN TRO PROTEIN	CASSAVA LATENT VINUS (STRAIN WEST RENTALL								
INTODITE INCL. 1 S. ED FODIEN S. E. PROTEEN S. E. P. E. E. P. E. E. P. E. E. P. E. E. P. E. E. P. E. E. P. E. E. P. E. E. P. E. E. E. E. E. E. E. E. E. E. E. E. E.	711 ELVR	RIBIOS GALLET	CASSAVA LATENT VIRUS (STRAÍN NICERIAN)								
INTODITE IN CALL 15 TO PROTEIN SULFOLOBUS VIRUS, LIKE PARTICLE SSY: 1.15	PVIJK MVOF		ORGYIA PSEUDOTSUGATA ART TICAPSID POLVIIEDROSIS VIRIL								
	PY11K SSVI		SULFOLDBUS VIAUS-LIKE PARTICLE SSVI	2						ŀ	L
	PVIAK SSVI	HYPOTHETICAL IN TRUTHETIN	STATE OF CHILS LIKE PARTICLE SSVI								
INTRODUCE INCL. 19 NOTES STATEMENT OF THE PARTICLE SIVI INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN INTRODUCE INCL. 10 NO PROTEIN	PY166 ADE07	SIYPOTHE SICAL 13 7 KD PROTEIN	AND A PERSONNELLY TYPE 2	119.166							
	1 SS X 1 A	HYPOTHETICAL PROTEIN C.164	HOMEN ACTION TO BE BARBER & SAVI	1:1	13.111						-
	PY IN SSVI	INVESTIGATION OF THE PROPERTY	SOLI GLOBO VINOS VINOS PARA PARA PARA PARA PARA PARA PARA PAR	9	118-150						\downarrow
INVOING TICAL 16 OR D PAOTEN INVOING TICAL 20 A CD FAOTEN INVOING TICAL 20 A CD FAOTEN INVOING TICAL 20 A CD FAOTEN INVOING TICAL 20 A CD FAOTEN INVOING TICAL 20 A CD FAOTEN INVOING TICAL 20 A CD FAOTEN INVOING TICAL 31 A CD FAOTEN INVOIN	1735 267	HYPOTHETICAL 13 BED PROTEIN	SIGN COLORON STATE	102-136							
INPOTIETICAL 26 A EO PROTEIN INPOTIETICAL 26 A EO PROTEIN INPOTIETICAL 26 A EO PROTEIN INPOTIETICAL 26 A EO PROTEIN INPOTIETICAL 27 A EO PROTEIN INPOTI	1010	HYPOTHETICAL ISOND PROTEIN	SULFOLGED VINOS CINCE CONTRACTOR	13.107							
INVOING TICAL 35 14 D PROTEIN SULFOLOBUS VRUUS, LIKE PARINCLE 33 1		INVESTIGATION TO A KD PROTEIN	SULFOLOBUS VIRUS LIKE PARTICLE 33.1	137.180							
INVOIDE RICAL TO PROTEIN SOURCE ARE CAROLIC LOSTILE VAINTS INVOIDE RICAL STATE PARTICLE SSVI INVOIDE RICAL STATE PROTEIN SULFOCUS VIRUS-LIKE PARTICLE SSVI INVOIDE RICAL STATE PROTEIN SULFOCUSION SVIRUS-LIKE PARTICLE SSVI INVOIDE RICAL STATE PROTEIN SULFOCUSION SVIRUS-LIKE PARTICLE SSVI INVOIDE RICAL STATE PARTICLE SSVI INVOIDE RICAL PROTEIN SULFOCUSION SVIRUS-LIKE PARTICLE SSVI INVOIDE RICAL PROTEIN SULFOCUSION SVIRUS-LIKE PARTICLE SSVI INVOIDE RICAL STATE PARTICLE SSVI INVOIDE	100	NI SECRETARIA SECRETAR	SULFOLDBUS VIRUS-LIKE PARTICLE SSVI								
INVOIDE IN A FOR FOLIS SULFOCIOUS VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SIND INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SAVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE IN A FOR FOLIS SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE FABILICE SSVI INVOIDE SULFOCIONES VIRUS-LIKE STATICE SAVI	23001		SOYDEAN CID OROTIC MOTILE VIRUS					<u> </u>			
HYPOTIGETICAL 11 TO PROTEIN SULFOCOMIS VIRUS-LIKE PAATICLE SSVI INPOTIGETICAL 11 TO PROTEIN AUTOCAAPIA CALIFORNICA POLITICATOSIS VIRUST INPOTIGETICAL 11 TO PROTEIN SOVIEMA CALIFORNICA POTICE SVI INPOTIGETICAL 11 TO PROTEIN SOVIEMA CALOGOTIC MOTTLE SVI INPOTIGETICAL 11 TO PROTEIN SOVIEMA CALOGOTIC MOTTLE SVI INPOTIGETICAL 11 TO PROTEIN SOVIEMA CALOGOTIC MOTTLE SVI INPOTIGETICAL 11 TO PROTEIN SOVIEMA CALOGOTIC MOTTLE SVI INPOTIGETICAL PROTEIN SOVIEMA CALOGOTIC MOTTLE SVI INPOTIGETICAL PROTEIN SOVIEMA CALOGOTIC MOTTLE SVI INPOTIGETICAL PROTEIN SOVIEMA CALOGOTIC MOTTLE SVI INPOTIGETICAL PROTEIN SOVIEMA CALOGOTIC MOTTLE PARTICLE SSVI	PYSIK SSVI	HIVE ILAL PROICES	SIR FOLDBUS VIRUS-LIKE PARTICLE SSVI		3			Ť		L	L
INPOPERICAL II TAD FAULTIN AUTOGLAFIA CALIFORNICA NACLETA POLYREDADSIS VIRUS INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN INFOTIE RICAL FOOTEN SUCCESSAR CALOROTIC SOUTE SIVI	PY 12K SSVI	HYPOTHETICAL 31 3 KD PROTEIN	CON SON CALLS VIRUS-LIKE PARTICLE SSVI	110-111							L
INVOIRE IICAL 13 % DP MOTEIN SOVYBEAN CAGAGITE MOTTLE VINUS INVOIRE IICAL PROTEIN SUNTE WILL SOVYBEAN CAGAGITE MOTTLE VINUS INVOIRE IICAL PROTEIN SULFACE SOVYBEAN CAGAGITE MOTTLE VINUS INVOIRE IICAL PROTEIN SULFACE CAGAGITE WAS SOVYBEAN CAGAGOTTE WILLS INVOIRE IICAL 13 % DP MOTEIN SOVYBEAN CAGAGOTTE WAS SOVYBEAN CAGAGOT	PY 11K MPVAC	INTONETICAL 11 TED PROTEIN	A IT CORAPITA CALIFORNICA PUCLEAR POLYTIE DAOSIS VIRUS	133-341							
INYOTHE ICAL PROTEIN SULFCORUS VIRUS-LIDE PARTICLE SSV1 INYOTHE ICAL STAPFOLEIN SOVERAN CRECAGOTIC MOTTLE VIAUS INYOTHE ICAL STAPFOLEIN SOVERAN CRECAGOTIC MOTTLE SSV1 INYOTHE ICAL PROTEIN SOVERAN CRECAGOTIC AND STAFFUL SSV1 INYOTHE ICAL PROTEIN SOVERAN CRECAGOTIC AND STAFFUL SSV1 INYOTHE ICAL PROTEIN SOVERAN	PY1 SOCHY	IN POTIETICAL STREEPROTEIN	SOUTH AN CAN DED TIC MOTTLE VIRUS	113.149				1			-
INVOING FIGAL 59 KD PROTEIN SOURGEAN CREADITE MOTTLE VIAUS INVOING FIGAL PROTEIN SOURGEAN CREADITE MOTTLE VIAUS INVOING FIGAL 13 KD PROTEIN SOURGEAN CREADITE COTTLE VIAUS INVOING FIGAL PROTEIN SOURGEAN CREADITE COTTLE VIAUS	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	IN POTIETICAL PROTEIN)	SOLDEN CALCADOR JUNE PARTICLE SSVI	=							-
INYDOING TICAL PROTEIN SOVERA CALDED IN STATE SAVICATION SOVERA CALDED IN STATE SAVICATION SOVERAN CALDED IN STATE VIRUS	AND CAR	INPOTITE FICAL SOKO PROTEIN	SULFOCUSION VINOS CONTROL MANAGEMENT	2 3							-
INTOTINE INCL. 51 7 ED PROTEIN SQUARM CALDIFOLISTICS VINUS TING VINUS INTOTINE VINUS TING VINUS	NO.	INPOSIGE TICAL PROTEIN?	SOVEEN CREMENT TO THE TIME SOLIT	81:13	503-537	\$46-587	638-700				
HYPOTHETICAL PROTEIN	VI. 100	INTOTICE TICAL 85 7 KD PROTEIN	SULFOLOUGH VINDS-LINE PARTICLE 2371	6-9						1	_
	10000	Т	SOVELAN CROPOTIC MULLS VINGS	14.111	164-331						
MONTHER TICAL BANDII ORTI PROTEIN FOWLDOX VINUS (1500, ATE ID ASSAULT II)	The same	Т	FOWLPOX VIRUS (ISON ATE ID 414 MUNICHI)								

		All Vigures (no beeltribghages)		1 4 4 4 4 4	AREAS	, REA	385.32	ABIA	ABEAT	47.00
,	PROTEST	WALS.	Τ	T		Г				
TOWN TOWN		TOWLPOX VIRUS (1504 ATL 10"-610 AND WATER	T	1						
Ī		OWIPOX VIRUS (ISOLATE IIP-418[ATUNICII])	T							
		TOWARDS VINUS (150LATE 10" JIHANUS/CHI)		i						
Nan Johnson		FOWLPOX VIRUS (ISOCATE ID-A) I (MUNICILI)	11.13							
L'ANDI DIOLA		OWL POX VIRUS (ISOLATE 10-4) ([NUNICH])	162-233							
P. BIS TOWN	INTO THE ACTUAL OF THE PROPERTY	FOWLPOX VIXUS (ISOLATE 112-431[A(UNICHI)	=	2 2						
PARIS FOWEN			137-163	j						
77RL3_EBV	Olem	MILKPESVIRUS 4)	158.506							
P10311 165157	20.0	HER PECKARITE CAINING 15 TRAIN 121-73	147.118							
PV.F 10 FOWP1	NO DE LECTO	TOWN BOY CORIS OF A 10 FP. II	160.204							
PI GAI JISVA		STEAM INC. IN CARDING	116-311							
PIGAL HSVADI	COPROTE		136.311							
PHILL VACCV	COPROTEI	IALER'S DISEASE HERE'S VIRUS (STRAIN HILD) (THE TOTAL	14.71	100						
PHIR) VACCV	Z	VACCINIA VIRUS (STRAIN WR)		111.33						
P. K.R. CBV	KD PROTEIN	VACCINIA VIRUS (STRAIN WR)								
PALLY ADEAL		EPSTEIN: BARR VIRUS (STRAIN BOS-I) (HUNIAN HERPESVIRUS 4)		Ì						
	IN 33 KD PROTEIN		1							
100		ERFESVIRUS 4)	64-123							
TOTAL CONTRACT		CONDIETINA YELLOW MOTTLE VIRUS (COTALY)	94-143							
2007		COMMELINA YELLOW MOTTLE VIRUS (COMMV)	11.11							
יייייייייייייייייייייייייייייייייייייי	,	LELYSTAD VIRUS (LV)	100-134							
NOT TAKE		THE BAIDPROTEUS TENAX VIRUS I (STRAIN KRAI) (TTVI)	10.50							
PIONI ADEGI		WANN ADEMOVIEUS GALLISTRAIN PIELPS) (FOWL ADENOVIR)	70-127							
PLORA TIVI		ALIAN ALCHONING STRAY VIOLE LATER IN ERALLITIVE	21.67							
PLUED TIVE	IIVPOTITE TICAL B I KO PROTEÍN	HERMOTEUS ILTAA VIAUS I (SIRAII)	-	96.130						
TOME TIVE	ILYPUTHETICAL IS & KID PROTEIN	THERMIOPROTEUS TENAN VIRUS 1 (STRAIN KRAI) (FIVE)								
Picht IV	HYPOTHE FICAL IS 3 KD PROTEIN	THE RAIDPROTEUS TENAX VIRUS I (STRAIN K.A.I) (1171)								L
11VI	HYPOTHETICAL 16 B KD PROTEIN	THE ILICHROTEUS TEMAX VIRUS I (STRAIN RIAT) (TIVI)								
PYCON TANK	IIYPOINETICAL 73 KD PROTEIN	THERMOPROTEUS TENAX VIRUS I (STRAIN KRAI) (TTVI)								
1212	HYPOTHETICAL 18 7 KD PROTEIN	HERMIOPHOTEUS TEMAX VIRUS I (STRAIN KRAI) (TIVI)								
PAPEL B18V	ILYPOTHETICAL 13 1 KD PROTEIN	HERAIOPROTEUS TENAX VIRUS I (STRAÍN KRAÍ) (TTVI)								
278	NYPOTHETICAL PIS PROTEIN	AICE TUNGAO BACILLIFORM VIRUS (RTBV)	27-12							
	HYPOTHETICAL PLY PROTEIN	RUCE TUNGRO BACILLIFORM VIRUS (1504 ATE PHILIPPINES) (RTG								
200	HYPOTHETICAL P14 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (RTBV)	\$1.101	2						
781	NYPOTHETICAL P14 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PITILIPPINES) (RT	31-101							ļ
SVEAL BIRVE	HYPOTHETICAL P46 PROTEIN	AICE TUNGRO DACILLIFORM VIRUS (RTBV)								
TAVEL PARTY	IIVPOTITE TICAL P46 PROTEIN	RICE TUNGRO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (RT		10.4				1		
P. P. P. P. P. P. P. P. P. P. P. P. P. P	HYPOTHETICAL PROTEIN IN PO S SREGION	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUSA								
PVPOII KPVAC		TOBACCO MECROSIS VIRUS (STRAIN A) (TNV)	•							
PYPOL IPNY	HYPOTHETICAL 23 6 KD PROTEIN IN PULYHEDRIN S	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS I								
PYO! ANIEPY		INTECTIOUS PANCHEATIC MECROSIS VIAUS (SENOT THE MAYEN								
PYOJ AMERY	INPOTESTICAL 14 KD PROTEIN IN TK STEGION	AMSACTA MOORE! ENTORIONOXVIRUS (AMERVI)		20.50	140.113					
PYRJ 115V6G	HYPOTHETICAL PROTEIN IN TR TREGION	ANSACTA MODILE ENTONIOPOR VIRUS (ANIETY)	776.101							L
PYTE HISVEG	HYPOTHE TICAL PROTEIN RFT	MENDES SINGLEX VIRUS (1 TTE B) SINGLES								L
PYRC HSV6G	HYPOTIGITICAL PROTEIN IU)	HEADES STAULEX VIXOS (1772 6/3) MAIN US)		404.443						
PYEN BY6	INPOTIETICAL PROTEIN RF4	HEILPES SINDLES VIRUS (1 TPE 6/ 3) FAMIN US)								L
PYRAI ERV	AEPETITIVE PROTEIN ORS?	CHE O INDESCENT VINUS (CIV) (INSECT INDESCENT VINUS 1TH								
Ves tayye	HYPOTHE TICAL BRUE! PROTEIN	EPSTEIN-BARA VIRUS (STRAIN BOS-E) (HURLAN JEHVESVIRUS 4)								
	INVOING TICAL BERF! PROTED	EPSTEIN-BARA VIRUS (STRAIN 895-8) (IMBIAN HERPESVIRUS 4)	_					-		-
THE PERSON	INPOTIGETICAL BIRE I PROTEIN	EPSTEIN-BAKK VIRUS (STRAIN 095-4) (HUMAN HERPESVIRUS 4)	200							
2001	LIVEOUR IKAL 14 0 KD PROTEIN IN UBIQUITIN 11	ORGYTA PSEUDOTSUGATA MULTICAPSID POLYIEDROSIS VIRUS		10.00						L
2000	HYPOTHETICAL IN O KD PROTEIN	VACCIMIA VIRUS (STRAIN COPENHAGEN)						ļ		
NAVA VACCE	HYPOTHETICAL 93 KD PROTEIN	VACCINGA VIRUS (STRAIN COPENHAGEN)								
NAME OF THE PERSON NAME OF THE P	HYPOTIGTICAL 14 5 KD PROTEIN	VACCINIA VIRUS ISTRAIN COPEMIAGENI								
ALVAIN CALLE										

क्षारु ।	
AREA AREA	
AREAL AREAL AREAL AREAL	
2000	
AUCAV	
DEEA!	
11-51 11-51 11-48 11-48 10-80 14-10 10-51 10-51	
ALI Virus (to beteriophyte) VACCHA VIRUS (STAAN COPENIAGEN) VACCHA VIRUS (STAAN COPENIAGEN) VACCHA VIRUS (STAAN COPENIAGEN) VACCHA VIRUS (STAAN COPENIAGEN) VACCHA VIRUS (STAAN COPENIAGEN) VACCHA VIRUS (STAAN WE) VACCHA VIRUS (STAAN WE) VACCHA VIRUS (STAAN COPENIAGEN) VACCHA VIRUS (STAAN COPENIAGEN)	
All Vieuri (ne britriughage) VACCIDIA VIRUS (STIALIN COPENILAGEN) VACCIDIA VIRUS (STIALIN COPENILAGEN) VACCIDIA VIRUS (STIALIN COPENILAGEN) VACCIDIA VIRUS (STIALIN COPENILAGEN) VACCIDIA VIRUS (STIALIN WE) VACCIDIA VIRUS (STIALIN WE) VACCIDIA VIRUS (STIALIN COPENILAGEN) VACCIDIA VIRUS (STIALIN COPENILAGEN)	ĺ
ALI Virges (no instrumbage) ALI Virges (no instrumbage) ALCENIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC VACCINIA VIRUS (STRAIN CC	
All Vines VACCINI, VACCINI, VACCINI, VACCINI, VACCINI, VACCINI, VACCINI, VACCINI, VACCINI,	
19 KD PRO 19 KD PRO 19 KD PRO 19 KD PRO 19 KD PRO 19 KD PRO 19 KD PRO 19 KD PRO	71.24
HETICAL HETICAL HETICAL HETICAL HETICAL HETICAL HETICAL	VENT NET IN
	2
TENE VICE VACC VICE VACC VIDE	
RIBSISISISISIS	L

TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

- 		All Victors (so beck-roping)	AOFA	ILV 2	ARES I	AREA	AREAS	10110			
7 			T	97.	1143-1169						1
	Z.O.I.L.	CCO NATTLE VIRUS (STRAIN S134)	Т	İ						1	:
				; 			İ				İ
				:	1						
				i	-						! i
			-		-						
			٦		į						
۲			10.43								!
		TOTALIST COLON CONTRACTOR AND AND AND AND AND AND AND AND AND AND	104-133					1			!
DAVID TANK			20:10								
+	A LIPTURE CALCADA. HT MOMOLOG	4 Julyi Chiltrid	Γ	69.04	430.032	\$10-625					
7			Ī	100	100						İ
_	M KD A. TYPE DICLUSION FRO			3							
	II KD A. TYPE DACE USION PRO		306-315								1
	AT PLAT TRANS. DED FACTOR 78 KD PRO		100.115				į	ļ			:
	THE PARTY OF THE P			-	-						
	ALTIA BANDON ALTIA	Cardy Nichal St. Rep. M. Cardy Barrier	2								
L	ALPIN TRANS-DO FACTOR 63 KD FRO		35.210								
Ţ,	AT BUTA PRANCING PROTEIN	EQUING IGADES VIRUS TYPE I ISTINATE ABOUT	T		176.478	111.620	<u> </u>	914.970	1214-120	-	
A I IM RISVES	The second secon		ī								
PATI COMPX	A.ITTE DELLOSON FROIEN	Vinite (CIBAN 895.6)	_								
WZLS EBV	BELL'I TRANS-ACTIVATOR PROTEIN	College Service Colleg	=	117.104							
20000	FELT GREACE BOODING PROTEIN	VACCINIA VIXUS (STRAIP COTETTION	-	117.144							
NIN ANCE	COLL SIMPACE BROWN PROTEIN	VACCINIA VIAUS (STRAIN WR)	Ī								
CAMPI VACCV	CELL BURN ALL BURNSHIP SECTION	VARIOUS VIEUS	1								
CASH VARV	CELL SURVACE-BUNDING PROTEIN	The state of the state of the state and ky A)	112.339					ļ			
Act to the trees	CELL FUSION PROTEIN PRECURSOR	EQUINE REJUES 1172	23.154								
	NAME OF TAXABLE OF	HERPESVIRUS SADAIRU (STRAIN !!)					L				
COO 10 VA	C I CLIC MANAGEMENT	HAMSTER POLYONAVIRUS									
PCOAL POWIA	COAT PROTECT VF	SUBINITIES ENGINEERING PROPERTY OF STREET	2								
PCOAT REDV	COAT PROTEDY VP2	BUILDERICAN	2.5								İ
	COA P BEOTTON VP2	BOVING POLYCALAVIRUS									
200	The state of the s	POLYDMANTALIS IC									
KOAI POVK	COAT PROTEIN VIZ	SOCIAL PORT PORTA VIRUS	30.204	İ							
ROAJ POYLY	COAT PROTEIN VP2	CANADA SOLONIA CONTRACTOR AND MILITARIA	33.49	ĺ							
PCOAT POVICE	COAT PROTEIN VP2	MOSE OF TOTAL STATE OF THE STAT	178.205								
5000 EVE	COAT PROTEDY VY3	SDAIAN VIRUS 40	2 00								
5	PROBABLE COAT PROTEIN 3	ADENO-ASSOCIATED VIAUS 2	5								
202	100000000000000000000000000000000000000	THERMOPROTEUS TENAX VIAUS I (STRAIN KRAI)							L		
יייון אסטי	COALPROIEM	AL PITTIAN MINK DISEASE PAR COVINUS (STRAIN G)	177								
MOAT ADVG	COAT FROIEIR VF	DE AN I EARBORT WRUS	123	į							
PCOAT BLAV	COAT PROTEIN	STATE OF STA	8.6	143-220	191.181						
TVALA PANY	COAT PROTEDI	CALL DIOWER MUSAC VINOS (STATES)	18.81	25.22			_				
200	COAT PROTEIN	CALL IS LOWER MOSAIC VIRUS (SIRAIN LAIL)		101.330							
1	20.000	ICALE DI OWER MOSAIC VILUS (STRAIN BBC)	2		1						
COAT CAMM	COALTRUIE	CASH THE DWER MOSALC VIRUS (STRAIN WARIS)	B.C								L
COAT CACA	COAT PROTEIN	TANK HI DUNER MOSAIC VIRUS (STRAIN STRASBOURG)	64-91								
PCOAT CALVIS	COAT PROTECT	CACALLIANTE CAPITE]								
PLOAT CALLIV	COAT PROTEIN	CARATION MOUTE VINOS	11.16								
SOAT CINE	MAIOR CAPSID PROTEIN	PARAMECRIM BUTSAUM CHUCKLEN TINGS	134.163			L					
	TO A DESCRIPTION	CUCUNDER MECROSIS VIRUS						L	L		
5	2000	CHOOMIS STRUATE MOSAIC VIRUS				-					
NOV COM	COASTA	I'M OVER YELL OW MOSAIC VIRUS	20.20								L
COAT CARY	COAT PROTEIN	CE: FOR PAINTING STRAIN CFUSE FIVE	×64-400						1		
POAT FCVC	COAT PROTEIN	TELEFORMATION OF THE AND AND COMMENTAL OF THE PROPERTY OF THE	516-543	246-600 546-600					\downarrow		
MCOAT BEVEA	COAT PROTEIN	PELWE CALLIVORY	410.546	(09-69)		_	_				
	COAT PROTEIN	SELINE CALICIVILIS (STRAIM PT)		311			L				
200	TOTAL STATE OF THE PARTY OF THE	FIGWORT MOSALC VIRUS (STRAIN DXS)	1000						L		L
PCOAT FAND	PROBABLE CUAL PROTEIN	H Y SYLONOLESS VIRUS	3-700	26.2			1	\downarrow			
PCOAT LSV	COAT PROTEIN	THE STATE STATE AND THE STATE OF THE STATE O	139-166				_				
PCOAT MOSV	COATPROTED	MUSCANIANS SERVICES CONTROLLS	106-133					_			
PCOAT ONSV	COAT PROTEDY	COOKIOGOS COMPANION COMPAN	324-551	368-996							
PCOAT PAVIG	PROBABLE COAT PROTEIN VP	KOMAN PALVOVICES BIT	3								
AND LACT	COAT PROTEDY	POPLAR MOSAIC VIRUS (INCLASE ATTENTY)	138.163					-			
2702	COAT PROTEIN	SOYBEAN CILCROTIC MUTILE VIRUS	1					L			
200	CENOME POLYPROTEIN	TAKARILO MOSAIC VIRUS	916			L	L				
1	TO A T SECTION	TOMATO ASPENANT VIRUS			ļ				-		
VOAT TAV	COAL CROSSES	POMATO BUSHY STURT VIRUS (STRAIN BS.))	1			 			-		L
PCOAT TISVE	COALPROIEDA	TOWATO BUSHY STUNT VIRUS (STRAIN CHERRY)	97:134			-					
PCOAT TBSVC	COAT PROTEIN										

							r	-	-	-	Γ
PCCENE		All Virus (se secreting life)	ARGAL	AREAL	163KA	ONTA C	SKA S	METAL ABEAL	12 SHEAL	38.	-1
THE RAPIE	COATEGO	TURNIP CHINALE VIRUS	П					<u> </u> 	<u> </u>	 	;
PONT PROTECTION		TOBACCO MILD CREEN MOSAIC VIRUS	104-131					1		1	1
POAT TAV		TOBACCO MOSAIC VIRUS (VULGARE)	2			İ		1		4	1
PCOAT DAVCO		TOBACCO MOSAIC VIRUS (STRAIN COWPEA)	Ē			İ	1	+	1	<u>:</u> T	1
PCOAT THYBA		TOBACCO MOSAIC VIRUS (STRAIN DAJILEMENSE)	2			1	Ì	1	1	1	<u>.</u>
PCOAT THYER		TOBACCO MOSALC VIRUS (STRAIN ER)	3			İ	1	1	<u> </u> 	Ť	1.
PCOAT THVO		TOBACCO MOSALC VIRUS (S) RAIN O MA KOKUBU)				Ì	İ	1	<u> </u>	1	i
PCOAT THYOM		TOBACCO MOSAKC VIRUS (STRAIN ON!)		Ī			<u>:</u> 	<u> </u> 	: 	:	
PCOAT TAVTO	COATPROTEIN	TOBACCO MOSAIC VIRUS (STRAIN TOMATION.)				Ì	<u> </u>	<u> </u>	<u>:</u> -	<u> </u>	;
PCOAT THYA		TOBACCO NECROSIS VIRUS (STRAIN A)				Ì	1		<u> </u>	<u> </u>	ī
PCOAT TRVPS	COATPROTEIN	TOBACCO RATTLE VIGUS (STRAINS PSG and PLB).				1	1		 	1	ī
PCOAT TYDVA		TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	3				Ì	<u> </u>	-	-	Ī
PCOAT TYMY		TURKE YELLOW MOSAIC VIRUS					1			-	Ī
MOAT TYNA		TURNIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)	=			İ			<u> </u>	<u> </u>	1
PONES ADEST	A-BINDING PROTEIN	HEMAN ADENOVIRUS TYPE 1	-		-			1	<u> </u> -	<u> </u>	i
VE 55		EPSTEIN-BANA VIRUS (STRAIN DOS-8)	8	200		Ì		1		+	ī
PDRGI HOKYA	MAJOR DNA-BRYDING PROTEIN	IRDIAN CYTOMEGALOVIRUS (STRAIN AD169)							 -	<u> </u> 	ī
PENEL HEVSA	MAJOR DNA-BROOMS PROTEIN	IERPESVIRUS SAIMIN (STICKIN II)							<u> </u> -	-	ī
PDINES MICHAE	ROTEIN	MUMURE CYTOMOGRALOVIRUS (STRAIN SAITTE)						\mid		-	Ī
PONTE POVIC		POLYOHAY BUS AC		917 117		Ì				-	ī
PRO FONC	BINDING PROTEIN	Spidan CTICACCALOVINOS (STRAIN COLBURA)	10.00		131.115	Ī		-		<u> </u>	Ī
PONEL VACCO		VACCINIA VICO (SINGER COTENIA CENTA COTENIA CENTA COTENIA COTE	9	8	38.183	İ		-	<u> </u> 	<u> </u>	i
אכני		VALUENA VICTORIA WAS	1	3.18	1	Ì			 -	 -	ļ
PDP&J VARV		VAUULA VIRUS					ļ		<u> </u> 	<u> </u>	I
PDPOL ADEIL	POLYNERASE	HONAN ADEXOVALUS TYPE 17		303.340		Ì		T	 -	L	Ī
POPOL CREDV		CHOUSING LIKE BEET SCHICK CONTROLS	110.141					-		L	
PDPOL CIVINS		CALCHELLA VICOS PIECAS	110.363			Ī			-	L	Γ
Pord Chivi		Course to the second se	=	30-416	250.03	27.78					1
POPOL FOWN	DAY FOLTMAAS	STATE OF THE PARTY OF THE AND ADDRESS.	153.780						L	L	<u> </u>
POPOL HOPVA		CONTRACTOR OF THE CONTRACTOR STANGED DICK ISOLATERS	2				T				
Neg Code	DAY POLYMERASE	DUCK HEPATITIS & VIRUS (STRATH CHINA)	=								
AUGUS PORCE		DUCK HEPATITIS B VIBUS (WILLE SHANGIAL DUCK ISOLATE 511)	=	10.20							
SOLON NO.		GROUND SQUIDLEL HEPATITIS VIRUS	211-335								ī
POPOL IDENT	DNA POLTNERASE		9.39							4	1
POPOL HOBAY	DNA POLYNGAASE	STRAIN PHILIPPINOPFDW294)	434-41)				1			4	Ī
POPOL HUBYZ	DHA FOLYNGRASE	HEPATITIS B VIXUS (SUBTYPE ADYW)	40.470						 	+	ī
POPOL HSVII	DHA POLYNGAASE	ICTALUNID HEAPESVIRUS I	326.364	110.117		Ì	1		1	1	ī
PDPOL HSVSA	DNA POLYNGRASE	IEDESVEUS SADERI (STRAIN II)	200			Ì	\dagger	1	1	 	1
POPOL NOVAC	DNA POLYNGRASE	AUTOGRAPHA CALE GRANCA NUCLEAR POLITIEDROSIS VIRUS				Ť	Ť		+	-	Ī
POPUL MANEE	COA POR VICEBACE	VACCIDA VILLE (STRAIN COPENHAGEN)	10.101				İ				
PDPGL VACCV	DNA POLYNEJAST	VACCEMA VEUS (STRAIN WA)	730-797							-	ĺ
PDPOL VARV	DNA POLYMERASS	VARIOLA VIRUS	769.786						+	+	Ī
PDPOL WHY!	DNA POLYMERASE	WOODCHACK REPAILITS VANUS I	20.					+	1	\downarrow	1
PDPOL WHYS9	DHA POLYNGRASE	WOODCHUCK HEPATITIS VIRUS SO	2			1	\dagger	1	 	1	Ī
TDPOL WHY	DHA POLYMERASE	WOODCHUCK REPAILITS VIRUS 7				1	1	1			ī
POPOL WHYS	DNA POLYNGJASE	WOODCHUCK HEPATITIS VITUS I	200	2 2			t		+	+	Ī
PDPOL WHYS	DNA POLYMEJASE	WUCKULACK METAILIS VIAUS .				Ī	t	<u> </u>	+	H	ī
POLICE COLUMN		COLYMERIAGE BETA	33.340				T	-	-	Ļ	Π
100 X CO.	DESCRIPTION TOWN PRECITED	CONTRACTOR DATE TA	516-313							_	Ī
1	DETRIBUTE VEHICLE OF THE CONTROL A CE	EALTH MEDERATE TYPE 4 (STRAIN 1942)	110				T		-		Ī
POUT HEVEA	THEORY OF THE PRINCE PROCESSES	INERPESYDUS SADIOU (STILAN !!)	34.35								1
1	EIB PROTEIN LARGE T-ANTIGEN	HUNKAN ADENOVIRUS TYPE 1	138-153								
L	EIB PROTEDY LANGE T-ANTIGEN	HEDGAN ADENOVIRUS TYPE 40	134-163						-	-	Ī
PEUNS ADEIN	EIB PROTEIN, SMALL T. AMTIGEN	INDIANA ADENOVIAUS TYPE 12	2				1	$\frac{1}{2}$	$\frac{1}{1}$	$\frac{1}{2}$	7

			П	_			1	ABEAG	AREAS	AREAS	AREAS
PCGENE	167617824		3	7	7	_		•			
FILE HAME	PROTEIN	CARLO ADEMOVIATION TYPE I	2	-		:	į	i !		:	i
PEIBS ADEMI	EIB PROTEIN, SMALL T.ANTIGEN		= =	Ì							
PEDIA ADEGS	EARLY EIB 14 KD PROTEIN						T	Ī			-
PEJ14 ADE07	EARLY ED 15 1 KD PROTEIN		٦	B	1		†				<u> </u>
PEJ 78 ADED3	EARLY ED TO 1 KD GLYCOFIOTEIN		ر اهر				İ	ĺ	Ì		
PEIN ADES	EARLY ES 20 S KD GLYCOPROTEIN		133-101	-		:	!		į	_	
PELLI ADELS	EARLY ES 20 6 KD GLYCOPROTEIN	HUMAN ALCONOMINE TOWN	¥.	_			_			_	
PEIG ADENI	EARLY ES 17 1 KD GLYCOFROTEIN		£.2	-	!		-	1			!
PEAR EDV	EARLY ANTIGEN PROTEIN R		107-701	470.497							
VERT VALV	EARLY TRANSFACTOR TO KD SUBUNIT		430-468								
PENN AVIET	ENV POLYPROTED ⁴	S VINOS	13	426.474							
2	SAN BOL VERNIEN		1								
PENV AVION	THE COMPANY OF THE PARTY OF THE	BABOON ENDOCENOUS VIRUS (STRAIN KIT)	Т	197.05	631.005						-
PENV BARYM	EN POLITICISM	BOVING INCAMPRICE PICE NOT VIRUS (ISOLATE 196)	1								
PENY BIVE	ENV POLYPROTEIN	SOUTH BANADAPETITIENTY VIRIS (ISOLATE 127)	7.44	313-637	3						
PENV RIVE	ENV POLYPROTEIN	BOVINE INDUNATION OF THE LAND AND AND AND AND AND AND AND AND AND	304.13								
AKAN BI VAR	ENV POLYPROTEIN	BOVING LEUKEMA VINOS INTERNATIONALISTA	104.33								
	Manual Value of the Party of th	BOVINE LEUKENDA VIRUS (AUSTRALIAN ISOLATE)									
PENV BLVAU	ENVIOLENCE DE LA COMPANION DE	POVDNE LEUKEADA VIRUS (AMERICAN ISOLATE VON)			ĺ						
PENV BLVAV	ENV POLYFRUIEM	BOOME I FIREMA VIEWS (BELGIUM ISOLATE LB385)									
PERV BLVB2	ENV POLYPROTED	TOWNE TELEVISION VIBILE (REL CATALISOLATE LB39)	304.177								
PENY MALVES	ENV POLYPROTEIN	BOVER LEGISLAND AND AND AND AND AND AND AND AND AND	304-373								
N N	FNV POLYPROTED	BOVING LEUKEMIA VIKUS (196 ANG) CONTROLL CONTROL	165-192								
TEN PERSON	ELIV BOIL YPROTEIN	CAPIDIE ARTIQUTIS ENCEPTIALITIS VIRUS (STRAIN CO.)	215								
	THE PART WAS DIEDE	EQUINE IN ECTIOUS ANEAUA VIRUS (CLONE 7) 2-1)									
PDV ELAVI	- ENVIOLEN	FORDOR BEECTIOUS ANGINA VIRUS (CLONE P.) 2-2)									
PENV ELAVI	ENV POLYPROTEIN	PROPERTY THE CONTRACT AND MINISTER COLONE P. 3.3)	644-712								
PENV ELAVS	ENV POLYPROTEIN	ECONE DE CONTRACTOR CONTRACTOR DE 2.5)	247-675								
PENV ELAVS	ENV POLYPROTED	ECUINE DATE INCOME AND A CONTROL OF TAKE A LAND A L	211. 999								
200	ENV POLYPROTEDI	EQUIPE INFECTIOUS AVENIA VIRUS (CLOVE 139)	506-024								
200	FNV POLYPROTERY	EQUING INTECTIOUS AVENUA VIAUS (LLUNG LLUS)	216-975								
	ENV POI VPROTEDA	EQUINE DIFECTIOUS ANEMA VIRUS (STRAIN WAS)	\$16.313								
PENV ELAVA	SAN DO VERDISON	EQUINE DOECTIOUS ANEMIA VIRUS (ISOLATE WYOMING)		77.							
TENV ELAVI	Service vehicles	FELTING ENDOCENOUS VIXUS ECE!	2000								
PENV PENVI	- Car Country	I FEI THE INDIADODE FICTENCY VIRUS (ISOLATE PETAL UPIA)	200								
PENV STATE	ENV POLYPROIECE	THE WAR HANDON'S HOUSENEY VIRUS (150LATE SAN DIEGO)	639-442	120-141			Ţ				
PEN FIVE	ENV POLYTROJEDN	TEL THE HANDHODE ICENCY VIRUS (ISOLATE TAU)	640.678								
PEN HYTS	ENV POLYPROTEIN	STINE STREAM PROVIDE CLONE CFE-4)	504-514								
PENV FLVCA	ENV POLYPROTEIN	THE TANK THE PARTY CONTINUES OF THE ARCH A SCHOOL !	490-519								
PENY FLVG	ENV POLYPROTEIN	SELING LEUKEPUA VICOS (SINGERA) ANGRA EL	\$10-579								
B IV S VICE	ENV POLYPROTEIN	FELING LEUTEMAN VINOS (31 PART)	497.516								
PACA EL VICA	ENV POLYPROTED	FELDAT LEUKENDA VINUS (STRAIM SANAMA)	1	118.33	166.69)						
200	EMV POR VPROTEIN	INDIAN SPUNARETHOVINUS	415 410								
1000	ENV BOT VPROTEDI	FELTINE SARCOMA VIRUS (STRAIN GARDMER-ARMS) EIM)							L		
200	TO NO CONTROL	FELDE SARCOMA VIRUS (STRAIN GA)		İ							
NA SAC	THE POST OF THE PARTY OF THE PA	FEL ING SARCONA VIRUS (STRAIN SM)	200								L
	The same of the sa	GRACIN APE LEUKENDA VIDUS	100			1					
ADA CET	ENV POLITICAL	HUBANN FOEL LEUKENDA VIRUS TYPE I (STRAIN ATK)									
PEN HILLY	ENV POLITICAL ENV	HABIAN POELL LEUKEADA VIRUS TYPE I (CARIBBEAN ISOLATE)	2			1					
PERV HILLIC	ENV POLYTHUI EUR	INMAND TARES SECREDADA VIRUS TYPES (ISOLATE MIT.S)	142.176								L
YEAV HITLIN	ENV POLYPROTEIN	HANDAN PARTILIER BADA VIRUS TYPE II	336-370						1		
PENV HTLV2	ENV POLYPROTEIN	LINESCO BALL BANDERICHENCY VIELUS TYPE I (ARVUST 2 150LATE)	344-592	430-462	30.62						
PENV HVIAL	ENV POLYPROTEDI	THE PROPERTY OF THE PARTY OF TH	345.594	631-663	191-818						
PEN HVIBI	ENV POLYPROTEDI	HADRAN BONGACO PLETA CONTRACTOR I MILE ICOLATES	\$40.519	676.478	116-613						
PENY HVIBS	ENV POLYPROTED	PRINCIPLE RULE PLUE TO CARDO A CORTO A	263.784	116.365	262.500	628.679	717.615				
MILAN VALIDA	DAY POLYPROTEDA	INDIAN DOMINER REPORT VINOS 1 10E 1 100 A 111	526.589	110.610	20.00	L					
SIAT AND	ENV POLYPROTEDY	INDIAN DOAMOOF KIESKY VIRUS LITTE LENG 1905ALL	167.590	133.404	643.695	803.63					
200	DAY FOLYPROTED ^A	HUMAN BOMONODERCIENCY VIRUS 177E 1 ICUC. 131 ISUC. 113	2	79	343.301	678-650					
EIN AU	ENV POLYPROTED ⁴	KINDAN DOGNODES KIENCY VIRUS 177E 1 (EC. 130L. 11.)	1	3	919:165			Ŀ			j
	SAV POLYPROTEDA	INDIAN BORRODE ICENCY VINUS 177E I (IIXUZ 1301.A.F.)			1		-				
2 101	FNV POLYPROTEDN	HUNGAN DOGUNGOEDICKENCY VIRUS TYPE I (IIXI) ISOLATE!		19	3	607.629	-				
2 1	ENV BOLVED TEBL	MANAN BARANCHERIC WINUS TYPE I (III) ISOLATES				-			L		
THE PARTY	PAN IN VERNITOR	HEDLAN BACABODESICIENCY VIRUS 177E I ITAL SF ISSUANCE	il.								
PENY HVILL	DAY IN THE PARTY OF THE PARTY O										

PUCKAR	107:176:4	All Viruses (ne becteriophages)	П				$\overline{}$		П	т	
TILEMANIE	PROTEIN	YORK	_	3	A BEAL	7	1		No.	7	A PER
PENV HVIKE	ENV POLYPROTEIN	HEMAN HORINDDEFICIENCY VIRUS TYPE I (STRAIN KII-1-GP)))	R.	2			i	·	1	•	•
PENV HVIMA	ENV POLYPROTEIN	HIGHTAN INDAUNCOEFICIENCY VIRUS TYPE I (MAL ISOLATE)	Т	20.00				İ	1	\dagger	1
PERV HVING	ENV POLYPROTEIN	INDIAN INDIANODE/ICIENCY VIRUS TYPE I (AIFA ISOLATE)	٦	7				1			1
PERV HVING	ENV POLYPROTEIN	HUMAN DONONDEFICIENCY VINUS TYPE I (AIN ISOLATE)	34).370	267.782	27.014	101.00		Ì	1		Ī
PENY HVINS	ENV POLYPROTEIN	INSULAN BEACHOOCE ICIENCY VIRUS TYPE I (NEW YORK-) ISOLATE)	ī					1	1	1	ļ
PENV IIVIND	ENV FOLYPROTEIN	INDIANA DISALINGDES ICIENCY VIRUS TYPE I (NDK ISOLATE)	٦					T	l	1	l
PENV HVIOY	ENV POLYPROTEIN	HUMANN MOMINODEFICIENCY VIRUS TYPE I (OYI ISOLATE)	┰	970-10	787.670			1		1	-
PENV HIVIPY	ENV POLYPROTEDI	MAKAN DAKINODEJ KIENCY VIJUS TYPE I (PVZZ ISULATE)	Т			100				1	Ī
PENY HVIBI	ENV FOLYPROTEIN	HENDAN BOARMODEFICIENCY VIRUS TYPE I (RUALAT ISOLATE)	Ţ	201	200-00	7400		1	1	ł	
PENY HVISI	ENV POLYPROTEIN	HEBLAN GOODWODEFICIENCY VIRUS TYPE I (SFIEFISOLATE)	Т		×	53.78		1		\dagger	
PENY HIVISS	ENV POLYPROTEIN	HUBANI BOKANDOEJICIENCY VIRUS TYPE I (SFJ) ISOLATE)	ī					Ì	1	†	
PENV HVISC	ENV POLYPROTEIN	HUNGAN BOARMODES ICIENCY VIRUS TYPE I (SC 150LATE)	T	2				İ	1	+	i
PENV HVIWI	ENV POLYPROTEIN	HUBIAN HOMENODEFICIENCY VIRUS TYPE I (WALII ISOLATE)	7		3			Ì		+	
PENY HVIWS	ENV POLYPROTEIN	HUNGAN BLOADMODERICIENCY VIRUS TYPE I IWAITZ ISOLATE)	٦	3	200				1	+	
PERV HVIZ3	ENV POLYPROTEIN	HENCAN DOCUMENCIENCY VIRUS TYPE 1 (22CDC-2)4 (SOLATE)	Т	₹ 2	678-610	0.0		İ	1	<u> </u>	i
PENY HVI23	ENV POLYPROTEIN	HENCEN DOCTORENCY VIRUS TYPE 112 AIRE 1 (SOLATE)	7		i.			İ			!
PENY HVIZA	ENV POLYMOTERN	HIDDAM DOWNODERCIENCY VINUS TYPE I (ZAIRE & ISTRATE)	Т	200	9 10			1	1	1	•
PENY HVIZE	ENV POLYPROTERM	HIDRAN BOATHODE FICIENCY VIRUS TYPE 1 (2:84 ISOLATI')	╗	3					-	<u> </u>	-
PENY HVIZH	ENV POLYPROTEIN	HUNIAN INDAUNODERICIENCY VIRUS TYPE I (ZAIRE 1123)1 ISUI ATE)	z	9				İ		j	İ
PENV HYZBE	ENV POLYPROTEDM	INDICAM BOORDWOOESICIEMCY VIRUS TYPE 2 (ISOLATE DES)	П	3	2	100		i	-	-	-
PEN INICA	ENV FOL YPROTEIN	IRIBIAN BASONODES ICIENCY VIRUS TYPE 2 (ISOLATE CANIZ)	=	2	5						İ
PENY HYZDI	ENV POLYPROTEIN	HARAN BERAGOEFICIENCY VIRUS TYPE 2 (15OLATE DI94)	Ì	220	2	3			_	-	-
POW HYDGI	DAY POLYPROTECH	HARIAN BEADWOODINCIENCY VIRUS TYPE 2 HSOLATE GHANA-11		524.551	26.53	3	3	ļ	-	-	i
PEW HYDIG	ENV POLYPROTED	HERICAN DESCENDED RCIENCY VIRUS TYPE 3 (150), A IE NIH-2)	11:11	324.551	356-383	613.640	643.489		-		- i
PEN MYZEO	ENV POLYPROTEIN	HADLAN BEALINGDEFICIENCY VIRUS TYPE TIISOLATE BOD)	\$6.05	201.00	617-698						
PEN HVIST	ENV POLYPROTEDI	HADNAN DERTHODELICIENCY VIAUS TYPE I JISOLATE STATATOR	442-476	337.554	159.186	19 179					
PENY INTE	ENV POLYPROTEDI	INDALAN DENDOCED KIENCY VIRUS TYPE I (ISULATE SHLISY)	311.544	100			İ				
PEN INTST	ENV POLYPROTEIN	HUMAN DEATHODES ICIENCY VIRUS TYPE SHSOLATE ST)	443-436	377-534	150.584	648-642					
PEN MOT	ENV POLYPROTEIN	HIDAK CELL FOCUS-FORTING FORTINE LEUKEAHA VIRUS	633.513								-
PEN MOTE	ENV POLYPROTEIN	MIDAK CELL FOCUS-FORMING MURINE LEUKENIA VIRUS (ISOLATE CI-))	462-515						<u> </u>	<u>!</u> 	-
POW MENAV	ENV POLYPROTEIN	AKV KURDÆ LEUKEMA VIRUS	517.544							<u> </u>	-
PEN MANCE	ENV POLYPROTEIN	CAS-BRIE WITHOUT LEUNENIA VIRUS	110-539								
JENY DE VTS	ENV POLYPROTEIN	FATEND MADRIE LEUKEMIA VIRUS (ISOLATE 51)	<u> </u>					1		+	1
PON MATE	ENV POLYPROTEIN	FALEND MARINE LEUKEMIA VIRUS (1500-ATE FB29)	20.50					1		1	
POV MAY	ENV FOL VFROTEIN	FALEND BUILD LEUKENBA VIKUS (ISULATE TYC. 111)	100					1	1	\dagger	1
The Party	EN PALTEURIN	DUMBLE TOTAL TECHNIST						1	1	\dagger	Ī
PLAN ME VAL	TENY FOLITHOUSE	MINISTER MONTH LEGISLING WAYS	5	Ī				1	 	\dagger	Ì
100	END AN USED TEN	PANATION LAMBER FIREIN VIEWS	407.533				Ī	Ī		\dagger	
1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N 1 N	ENV POLVPROTEIN	RADIATION MIRDRE LEIRFMIA VIRUS ISTRAIN KAPLANI	103.10					T		t	Ī
PDV MATY	ENV POLYPROTEIN	MOUSE MANDARKY TUNOR VIRUS (STRAD) BR6)	Т	\$2.500						l	Ī
PEN MARTYO	ENV POLYPROTEIN	MOUSE MANDRARY TURNOR VIRUS (STRAIN GR.)	П	263-589					_		
PEN MIN	DIV POLYPROTEDI	SINGAN MASON-PRIZER VIRUS	432-476								
PENV MSVFB	ENV POLYPROTEIN	FE) MURDAE OSTEOSARCOMA VORUS	23-64							1	
ADA ORAN	ENV POLYPROTEDI	OVING LENTIVIDUS (STILAM SA-OAIVV)	43.49	2	760-t0/				+	+	
PEN ENCY	ENV POLYPROTEDI	RAUSCHER MINIK CELL FOCUS-INDUCING VIRUS	_							1	
PDV STVI	ENV POLYPROTEDI	SDGAN FOAMY VIRUS (TYPE 1)	٦	104-10						+	
PEN STVIL	ENV FOLYPROTEDI	SOCIAN FORMY VIRUS (TYPE 1/8TRAIN LK1)	Т	15.33	2.78	65.00				1	Ì
PON SIVAI	ENV POLYTROTEDN	SOCIAN DOCUMENT VINUS (AGAISS ISOLATE)	269.310			623.678	Ž.	1	+	+	
PDIV SIVAG	ENV POLITICIEM	STRUCK BENEVIALE RESERVED VINES (NOW) 1904 A 12)	26.50	11.	107 97	114 Mg	2	1		\dagger	Ī
7	ENV POLTFRUIE	STREET STREET STREET STREET STREET STORY STREET STREET STREET	T					1	+	1	Ī
PEN SIVAT	DAY FOLYFLOTEDA	SUMMAR DESCRIPTION OF THE STATE		147-117		7	17.	†	+	\dagger	Ī
TWI WO	ENV FOR TYROIGIN	COUNTY AND AND AND AND AND AND AND AND AND AND	Т		97.00	711.71		1	+	\dagger	Ī
PENV SIVE	EAV POLITICOLEUM	STATE MACHINES OF VIEWS AND 1509 ATE	9	\$30.609	631.311				+	\dagger	Ī
PENN SINGO	DAY POLYPROTEDI	SDAAN DAADOOFFICENCY VRUS OP4251 ISOLATES	Т	277.289				T	\dagger		T
MANY VICE	ENV POLYPROTEON	SENDAN BARDHODEFICIENCY VIRUS (KOW ISOLATE)	Т					T	-		Ī
								1		l]

		AB Vivies (se betterioghegy) YARUS (K78 ISOLATE)	$\neg \neg$			1000			+	\dagger	
			Т	ī					_		Ī
				1	9 677 (77	811.109		-	1		
			т	T	Т					1	1
			٦					-		-]
			100-00	1	j	Ī		-			إ
			117-609		Ť			-			
			11-62	8				-			•
			Ī	101-01					1		
		TOTAL TRANSPORT OF TRAIN 1514/ CLONE LVI-1KS1)	T	383.809				+	1	t	
			Ţ					_	+	1	1
- <			┑	7						1	1
П	TUNDEND SUBURIL		304-360	_ [
П	Ţ		Г	(\$-2)							
I	1		Т	107.027					1	İ	
			Т		11111			1	<u>:</u>	:	
T	_	VACCIBIA VIIIUS (SI INCIII)	,	2							į
PETFI VACEV	Γ	VACCINIA VIRUS (STRAIM CUTEMINALY)	20.3	174.210	101:10				<u> </u>		
	Ī	AND A WRUS	9							t	
Ī		CIMING REPORT OF THE PROPERTY								1	
I		VAUCELIA-2031ER VINCE	13-50						_		
		REMAN ADEMOVIRUS TYPE 40	178-216								
14 4 KD		TABLES AND VIRUS TYPE 41	11,000							T	
	ALA KO FIRES PROTEIN	Take to the second seco							1	Ì	١
Ţ		HUMAN ADEMOVIACIO	٦	440-473							
		MINAN ADENOVINUS TYPE 40	110.)44	141.488							
		A ANEXOVALISTY OF 41	۲	161.191					1	Ì	١
l		RUMAN ALEX	٦							j	١
١		BOVING ADENOVIKUS I THE 3	275-705	123-132							
1	TROCKEN	MOISE ADEROVING TYPE I	1130-169		1						
Γ	FIBER PROTEIN	ASSESSMENT OF ARCOMIN VIRUS							1	Ì	
Ī	C. COLAROY THANSFORMUNG PROTEIN	AND MOUNTAIN							-	Ì	Ì
	TO THE PARTY PROTECT	AVIAN RETROVILOS PALIT	162-193							_	
PFOS AVBOX	PSS-V-10S TEAMS CONTROL PROTECTO	THI MORDAL OSTEOSARCOMA VIRUS	230.207					1			
	FOS TRANSPONDING PROTEIN	SUBJ. SIZE OF CROSS SIZE OF CR				_			İ		
Ī	OL YPROTEDI	AVINA TELEVISION VINIS (130LATE WYOMING)					L		1		
١	NOTION VOICE	EQUINE Description	621-641		1		L		_		١
POAG ELAVY		HIDALN SPIRARETROVIEUS	396-442	467-476							
	ALTEROICE.	GINDON APE LEUKEADA VIRUS	91.111						1		
l	GAG POLYPROTEDY	THE STATE OF THE PROPERTY OF THE PARTY OF TH				L	_				١
Ī.	OL YPROTEIN	MUNICIPAL PROPERTY VALUE TYPE I (BIS 150LATE)					L			1	۱
Ī	CALCULATION OF THE DAY	HADAAN DOLUMENT THE TABLE I AND INCLATED	1				ļ				١
		INDIAN BERTRODEFICEMEN VIKUS TIVE TIMES TO SEE	1111								
POAD HVINON GAG	GAG POLYPRUIEUR	THE MAN MANAGERICENCY VIRUS 179E 2 (SULATE BUT)	1						1		
١	OLYMOTED!	THE STANDER PUBLIC VINIS TYPE 2 (ISOLATE DIM)				L					
١	CAL POLYPROTEDI	INDIAN BENEVISION OF THE TYPE 2 (150LATE NIM-2)			1			-		-	
١	ALA LA VERDITEDA	HUMAN DOMINACON CONTRACTOR OF STREET STREET	112		1		1				1
	The state of the s	HUNCH BOTH COLLEGE AND A STORY	136.30					Ī			
POAD HYTST GAD	GAO FOL TYRUIEM		971	49-103	133.259						
Γ	LETROVICE RELATED GAG POLITICAL										
Ī	DAMEN AND A TED GAG POLYTROTES		R				ļ	L			
1	THE VALUE OF VALUE OF STROTE!		24.53	*							
	WALKE STATE OF THE	-	11.48								
	CAG FOL YPROTEDS	CONTRACTOR TO SERVING (STRAIN CIVI)				L					
Ī	AAA HOL YPROTEDM	TOOTS TO THE TOTAL CONTRACTOR OF THE TOTAL CONTRACTOR				+	-				
T	NOT CONTROL	MOUSE MARGARY I COMMISSION	333-260			\downarrow	-				
,		SOUTH MASON PEREN VINOS (MP.M.)	497.531	624-651	_						
_	CAO POLTTRUILLA	TEACHARDAYCES CEREVISIAE VIRUS L.A	9	ļ		_					
Γ	KAJOR COAT PROTED!	THE AGAIN OF THE WORLD STOP ATE AGAIN CLONE GIV-1)				-	L				
0.00	AAA KAL YPROTEEN	SOUTH STATE OF THE PARTY OF THE PRINT ISOLATE!		1	1	1	+				
Ţ	CALCULATION VALOTEDA	SOCIAL BURGACOUT THE SECTION AND AND AND AND AND AND AND AND AND AN	=					-			
		SDALN DOGINOOES HOENCY VIRUS (31 PM 1905)			_			1			
	GAG FOLTFEU ELA	TENAN BOARDOE ICENCY VIRUS (FINASARIA ISOLATE)				_	_				
l	GAG POLYPROTEDI	STATE OF THE STATE		\downarrow							
100	A PAN YPROTEDI	SOUND BEACH STORY	197-441	-		1					
١	T LOS COMPANYS IN	SECIAN SALCOMA VACO	192-122				1				
اٰٰٰ	Contraction of the Contraction o	SPOAN LETROVAUS SRV-1	=======================================	321-348				1			
PONO SEVI	CAG POL THEOTEUR	EASTER HERPES VINUS TYPE I (STRAIN ADA?)				L	_				
	PROBABLE HELICASE	CALLEGE OF A PARTIE OF THE PARTIES O		7	1	-	-				
Ī	Same and it little be'A SE	HERESTANDS SAME TO THE PARTY OF	486-313	701-728			1				
1	1000 P. C. C. C. C. C. C. C. C. C. C. C. C. C.	VARICELLA-ZOSTEA VINUS (STRAIN DOPENS)	204-242	L				+			L
אינו אינו אינו וויין	CONTRACTOR OF THE PROPERTY OF	THE PROVING CORONA VIBLUS (STRAIN F15)	171	-	-	_		-			l
	MACCLITTOM ESTEANSE PRECURS	The President Villa (STRADALY-1)9)		1			-	L			
T	TANGET THE CONTRACT OF THE CURS	OR BOVER CONCENTRATION	7		-	-	1				
PIENA CVELY HE	MACCALLINE STATES OF THE PARTY OF THE	HOMACOLD I POWER THE NEW PROPERTY CONDITION (STRAIN ARE BUS)					ĺ				

PCCCXC	107117814	All Virget (se batteriophages)	ARTAI	ARTAL	AREAS	AREA	AREAS	ANKAS	ARTA1 A	ARGAL	PREA
ILE KAME		VIRUS	Т	Т	Т						
HEM CVBQ	LUTININ-ESTERASE PRECURSOR	BOVING CORORAVIROS (STEWN CORORA)	306.363							İ	
A CVIOC	ğ	INDAKAN CONCRAVIACIO LI INAMA CALLI INAMA	107-433							İ	
MEMA IAAIC	HEMACCI UTININ PRECURSOR	INCLUSION A UPPIN OF AN AMANGEORY OF	18.91	21.43							!
MENA IABAN	ILEMACKA UTOWN PRECURSOR	INCLUSION A VIRILE (STRAIN ANUDGENGAR/IONKAIDO/1/71)	381-451					1	+	Ť	
TOWN INDICA		THE TENZA A VIBILS (STRAIN ACADELLAIONGOLIME)	9.36		1			†	Ť	1	ŀ
HELLA LACKA	PEFCURSON	RELIENZA A VIRUS (STRAJN ACCIECKENAL ABANIAIM)	_	ī		T	İ	1	T	Ì	1
HELY INCO		RELUENZA A VIRUS (STRAIN ACHICKENGERMIANY MAY)	٦	2		İ	Ī	İ	Ī	-	1
HOEMA LACKE	HEMAGGLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIN ACHICKENTEMNS). VANIAIM)	200	į	:		:	•	:		
HEALA LACKO	HEMACOL UTINGH PRECURSOR	INTUENZA A VIRUS (STRAIN ACIDCICENTENNSVI, VANIAZI) 7091)	_				1	İ	İ	Ì	
MISTA IAPEV		HELLENZA A VIRUS (STRAIN ACHECKENVICTORIA/IA)	19.14	3			1	Ì	1	1	
HENT INTE		DELUENZA A VIRUS (STRAIN ANDLEIVALBERTANIVA)	٦				Ì	†	1	1	
HELL LAND		DALLIENZA A VIRUS (STRAIN ACUCICAL BERTAMOTA)	┑	3.8			Ì	1	Ì	Ì	
THE PARTY	CELLICE THREE BETTINGS	DATELENZA A VIRUS (STRAIN ADUCIOAL BERTATUM)	_		ļ				-		;
THEMA IADA	HENCE IN THE PARTY OF THE COMPANY	DELIENZA A VIRUS (STRAIN AUXCK/ALITIERTA/1976)		5	:	!		•	-	-:	:
VIII V	SECTION OF SECTIONS	THE LIENZA A VIRLIS (STRAIN ACCICACIOSLUVAKIAS)	301.431						Ì		
PIENA IADEZ	INCHARGE UTININ THE CONJUN	NET TENTA A VIBILS (STEAM ACCIDING AND) 1/56)	25:12	402-453	\$6.51 1				j		
NEMA IADEI	DEMACCI UTININ PRECURSOR	IN LUCYCA A VIRITO (STEAM ACHICKANDKKAIDOWN)	111-111	İ					į		į
HENA IADIII	HEMACGLUTININ PRECURSOR	THE THEFT A VISIT STATE AND CRAINER ADDRESS.	11711								
MEMA IADHI	PENACELUIRIN PRECURSOR	THE LIEUTA A VIBIL (STRAIN AMERICANCE KAIDOV) MO)	111-11						Í		
HENCY INDER	HEMACALUINAM PRELUASUR	THE LOCKET A VIEW ROOM AND A MAINTENANCE AND VIEW AND VIEW AND A V	11-11	ĺ							
HEMA IADIM	HEMAGGLUTING PRECURSOR	THE LEWIS A VIBIR REPLAN ANNICHMENT AND THE STATE OF THE	717-17		!	i	ı				
PIEMA IADIIS	HENAGGLUIMIN PRELUASOR	THE THE PARTY A A WRITE STRAIN AMERICANCE AND OF BASE	311-111								
MENA MON	NEMAGGLUTING PRECURSOR	SACTOMENT A VALUE (STEADS AND PERSONAL AUTOMOS)	10-15	ĺ							
MENA MOET	IIEMAGGLUTINE PRECURSOR	THE LIEUXA A VIBIR REPAIN AND CHARLE AND LIMIT	413-465								
PIEMA MOR	HEMAGGLUTING PRECURSOR	CALLESTA A UNIT (STRAIN ADDICKARMIS) (40)	25-12								
HENN MORE	PERACKEUTING THE CONSOR	MELLENZA A VIBIN ISTRAIN ADJUCKAGADIJSO2074)	387-483								١
MENA MAN	NEWACCH INTERNATION OF THE STATE OF THE STAT	DOLLENZA A VIRUS (STRAIN ADUCKALANITODA/1/3)	31.58						1		1
MIELIA TARAN	HEMACICA UTDOM PRECINCOR	DOLUENZA A VIRUS (STRAIN ADUCKAEW YORK/1278)	21.55							1	
PIEMA IADAZ	REMAGGLUTOWN PRECURSOR	DOLLENZA A VIRUS (STRAIN ABUCKĀRW ZEALANDVIIN6)	381-451	T			1				
PIEMA MDUI	HEMAGGL UTDON PRECURSOR	INSTITEMEN A VIRUS (STRAIN ADUCKATIRBAINE/140)	31.5					1	Ť	T	
PIESAN MOUS	HEMAGGLUTDWN PRECURSOR	DALUENZA A VIRUS (STRAIN A/DUCKAIXRAINE/1/81)	207-631				1		1	Ī	
A LAEDA	HEMAGGLUTDON PRECURSOR	RELUENZA A VIRUS (STRAIN A/ENGLAND/87848)						1		T	
A MEN	HEMAGGLUTOWN PRECURSOR	DGLUENCA A VINUS (STRAIN AENGLAND)21/77)	1					1		Ī	
PIEMA WIR	HEMACCLUTININ PRECURSOR	INGLEDIZA A VIELE (STEAM ANDWE PLACED VIRUSAUS ICHANA									ļ
NOT I	HEMACKE UTINEN PRECURSOR	DELICENCE A VICINE (STRAIN AND LAKEN LAND TOWN)	200.50	Ī							
	HENACO INTRA PRECIDENT	DOLLIENZA A VINUS (STRAIN AGULL/ASTRAICHAM117/14)	504-531								
400	LIETA COLI TITUM PRECITE SOR	DOLUENZA A VIEUS (STRAIN A/EQUINE/ALGIERS/12)	386-452								
TAIL A	INFLACTOR ITEMENT PRECINGOR	ROLLENGA A VIRUS (STRAIN AAIANDINIAN)	38-56								
MACA	IGMACHE LITION PRECURSOR	DALUERZA A VIRUS (STRAIN AÆQUINE/CAMBRIDGE//43)	3.50	186-221	2073				1		
A WHC	HEMACOL LITEREN PRECUNSOR	DOTI LENZA A VIRUS (STRAIN A EQUINE/CAMBLIDGE/1/7))	3 2	2	57-05				1	1	
HEW MICE	IEMAGGLUTBON PRECURSOR	BOLUENZA A VIRUS (STIALIN AEQUINESC DETROTT/1/64)	ž	2.4							
A WEDE	HEMAGGLUTDIN PRECURSOR	DETUENCA A VIXUS (STRAIN A/EQUING/DETROIT///A/)	2					1		Ī	
A LABEO	DEMAGGITTEN PRECURSOR	DIFLUEICA A VILUS (STILADA ARQUINEIRONTAINEBLEAUTA)				J		1	1	1	1
A LANKS	IEMAGGLUTDEN PRECURSOR	DOTLIDICA A VOLIS (STRAIN AEQUINEMENTICA VIZIA)		T						Ī	
A LABER?	HEMAGGI LYTHIN PRECURSOR	INTLUENZA A VINUS (STRAIN AEQUINEXENTULX Y/197)							T		
PHEMA IARE	HEMAGGLUTOWN PRECURSOR	DIFLUENZA A VIRUS (STRAIN ARQUINEA EXINGTONIAN)	2 2						T	Ī	
MEMA IMBO	HEMAGGLUTININ PRECURSOR	DAPLIERZA A VIRUS (SITIATA ARQUINEZ-ONDOROMA)							Ì	Ī.	
PIENA MEG	IIEMAOGLUTDON PRECURSOR	CALCACA A CALLA CATA AND A CALCACA MARKETON	186.453								
N N	HELLISON PRESENTATIONS	INCLUSION A URISINAM AFOIDEARY MARKETIAN	39.50	18.23	100						
PIERO MORE	HENALCH CHENN MECHESON	DELUENZA A VIRUS (STRAIN ARQUINE/RAGUE/1/34)	35-56	194-221	111.437						
MEMA IAIRO	HEMAGGLUTOON PRECURSOR	DELUENZA A VIRUS (STRAIN AFQUINE/ROMANIANO)	384-452								
MENA IAHEA	HELLAGGE LITTORN PRECURSOR	DOLLEDZA A VIRUS (STRAIN AEQUINE/SANTIACO/M))	186-452								
HESTA LANCE	HEMADOL LITTING PRECURSOR	DELLEDIZA A VISUS (STRAIN ARQUINE/SAO PAUROVIVA)	38-56	184-331	110-459						
		The section of the transfer of the transfer with the transfer of the transfer	7								

	1445.490.4	All Viruses (se batteriopheges)	ARCAL	ין שננאי	1	PRIO LARGA		2011				
CCENT	70.100	VIRUS		<u></u>	1	1	1	+	T			
TANK T	HELACOL UNDON PRECURSOR	BELUENZA A VIRUS (STILATIV ACQUINER OK VOCI)		<u>=</u>	! 	1	1	+	T	İ		
TOTAL PARTY	HE MACCOL LITTING PRECUTSOR	DOLUENZA A VRUS (SIRAM ALCONNEARING)		_ =	1	1	<u> </u>	t	T	Ī	ŀ	-
PHENA INTER	INTRACOLUTION PRECURSOR	DOLLENZA A VICOS (STRAWA ACCOUNTS)		٥	<u> </u>	+		+				
MININA IAIAP	HEMAGGLUTING PRECURSOR	INTURKA A VIACO (STATE AND	19.56	٦			+	t				
MELLA TAKEE	HEMAGGLUTHEN PRECURSOR	DELUEYCA A VINCE (STEEL AND AN ENDICALADISM)				1	+	\dagger				
HEN MEN	HEMAGGLUTINEN PRECURSOR	INDICATION A VINCE (STEAM ANIAL LAND/ASTRAKHAN/14/12)		2	1		+	t				
HIGHA IAMAA	HEMAGGLUTDEN PRECURSOR	INCLUENCE A VINCE (STREET AND ACIAL LABOVAS I RAKHAN			1	1	1	<u> </u>	Ī			
SHELLY TANAB	HEMAGGLUTBON PRECURSOR	DOLUENZA A VIKUS (STEATIN AAIA) ABDANTW YORKABTUTE)	67470) 387-453	T	1	1	<u> </u> 	İ			<u> </u>	
OVANA TANAS	HEMAGGE UT THON PRECURSOR	INTLIENZA A VILOS (SI LATIN ANTALIANIE)	40.63		13.431	<u> </u>	1	+				
1000	LIENACCE LITININ PRECURSOR	IN THEMS A VIRUS (STRAIN APIEND IN THE PROPERTY OF THE PROPERT	190		19761		+	†	T			
MA IME	SELVACE INTONIN PRECUESOR	INGLUENZA A VIRUS (STRAIN AMERICANOMIC)	14.51		111-111	-	-	1	1	Ī		
TENA ME	CONTRACTOR OF THE PARTY OF THE	DELUENZA A VIRUS (STRAIN AMEROPIEM)	831	Ī	182-441		1			Ī		
PIEMA IMES	ELACOLULIA PARCINEDA	INFILIENZA A VICUS (STRAIN AMINIC/SWEDENTA)		ء						:		
PHENA LANDA	HEMAGGLUT DED PRELUASUR	INGITIENZA A VIRUS (STRAIN ANTMONS)			<u>:</u>	<u>:</u> !	<u>'</u>	_				
HELLA LANTIG	INTERPROPERTIONS PRECUESOR	THE THE WAY A VIBIR (STRAIN APILOF WITHLIFT IN 17 12014)		٦	<u> </u>	<u> </u>		İ				
MICHAEL LABIT.	HIEMAGGLUTININ PRECURSOR	THE CONTRACT SEE AND ADDRESS OF THE PARTY OF	29.56	٦		1		Ť				
HELLY TABLE	HEMAGGLUTING PRECURSOR	INCLUENZA A VIACO (SI PACO A) INCLUENZA		_	<u> </u>	1	\dagger	t	I			
	THE LANGE IN PARCIASOR	DALLENZA A VIALIS (STEAMER TO THE METON THE ME	W 1EMSEY/47/851 381-451	÷		1		Ì				L
3	TOTAL PROPERTY OF	INCLUENZA A VINUS (STRAM MACON) 1002-101-101-101-101-101-101-101-101-101	Γ	Ę		-	+	İ	T			L
PIEMA IARUD	THE PARTY OF THE P	INCLUENZA A VIRUS (STRADA ASEALALASSACILUSE)	20.00	Γ	1	506-547	_	1				
MENA INSES	PHACKED IN THE CO.	THE LIENZA A VIRUS (STRAIN A/SHEARWATER/AUSTRALIA)		Т	384.445							1
EMA IASHU	IEMACCI UTRON PRECONSOR	THE HEAT A VALUE ISTRAIN ASTARLINGNIC TORING 1957)		Т	1	-						
PICEMA LASTA	HEMAGGLUTDION PRECURSOR	THE STATE OF THE PARTY AND INCOME.		•	1			ĺ				
SIESZA IATAL	HEMACCE UTINON PRECUASOR	INTERCEMENT AND STATE OF THE PARELANDING IN		15.45	<u>!</u> 	<u> </u>		Ī				
TALL VIVE	INTERNACIONAL UTINON PRECURSOR	THE LUENCA A VINCO COLOR COLOR EN ANDRESO AND		15711				Ť				L
	INTERNACIONAL PROCURSOR	INFLUENCA A VIRUS (STRAIN AND THE COUNTABLOW) 11/64)		\$01.534	-			1	Ī			L
1	LATILACIA LITINON PRECURSOR	INGLUENZA A VIRUS ISTACIONA CONTRA CONTRA ABIDALI		414-454	49)-539	1	1	1				L
MENA MINO	THE STATE OF THE PARTY OF	INTLUENZA A VIRUS (STRAIN ATURAS TONIANO		F	104-221	101-422		1				
DAM MIKE	LEST ACCES THE BATH PRECIDES OR	DOLUENZA A VIRUS ISTRAIN ANDRUCE TARRECULAR		2	\$00-536		1					ļ
HENY WILL	THE PERSON NAMED IN COLUMN NAM	DOLUENZA A VIRUS (STRAIN ATURAE TATIONALIA										ļ
HEMA INTEN	٦	DG LUENZA A VIRUS (STRAIN A/TERWAUSTRALIANO		T	117.653							ļ
PENA MIRA	٦	DOLUENZA A VIRUS (STRAIN ANDORWIOTAZ)		T	435.478	-	ľ					1
ENA IAUDO	٦	INGLUENZA A VIRUS (STRAIN AAUSSAVIOTT)		T	111.454							1
EMA WUSS	IEMAGGLUTURE MECUASOR	DATTENZA A VINUS (STRADI AVIC TORUANAS)		T	<u> </u>							
PIEMA LAVIT	HENCOLUTION PILECUSOR	THE PAPER A VIRUS (STRAIN ANIL SON-SLICTIVII)			+							_
HESA LAWE	HEMAGGLUTING PRECURSOR	CHITENS A VIRING STRAIN AXIANT ENCORT		7	†		1					
HELA LAIGA	HEMAGE LITERAL PRECURSOR	THE THE PERSON AND AND AND AND AND AND AND AND AND AN		٦		1	t	T			L	L
COLVE IVA	HEMAGGLUTEVEN PARCUASOR	DELUGICA A VOCUS (STORY AND		11711	j	1	1					L
MENT AND	HEDALOGI UTBABI PRECURSOR	DOLUCIAL A VICTORIA SERVINA ANA INCANDA KONCALIANTA	_		i	1	1				L	L
AMA AMA	HEMACOLLITION PRECURSOR	DOLUME A VICE (STANDARD AND AND AND AND AND AND AND AND AND AN		3 24-811	506-547	+	1					
1111	HELIACOL LITINGS PRECURSOR	DOLUENZA A VIRUS (SI INAIN MANUEL IN INC. OF VIL		X 217111	¥.5		1					L
	THE LANGE THE WAY PRECIED SOR	DOLLENZA A VILUS (STILADA AS WINEZNEW SENZE		117411								ļ
HENY MEN	TOTAL PROPERTY OF COMMENT	DELIGITAL A VIRUS (STRAIN AS WINEUR ELLINA)		L	110-41						1	1
AND MEDI	THE PARTY OF THE WAS DESCRIBED AND	INGLUENZA B VIRUS (STRAIN BUREUINGUS)	100	Γ	139-473							1
1	T	INGLUENZA & VIRUS (STRAIN BARONICAS)	100	Г	433-481						\downarrow	1
MENA BORO	HENCACH ANNAUL SECTION	DELUENZA 9 VINUS (STRAIN BENGLAND/22/82)		Т	439.471	-						1
FDA PEDA	٦	DATEURNEA BYRUS (STRAIN BAIONG KONGAZI)		T	411.411							4
PIESAS DESIGN		PAST (ENZA & VIXILS (STRAIN PALE)		Т		t						4
	7	PARTITION & VINCE (STRAIN BALARYLAND)		Т			T					4
HENA DEM	_	CAST TRANS A WARTER OF PRACTICE ACPUISANCE	1	7			Ť					
PIEST BONE	Ē	HALLENS A B VINIS (STRAIN BONE CONSAU)		7		†	1					
PHEDAN POOR	Г	SETTEMPS IN VINITE OF THE AIM INSTRUCTOR (2)		11.479		†	T			L	L	
HELLA DOS	Ī	THE COUNTY OF THE ACTUAL ACTUAL PAINTS (AVIOUS)	200	П	2	+	1			L	L	
PIESAA DEUS	Ē	HEATTERS & COLK (CTRAIN EVICTORIA/345)	66	٦	472-476	1	T				L	L
PHENA DANY	Г	COLUMN TO THE COLUMN TO THE BANCHORIANDS	9	٦		1	T			ļ		L
ALEKAA DARVE	٢	DOLULICA S VENA (SIEARIA CITALICANIA/III)	\$	115-549			1				ļ	ļ
ADDIA DICCA	T	DOLLERO C VICTO (STEAM CONC. AND GOLD.)		43.539		1				1	1	-
COM VICE	٢	DOLLDERGA C VINUS (SIENAM CICLEAT LAKE SVI167/34)		413-559	١				1	ļ	ļ	L
PACE PACE	T.	DOLUMENT & CARLO (SINGE CANDONIA))		441-358		1			1	ļ	ļ	L
	Ī	DESTRUCTOR CARLOS (STRONG OFFICE OFFI		7.2								
		ANIAN CONTRACTOR OF THE PROPERTY OF THE PROPER										

- COUNTY	100,170,4	All Virung (no becterfophoges)	П		15.00		ABEAS	AREA 6 AR	AREA? AR	AREADAR	AREAP
PIL NAME	PROTEIN	YIRUS	J			Т	1			Г	
MEMA MOXY	HEMACCLUTOWN PRECURSOR	INFLUENZA C VIRUS (STRAIN C/X YOTOMIRI)	200				T	-	-	H	
MENA DICK	HEMACGLUTININ PRECURSOR	INGLUENZA C VIRUS (STRAIN CALISSISSIPPUSO)	200				Ì				Ī
A STATE OF THE PARTY OF THE PAR	WELLA COCA LITTONINA PRESCITA SOR	BATUENZA C VIRUS (STRAIN CANAKATZ)	386				Ť		t	-	T
THE PARTY	ACTIVITY PRECIMENT	DELLENZA C VIDUS (STRAIN CPICAEIIING/10/11)	603-530				1		+	l	Į
MENT OFFI	IN MACAL LITORN PRECIDIOR	DELLENZA C VIRLIS (STRADI CPICARIJING/11591)	483-539				Ì		1	1	<u> </u>
PARTIA DATE	HEMACKE LITISAN PRECURSOR	DELLENZA C VIRUS (STRAIN CPICOEIIING419411)	13.5				1	T	1	1	į,
PASSAA MATAA	HE MACKELLT DOWN PRECURSOR	BELLENZA C VIRUS (STRAIN CTANLOWITHM)	120				Ì			t	1
PHOSIAL DACYA	HEMACOL LITBON PRECUMSOR	INFLUENZA C VIRUS (STRAÑI CYANIAGATA/1041)					Ť	<u> </u>	<u> </u>	t	
NOW ALTER	HE MACCELL IN INDIA NEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORUAVII)	19						$\frac{\perp}{1}$	t	
THE PERSON NAMED IN	HENACICA LITIDANANE LIRAMANIASE	INEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	<u>=</u>					1	+	+	Ī
	NEWA COLL TERMINISTER ANNUITA SE	INEWCASTI E DISEASE VIRUS (STRADY D2674)	64.91						+	†	Ī
THE PARTY	AND A COLUMNIA LINE IN A LANDING A CE	NEWCASTLE DISEASE VIDUS (STRAIN BI-MITCIPLE NAT)	£.93	İ					 	i	1
	LIFELA COST IN BOOM MET TO A LABORDA CE	INTERCASTLE DISEASE VIRUS (STRAIN ITALIEMAS)	64.91						<u> </u> 	-	
The state of the s	THE STATE OF THE PARTY OF THE P	NEWCARTLE DISTANT VILLE (STRAD) MIYADERANI)	16-191				Ì		1	 	
FIELDS FOUND	TENACOL INCIDENTIAL VEHICLES ANNUITA CE	NEW CATHE DISEASE VILLES (STRAM CUPENSLANDAS)	10-75					1	+	†	Ī
A STATE OF THE PERSON OF THE P	CHANGE IN THE LIE AND A CO	MEWPART REPARENTE VIRIAS (STRAIN TEXAS G B /48)	16-1-91						+	1	1
NEW ADVICE	THE PARTY OF THE P	NEWCASTLE DISEASE VIAUS (STRAIN OF STERVA?)	16-79						1	\dagger	
ALCONO.	TENNON THE PROPERTY OF THE PRO	PHYCOG DISTRAPES VIRUS	39-66	46-73						†	
MENA PRODV	TENCHALL INDICATION AND AND AND AND AND AND AND AND AND AN	MANAN BARANGE LENZA I VIRUS (STRAIN WASHINGTOW 1957)	76-110	166.393				-	<u> </u>	+	
PIEMA PIEM		BANKA BABANSI IBNZA I VIRUS	(6-33						1	+	
PIEMA PUB	IEMANCAL I INTRACTION SE	CHALAL DAS AND LINEAR A VIBIL (STRAIN NIT 4785)	13-41							1	
PIEKA PURA	HEMACOLUI MINIMELINAMININASE	HANDER STREET STREET STREET STREET AUGUSTON	27-61							1	
MEN TOW	I CHACCLUI DUN VEUICAMINUASE	THE WAY TO A DATE OF THE WAY A VINITE OF THE AND THE WAS A STRONG	37-75							1	
PIEDA PISHT	HEMACCLUTING NEURANINDASE	TOTAL STATE OF THE PROPERTY OF	21.00			L					
MENT MINE	HEMACCUTION-NEUTAMINIDASE	THE PARTY FACTOR AND THE PARTY OF THE PARTY	13.41								
PIEMA PUNY	HEMAGGLUT DIDY-NEUTAMINIDASE	INCOME. C.	37.41								
PIEMA PUIN	IEMAGGLUTINDI-NEURAMINIDASE	HUBILAN FACINETAL MENON OF THE MANAGEMENT OF THE STATE OF	27.41			L			L		
PIEMA PUHX	IEMACGLUT DON NEUTOMINIDASE	HUMAN FACING LUCIAL A VINCA LA CONTRACTOR A	166-314	336.283							
MENA MACH	HEMAGGLITTEN PRECURSOR	CALCAL CASTR 26TS AND 7 MOST MITTANTS 1	79.106								
HEAT SEAS	HEMAGGLUT BY PAR GRANIPLY SE	PENDAL MANUEL AND ELICIPATION	79.10								
PIEMA SENDI	HEMACKALUT DAIN-YE UKAMININA SE	REPORT VIPE (CTAIN MARKE)	79-106								İ
HEAL SECTION	INCIACACIONI INTERPREDICAMENTA SE	GENDAL VIBILITY IN HVD	3.18							1	
MENA SENO	SELECTION OF THE CHANGE AND A COMMITTEE OF THE COMMITTEE	GENDAL VIDUS (STRAIN Z)	39:62							1	
TIENA PEROS	SEASON SECTION OF THE ALCOHOLOGY	STATAN VIRUS 41	11-51	194-431					-	1	1
MENA SVA	LIEUA CONTINUE DE COMPANIO		115-146	175-203	316-343				-	1	
1000	HEMACKET ITTOWN PRECIMENT	VACCORIA VIDUS (STRAIN BID-I)	109-146	173-202	116-243					1	T
PIETA VACCE	HELLANGE LYTDEN PRECURSOR	VACCINIA VIRLIS (STRAIN TIAN TAM)	139-146	22.23	2				1	1	
PIEMA VACCV	HENAGGLUTDEN PRECURSOR	VACCINIA VINUS (STRAIN WR)	30	2					+	T	T
PIEMA VARV	HEMAGGLUTDON PRECURSOR	VALUOLA VIDUS							\dagger	\dagger	Ī
PIEXO ADEOL	HEXON-ASSOCIATED PROTEIN	HUNGAN ADEMOVIALIS TYPE 2	3							t	Ī
PHEXIS ADEON	HEXON-ASSOCIATED PROTEIN	INDIAN ADENOVINIS TYPE 3							\mid	1	
MEXS ADEO?	IEXON-ASSOCIATED PROTEIN	HIDAAN ADENOVRUS TYPES 1 and 7	1,1,1,1	700 000	977			+	-	\dagger	
HEX ADEOS	HEXON PROTEDI	HERAN ADENOVIRUS TYPE 2						\dagger	\dagger	\dagger	Ī
MEX ADEOS	HEXON MOTEDA	MIDALAN ADEROVATUS TYPE S							l		Γ
MEX ADEA0	HEXON PROTEIN	HUNCAN ADENOVICUS I TVE 40	110								Ī
NEX ADERI	HEXON PROTEIN	-							-	t	
NEUS COWPX	IEMOKRHAGE-DEDUCING 18 KD PROTEIN	-	2007						-	t	Ī
PIGG COWPX	HOST MANGE PROTEDM	COWPOX VIXUS	10 TO 10 TO					$\frac{1}{1}$	1		
FILM ASFB?	LATE PROTEIN 1196L	AFRICAN SWINE FEVER VIRUS (STRAIN BATTY)							-	t	Ī
PLESS ASFIBI	LATE PROTEIN IZION	APTRICATE SWITCHER VENUE (STRAIN BATTY)	1					+	H		Γ
200	DACE USION BODY MATRIX PROTEIN	CALL THE SAME LANGE IN COME AND AND	77.5					-			Γ
JEND CUND	DICEUSION BODY MATRIX PLOTEDI	CAULDIOWER MODALC VICTOR (STEAM OFF)	417.7			ļ		1	l	T	
PER CANY	DECLUSION BODY MATRIX PROTEIN	CAUCIFLOWER MOSAIC VIRUS (STRAIN FY147)	1					-	l	\dagger	
VIEW CERV	DICTUSION BODY MATRIX PROTEST	CARACILOM BILDED TONG TONGS	107-611							Ì	
2000	INCLUSION BODY MAINLY PROTEIN	LOVE AN CHI PROTECT LOTTE IL VIBLIS	7	56.16							
200	DOLLSON BUDY MAINA PROJECT	HENCEN CYCOLOGICAL COURTS (STRAIN AD149)	1111		L	L			H	П	
PICIE HOWA	PROB PROC & TRANSPORT FRO CLIFE	NUMBER OF THE PROPERTY OF THE									

			Ì	Ì							F
		An Vinces (no become plants)	т	Т	AREAD	AREA	AREAS	ARTA	1418	TOTO	されず
PCGENE	T		1	~~~	Т	Т			j	1	·
	PROTEIN STATE OF STAT	SVIRUS SAIDGING (STRAIN 11)	Т					;	:		
	T	AIN SMITH	_	Ī			į				-:::
2	T			1							ļ
				Ī							-
ELL HEVII	-			Ì							
		THE STANKING AT AMERICA (STANIA AD160)	7	Ì	Ī	Ī					•
			74-162	j		Ī			1		•
Ī			7			!	1		:		
Ī			9								
	**			1	1	í -					1
_			76.07								
	3	BLINE PARCOMA TINGS TO THE STATE OF THE STAT	127.363								
Ī,	K	FEDE SAICONA VIRUS (STRAIN FILESCOCK)	196.341	149.301					İ		
		FURNAMI SARCOMA VIRUS	Ť								
PLYES PLESS	1	THE PERSON NAMED IN COLUMN TO A SECOND SECON			Ī						
		ALCACIA MUNICI EVICINO	7			ļ		:	:		
		CAPAIPOXYIAUS (STRAIN R.S.!)	41, 41,	İ						•	
MUTH CAVA		HE DECYMENT LAIMING (STRAIN 11)			!	!	:		_		į
PKITE BOYA		THE STATE OF STATE ACTUALIST STRAIN NEWS IN VIOLENCE CO.	134.341								
The second second	TAYALIDDAE KDCASE	De ECHOUS LANDON	115.18		1						
	TO SECURITION AND ASS.	KTALIMID KEAPES WALUS I	141.146								
PERT HEVIL	CONTRACTOR AND AND AND AND AND AND AND AND AND AND	UAPPORA VIBILE (STRAIN COPENIAGEN)									
PERRI VACCC	NO ICD PROTECTI ICONA SE PICIPALICA	TATAL CALLS OF DAILS WEN	101-101						L		
WALL CAPTU	19 KD PROTEDI KDIASE HOMOLOG	VACCINIA VINOS (STICK)	147.134								
	SOCIAL E DECTETAL EDITAGE BIZ	VACCEDIA VIEUS (STRADA COPENIANCEN)	761.77								
PERSONAL VACET		VACCEDIA VIRUS (STRAD) WR)		١							
PKALES VACEV	POSSOR I PROTEIN KINASE DIE	CONTRACT CONTRACTOR AND CORRESPONDED	1								
WALL VACOR	POSSIBLE PROTEIN KINASE F 10	AALLMA VAUS (OTTOWN: CO.	11.74								! !
79.0	SOCKER OF STATE OF KINASE FID	VALUE VIEWS	=		_						
W. T.	MALONE SALACE TO ANCE PROTEIN	AVIAN SARCOMA VIRUS (STRAIN URZ)									
PKAOS AVISU	ROS IVROSINE ALPASE INCOME PAGE	AVAN RETROVIAUS APL 30						L			
PERYK AVEU		A CONTRACTOR OF THE COLD AND A TO	14 S								
W VEC AVIEV	TYROSON KONSE TRANSF PROTEIN TES	A VIAN DALLORA VANCE (STATE OF THE STATE OF	200-415						1		
	I ATT 100 KD PROTEDY	MAKAN ADENGYIRUS 17FE J	386-413								
	TAR AND PROTECTION	HIGAN ADDIOVENUS TITLES	167								
P. IS ALKE	Contract of the Contract of th	HIDAAN ADENOVIAUS TYPE 40					L				
A LISO ADEAS	LAIR 100 to 100	HABADAN ADENOVIAUS TYPE 41	3								
PL 100 ADEA1	LATE 100 ID PROTECT	FERTHER DAME OF US (STRAIN 895.0)						-			
Vise i Div	LATENT MEMBRANE PROTEIN	EXTERNOLOGICAL CONTRACTOR OF THE PARTY.	141.13					1			
HADE BAVE	LATENT SELVERANE PROTEIN	E.S. E.M. CALLE STORY IN CO.	140-175								
	I ATTEND LENGTHAND PROTEIN I	EPSTEIN-BALK VILLS (3 I PAIN PAN)	36.133								
1	CENT PERSONAL PROTECT	EPSTEIN DARK VIRUS (STRAIN BV)-1)	7	244.314	493.524	612-656					
1	THE PARTY OF TABLE STREET		T		410.411						
Į	MUNA CATTON DAY I AND TABLES		T			1					
	JOHN CAPPIO DALTIME, LANDE SUBUR	SAPERA CORING (CIRAIN WR)	٦	21-16			ļ				
L	MONA CAPPON DIZ THE, LAKUE SUBUR	-									
	HANN CAPOND ENGINE, LAKEE SUBURI	-	119-111								
ł	LABORA CAPPORT DICTOR	APLICAN SWING FEVER VIXUS (3) IKAIN BANIN	136.161			L					
	CONTRACTOR DE CARROL	CUCIBIDER GREEN MOTTLE MOSAIC VIRUS (WATER MELLUN STRAIN "						-			
MOV COM	MOVEMENT PROTEST	THE MARKE CAREN MOTTLE MOSAIC VINUS (WATERLIELON STRAIN SHI	2								
PLACE COLON	_	CANADATA OKITA RINGSPOT VIRUS	20.00					-		L	L
PACOVE CRESV	=	SALATO LANGARY VIRIUS (STRAD) LILA)	-								
PACOVE TOLIVA	7	TOTAL CONTRACTOR CONTRACTOR AND THE	3						1		
TOTAL STORY	۳	TOWN DECEMBER 1 AND 1 AN	143.130	129-256					1		
	т	CICCOLLIA VICUS MC-IA		110.172		L					
	TANAMATA HOM LASTING ASE CYIASE	PARAMECTION BURSALIA CHEORELLA VIRUS I		107.15				L			
	MODO PLATITUDE STATE OF THE STA	AVIAN MYELOCYTOMATOSIS VIRUS CMIL	777.7			1					L
PAYTE AVBAD	MYC TLANSFORMAN PROFES	THE PROPERTY OF THE PARTY MALLS INCOME.	233-267	376-403			ļ	-			
PLYC AVDIC	MYC TRANSFORMOND PROTEIN	A VACA A A A CONTA A A CONTA MAIL MAIL	23:32 23:32	26-40							
COMM JANA	LAYC TRANSFORMOND PROTEIN	AVIAN MILLOLI IOMA IOSIS VINOS IOSI	239.260	373.404							
T WAY	LAVE TRANSFORMENS PROTEIN	AVIAN RETROVERUS MOLEZA	337.246	170.197	L	_					
200	LANCE THE AMERICAN PROTECT	AWAN ALTROVAUS OK 10	161.436								
PACE AVIOR	THE PROPERTY OF THE PROPERTY OF THE PARTY OF	FELDIG LEUKENDA VIRUS							L		
PATC FLV	MIC INVESTMENT AND THE	FELINE LEUKENDA PROVINUS FTT	2	1		ļ		-			
MAY NATI	MYC TRANSPORTER TROTER	INFRAM VINUS	į	2		1	\downarrow	-	-	L	L
PNCAP BEV	NUCLEOCATSID PROTEIN	Brigger visite LA CROSSE	13-113		_	\downarrow	-			ļ	L
THE MALE		STATE OF THE CANADA STATE	1						+	ļ	ļ
PACAS MAKE	Г	BUNTA VALUE BROWNING TO CO.	46-35	189-330				-	$\frac{1}{2}$		
THE REAL PROPERTY.	MAICH EOCAPSID PROTEIN	BUNY ANWERA VIRUS					1				
	7										

PCGINE	167117844	All Viruses (see besterlaphinger)			A BEAL	AREA 4 AR	AREA ! AREA 6	4 AREA?	AREAG	ARIAS
FILEHAME	PROTEIN		Т			7	_	Г		
PICA COST	MUCLEOCAPSID PROTEIN	VIE COROTAL				<u> </u>		-		İ
PICA COVO	MUCL EOCAPSID PROTEIN	NDI.RSTEPOORT)		Ì	i	<u> </u>				
PMCAP CHAV	MUCLEOCAPSID PROTEIN	CHANDIPURA VIRUS (STRAIM 1653514)	2	İ		1			ľ	
PACAD CVCAE	PACLEDCA7SID PROTEIN	CANDE ENTERIC CORONAVIRUS (STRAIN K118)	///		İ	1		I		!
PALTAR CVPM	MAIN FOCAPSID PROTEIN	PORCENE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIM PURD	2			1	<u> </u>	1		1
PACAB CVPA	MICH FOCAPEIN PROTEIN	PORCING RESPIRATORY CORONAVIRUS (STRAIN 64/137004 / BILLTISH ISOCAT			1	1	1			
Mary avain	MAIN BOCAPSID PROTEIN	PORCENTE RESPIRATORY CONONAVIRUS (STRAIN RAM)	191-327	۱			1	1		
Control March	MAINT BOCABOTTERS	DUCINE VINUS	338-365		İ			1		
200	National States and St	FEET DATE THE CONTROL MENT ON THE STRAIN 79-1146)	113-209							
	TALEGOAN TROITING	DAYABA VIBIR (ISOLATE ICHO)	1	134-261						
NAME OF THE PERSON	MUCLEUCALSID PROTEIN	COUNTY OF THE PROPERTY AND INCOME.	T	Т	101:21					
TICK TOTAL	MUCL EDCAPSID PROTEIN	T	١	T						
PEC ISSVA	MUCLEOCAPSID PROTEIN	TIAL VIRUS (STRAIN AZ)	1		†					
1757	MAICH ECCAPETH PEOTED	LASSA VIRUS (STILADY GALM)		147-174		1				
	The section of the se	FARSA VIRITS (STRAD) DOCAN	* 1	4 3.2						
3	MALEUCA SID TRUTEIN	CANADATATATATATATATATATATATATATATATATATAT	10.13							
TICK LYCY	NOCE EDCAPSIO PROTEIN		Ī	017.710			<u> </u>			
PHCAP MAGV	INCLED CAPSID PROTEIN	.73	Ī		ļ	<u> </u>				
PACAP LEDPE	NUCLEOCAPSID PROTEIN	MOPELA VIRUS	٦		1	+				
201.00	Later Englanden Denge Da	HIDAM PARADGLIENZA I VIRUS (STRAIN C19)		455-463						
	CALCULATION SERVICES	HINGAN PARAMOLIENZA I VIRUS (STRAIN WASHINGTON 1957)		11733						
	POCESSION OF THE PROPERTY	TOTAL SABARET INVA 1 CIRCL CTRAIN MINISTER	176-40)							
PHCA PUR	MUCLEOCALSED FRUIEIN		9				<u> </u> 	L		
25. 117.	NUCLEOCAPSID PROTEIN	PUNTA 1UNU PPELLO VIRUS		İ			1	-		
PHCAP PLABON	NUCL EOCAPSED PROTEIN	PUDDALA VIRUS (STRADH HALLMAS BI)			Ì	1				
PACTAR BIRBAY	NAICH SOCKAPED PROTEIN	PUTDALLA VIRLIS (STRAIN SOTKANO)	2.2							
	AND ROLLEGE BROTEIN	PARTIMENTA VIRIS OF MICE	93.120							
	MULEUMASIDIFIE	A - Bridge Committee of the Author	133.167							
PHCAP BABVA	NUCL EOCAPSID PROTEIN	KABUS VIRUS (SILVAN AVO.)		İ						
PICA EADV	NUCL EOCAPSID PROTEIN	EASIES VILUS (STEATH PV)		İ		<u> </u>	<u> </u>			ĺ
PHCU EABVS	MUCL EOCAPSID PROTEIN	RABIES VIRUS (STRAM SAD B19)			1	1	<u> </u> 		I	
PACAP LEBERS	MUCL EDCAPS OF PROTEIN	SENDAL VIRUS (STRAIN 2 / HOST MUTAMTS)	20.00							
Service Charles	MANY BOCAPKID PROTEDA	SENDAL VIBUS (STRAIN ENDERS)	363-404				_			
	TANKS BOARD BOARD	CENDAL VIRIAS (STRAIN 2)	363.404				4			
	TOTAL STATE OF THE PARTY OF THE	CANDET V GEVTER SICH IAN VIRIS	15	Ī		_				
	TOTAL TOTAL TOTAL	CHAN WELL AT	\$07.534							
	NOTE OF STREET	21 14 14 14 14 14 14 14 14 14 14 14 14 14	\$0.77	İ	-					
TACK TACK	NUCLEUCATSID PROJEIN	INCOME VALUE			İ					
TCU 105V	NUCLEOCAPSIO PROTEIN	TOSCAMA VIXUS		Ì						
PHCA UUX	MUCIEOCAPED PROTEDY	CURUNDAD VIDUS				Ì	1			
PICS VIEW	KUCLESCANSID PROTEDM	VILL REMOREHAGIC SEPTICEMIA VIRUS (STRAIN 07:71)	T			+	1			
ACC VISA	NUCL EDCAPSID PROTEIN	VIDAL HEMORIHAGIC SEPTICEMIA VIRUS (STRAIN MAKAN)	2	284-314	1	+	1			
PART VENE	NAXO EOCAPSID PROTEDY	VESICULAR STONATITIS VIRUS (SEROTYPE INDIANA / STRAIN CLASCOW								
1	ANICH PACABOTTEN	VESICILIAN STONATITIS VIRUS (SEROTYPE NEW VERSEY / STRAIN OCDEN	14-60	336-365	-					
	Control and the Control	VECKTIB AB STONATTIS VIDUS (STEATM SAN TUAN)	1			_		_		
2	NOCECUA SIGNATURE	INTELLISOR AND PROPERTY VIRIA TYPE I (FLISOR ATE)	91111			-	_			
	TECHNIC CALLOR	MANAMINAMINAMINATIVE NEW VIEWS TYPE I MOK ISOLATES	911:11			-	L			
	INCOMING FACTOR	INDIAN BARBUTETTO VIEW TYPE I (ZAIRE & SCH ATE)	14-134				-			
Mary By 126	MEUA II VE PALIUR	PRODUCE DESCRIPTION OF STATE ACTUAL COLUMN C	1							
VAS AV	NELM IVE PALIUM	DATE HOLD A CONTROL OF A AND A CIT PAINTED AND LANGUAGES	47.41		T					
MOAN MADA	MEURAMANAS	MALLESTIA A VIDELE ACTOR AND AND AND MONICOL LAND	**	Ī	T	-				
WANT MCAS	NEUROPANE	ANTONIA A MANAGEMENT OCCUPANTO	1	2						
WEAN IACK	NEURANDASE	Matches A visco (strong Actual 2017)		Ī		+				
PIRAM MDAI	NEIBANDADASE	DELUEYZA A VIRUS (STRAIM ADUCEAAL BERTAVIA)		Ì	1					
PHILAM INDIGE	NEURANDASE	Det UDIZA A VIJUS (STRAIN ADUCINGERMANTIAS)		T	-	ł			I	
PRICE LATIV	NEURANDADASE	DOLLEDGA A VOLUS (STRADA AFOVE, PLACUE, VIRUSOWE Y BRIDGE)	1	T	***	+	1			
PHELAM TARCO	NEURALDADASE	DELUDIZA A VIRUS (STRAIN AEQUINECORVIATA)	2	_	1	+	+	+	\prod	Ī
THE WAY	NEUTA-MATDASE	DELUENZA A VIRUS (STRAIN AEQUINE/KENTUCK Y/I/II)	77	46.76	207	1	1			
POAM WEE	PEURANDASE	INCLUENZA A VIRUS (STRAIN A/KIEV/19779)	<u>=</u>							
PROAD INLEN	NE URANDADASE	INTLUDIZA A VIRUS (STRAIN ALEHINGRADYSVI)	=	Ī	j		-	1		
PROBAM TABEL	HE URANDADASE	DELLENZA A VIDÚS (ŠTRAIN AMENONIŠVIČIH-AMELLAMYAZN)	3	=						
PROCEET INDAK	NEURAND/DASS	INFLIENCE A VIRUS (STRAIN APARROTAL STERVI)	Ī	=	1		$\frac{1}{1}$			
PHEAM LANGE	NEURAL MONTO ASE	INFLUENZA A VIRUS (STRAIN APUERTO FUCORDA)	Ī		-	-	-	$\frac{1}{1}$]]

Ī	1		╗	ABILAL	7	4	7			_	į
PCCENE			49-63	İ				+			
1	AFIRA AMORDA SE		₩.B.				T	T	+		
1			:19					+	1	ŀ	
١	CALLE ALCOMODA SE		19.60					<u> </u>		Ī	
PRIME IAUSS			16-43						-		
Т		DELLEGIZA A VILLO (3 IZALIA A VILLO)	3								1
T			313.310								
T	PROP NONSTRUC PRO PRECURSOR		43-40						<u> </u>		
ASI SUCC	PENE MINKS TRUC PRO PRECURSOR		95.122							į	
T	WOOL STRIKE THEAL PROTECT	POATIENS NECROTIC NOT VIRGIS (STANISMINE)	3.33	÷.	!			:	:	١	
NA STATE	AND STREET WATER AT PROTECT		1 2 2						<u> </u>		
HES TSWVB	MILL OF THE PROPERTY.	TOMATO SPOTTED WILT VIRUS (STRAIN L.)	1						1	Ī	
PHSS TSWAL	NON-STRUCTURAL PROJECT	ANSACTA MODRE ENTONIGPOXVIRUS	Ī	103.114	155.52				1		
PATIFIE ANGEN	MUCLEOSIDE TRUMOSPILATA		Ţ	1	1				1		
VATE CREPY	PAJOL E OSIDE TRIPHOSPILATASE I	CHOCKES CASES AND CHEENING THE WINDOWS THE COMMENT OF THE WIND CHEENING THE WINDOWS THE CHEENING THE WINDOWS THE CHEENING THE WINDOWS THE CHEENING T	٦								
TO NO THE	MEN'T EDSIDE TRUPHOSPHATASE		65-93	7							
THE PARTY IN	THE PARTY TREPHOSPILATASE	VACCORA VALIS (STANT WA)	300-339	470-447	25.40						
TPI VACEV	THE PERSON AS THE PERSON OF TH	VAUOLA VIRUS	Γ	189.716	688.715	785-812			+	I	
PHITP! VARV	MOC EOSIDE HUMIOSTICATOR	WEAPES SINGLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	T								1
PETER HEVEL	MAJOR ANTIGERIC STRUCTL FROTEIN	CONTRACTOR IN COPENIAGEN									
NACCC	POLY(A) POL CATALYTIC SUBUNIT	VACCIONAL VICTORIA CONTRACTORIA									
	AND WAY POL CATALYTIC SUBUNIT	VACCIMIA VIMUS (STRAIN WA)	88-113				1		-		
1	THE STATE OF A PART SUBURIL	VARIOLA VIRUS	118-145								
ANI VARV	POLICAL DESCRIPTIONS	CAPIDOXVIDUS (STRAIN KS-1)	11.50							l	
PASS CAPYK	POCY(A) POL AEU BUBUNI	SOLVE POX VIRUS					_			1	1
PPAPE FORPY	(POCY(A) POL REG SUBURGY	COMPANIA CALIFORNICA NUCLEAR POLYIEDROSIS VIRUS	2								
2000	13 1 KD PROTEDNIN PE STECTOR	AUTOCATION CALIFORNIA TICABLIS POR VIEDROSIS VIRUS	6:-93								
20.21	THE PROPERTY IN PUR STECTON	ORGYIA PSEUDOLOAIA MOLITICA SILLIANIONI VIRUS	104.148								
MEIS NAVOL	THE PROPERTY OF THE PARTY PROTEIN	AUTOGRAPHA CALIFORNICA NULLEAR TOLVILLE SEGUEDA VIBILE	15:3	11.3			\downarrow				
PEN NPVAC	THE PERSON NAMED OF THE PERSON	AUTOCRAPHA CALIFORNICA MUCLEAN POLITICONO	100								
PEAS NOVAC	40 ND IN PACE IN LANGUAGE	AVIAN ABBNOVIRUS GALIO (STRAIN SAZ)	8	1775.1602	1336.3263]					1
PEN ADEGX	PENTON PROJECT	MARIEY YELLOW MOSAIC VIRUS (GEANIAN ISOLATE)		1356.3755		L	_				1
PATON DATE	GENOME FOR YTHOTELM	STATE OF THE LOSAL VIRUS (IAPANESE STRAIN II.1)	:1			-	-	L			
PROF. 1 BAYNU	GENOME POLYPROTEIN I	THE STATE OF A PERCENCE MOSAIC VIRUS	Т			1011					
VO. 1 100	RAKA I POL YPROTEIN	HUNDALA CASE OF CHARACTERS									_
715	RNA! POLYPROTEIN	CHACK VINE TANKE CON STANKE STRANK ST	1044-1123		ļ						L
	Married Venntell	TOWATO MACK MIND VINOS (3) PARTY SEE	346-201	101-126							
Tarks	TOWN THE PARTY OF	BARLEY YELLOW MOSAUC VIRUS (GENOMAN ISOLATE)	240-247	979-108							1
POL1 BAYNG	CENTRE POLITICAL	RABILEY VELLOW MOSAIC VIRUS (IAPANESE STRAIN U-1)					L				1
POLY BAYAU	CENOAGE POLYPROTEIN 2	IN THE AND THE A PRIVIDES CHRONG INDSANC VIRUS									
VIOU 004	KNA1 POLYMOTEDA	TOTAL SERVICE AND VALUE OF THE PROPERTY OF THE	200			-	ļ				
200	SALAS POLYPROTED	CEANBUNG PARLEY VANCOR SEE A CORERRY)	983-1009		_		1				L
100	THE PART WHEN THE PARTY IN	TOMATO IDMOSPOT VIXUS (ISULATE INSTRUMENT)	77.	1030-1037							ļ
POLI TRIVA	MALE TO THE OWNER.	BOVDE EXTEROVEUS (STRAIN VG-5:27)	470.446	1062-1117	100.1110	1333-2264	1476-2503	3 2609-2636	7617-7847		1
POLO BOVEV	GENOME FOLITACIONE	INVINE VIEAL DIABILIEA VIRUS (ISOCATE NADL.)		-			9 1333.3350	0			4
MACA D BOOM	GENORGE POLYPROTECH	TOTAL STATE OF THE STRAIN SO. 1)		-	-	-	-				_
AVOVA O SYNVE	CENCHE POLYPROTEIN		¥-13								L
	CENTRACE POR VOEDTEDA	BEAN TELLOW MUSAL, VANC.	3.34	100	1062-1096	000116	2				Ļ
	A STATE OF STATE OF	COXSACKEVEUS AZI (STRAIN CUE)	1040-1076		L						ļ
POLO COXAL	CENTRE IN THE PROPERTY.	COXSACKEVING A9 (STRAIN GRICOS)			1031.1053	165					4
Proto COXA	GENORE FOR THE SELECT	CONTACT WILLIAM			÷						4
MOLD COX	CENORAL POLYPROTEUR	XXXX FVRVALK B1	107-10				-				_
March (COLOR)	CENONAL POLYPROTEIN		64413	1022-103	-	$\frac{1}{1}$					L
A PANTA	CENCRAL FOLYPROTEDI	COXXVIAL	1000 1000 1000 1000 1000 1000 1000 100				1				L
	ATTENDED OF VERNETRA	COXSACKE WRUS BY	20.00		L	_					ļ
100 CO CO	CENCHE POLITICALE	CLOVER YELLOW VERY YIRUS	1000	2000-2015	13 2989-1016	=					<u> </u>
POLO CYW	CENCIAL POLYPROJECI	PENCIE VIETS TYPE I (STICATOR SINCAPORE 5215/40)			-	16 2043. 1016	11.11.11.1	=			<u> </u>
PROLO DENIS	CENONG POLYPROTEDY	Secure Chaire Prog 3 (CTLAIN 1661)	10.00				_	2011			_
PROLE DESTA	CENOPE FOL YPROTEIN	CELEGRAL CARTHE TOWN S & SCREAM (MAIL POR SI)			_			1			
TIMES OF STATES	GENORAL POLYTROTEEN	- Indiana Carata Santa Andrews Andrews	1344-1371		-	-	-	1			<u> </u>
LUCY V	CENTRAL POLYPROTEIN	DENGLA VALUE 110 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACHE 100 MACH 100	1344-133	1830-1115	1 2005-2912	11 107-501	-	-			Ļ
	CENTRAL BOX VPROTEDA	DENGIA VALUS TYPE JOHNAM THE STATE OF THE ST	1134-1161	1 1448.14	=						╀
	The Change of	DOIGHE VIRUS TYPE 3 (STRAIN TOPICA 1974)	77111	1342.1340	1637.1014	114 3494-3531	131 200-3014	14 1345-1372	2		4
HOTO DENS	CONTRACTOR IN THE PROPERTY OF	boxed vaus type)	2006 3000	101.1011			_				4
Prot o ben	GENORAL POLITICIONE	Now at White TYPE 4						-			4
A P POST	CHANGE FOR YPROTEDI			-							l
				1	1						

1000	1127-110-4	An Vicance (ne bacterlanhanes)		Ī		-					П
THE NAME	PROTEIN	VIRUS	AREAL	1538	48642	ABEAS	AREAL	AREA A	AREA? AB	ABEA A	1020
POLO EMCV	GENORG FOLYPROTEIN		╗	3	× ×	1	1	+	1	\dagger	
PPOLO EMCVI	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EAIC B NONDAMETOGENIC)	٦	200	22.12		1	1		+	
PPOLG EMCYD	GENOME FOL YPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN ENC.D DIABETOCENIC)	٤	120	2 2	1		1	+	1	
ŀ	GENOME POLYPROTEIN	NENCO ENCEPHALORIYOCARDITIS VIRUS (STRAIN 17A)	81.6		Ì	Ì		1	1	+	1.
	GENORAL POLYPROTEIN	AGINGO ENCEPHALOMYOCARDITIS VIRUS	7			Ì	\dagger			\dagger	;
- 1	GENOME FOLYPROTEIN	FUOT-AND-MULH DISEASE TRUS (STRAIN A10-61)	7		Ī	Ī	İ	Ì	1	t	-
PHOLO FADYA	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN ALZ)	-		İ		1	1	1	†	·
- 1	GENOME POLYPROTEIN	FOOT AND WOUTH DISEASE VIRUS (STRAINS OF AND UTBES)					İ		1	\dagger	
_	GENOME POLYPROTEIN	FOOT-AND-MUDIT INSEASE VIRUS IS HAIN CITSANIA FAU (C.SA)	2 2		Ť		T	\dagger	+	\dagger	Ī
POLO HCVI	GENORG FOLYPROTEIN	HEATTHS CYRUS (ISOCATE I)	100	104.1312	101.191	1414.1461	100.100	1406-1440		 	Ī
-	CENCRAS POL VPROTEDI	THE CHARLES WINE (STANIS AND A CONT.)			_		-			t	Ī
1	GENOME FOL YPROTEIN	HOG CHOLLEA VINUS (STRAIN BAT SCIA)	2			_	_	i	<u>:</u> 	-	:
- 1	CENORGI FOR VITIOUS IN							_	_		
	CHENCHAR POLYPROTEIN	HETAINS CARINA (NAME A III)		7				_	_	_	
Prote licyle	CENCACE POLYPRUTEIN	HEPATHER C VIRUS (FAILAN)		2			-	-		 	
1	GENORGE POLYPROTEIN	HEPATITIS C VIXIUS (ISOLATE HC.18)	ग	- ABA		Ì		1	+	\dagger	
	CENORG FOLYPROTEIN	HEPATITIS C VILLIS (150LATE LAPANESE)	╗	2.73	20.50	İ	İ	1		+	
ı	CENOME FOL VPROTEIN	HEPATITISE VIBUS (150LATE MC-17)	22.120	20.00			j			1	i
L	GENOME FOL YPROTEIN	IEPATITIS C VIRUS (ISOLATE TAIWAN)		045-1072	_		j	<u>-</u>	<u> </u>	-	:
PPOLO IPAV2	GENOME POLYPROTEIN	HEPATITIS A VINUS (STRAIN 21A)	703-237	20.104	-	1454-1481					
ı	CENOAG FOL YPROTEIN	HEPATITIS A VIBUS (STRAIN 43C)	201.237	1031-1046	1	1036-1421		ŀ		İ	
ł	CONTACT NO VOROTEN		T	021.1048	_	1636-1481				<u> </u>	l
L	Charles and the Attent	141	201.213	_		Ì	İ	T	<u> </u>	<u> </u>	i
- 1	CONCRET FOR THE OFFICE				Ì	Ì		-	İ	<u> </u>	Ī
1	CENDAG FOLYPROTED					Ì	i	\dagger	1	+	
PHOLO HOAVN	CENONG POLYPROTEEN	(75)			601	Ì	1	1	+	\dagger	
	GENOME POLYPROTEIN		107-102	201-120		Ì		1		+	
1	GENOME FOLYPROTEIN	HEPATITIS A VENUS (STRAIN AGB)	30.237	_	\$ 103.E	ĺ			<u> </u>	+	1
ı	GENORAL POLYPROTEDI	,	2	2 2 2 2		Ì		1	1	1	Ī
		IS (STRAIN CY-145)	-		∹					 	
PPOLO HEVIA		IRDAAN ENDWOYBUS 14		٠,	6.0	2		1			
			1133-1139	1035-1162						1	1
ı			1125-1152 1552-1593	552-1593	_				-	1	
	GENOMAL FOLTPROTEIN		916-1919	1	196.160	1862-1819		1		1	1
	GENORGI POLYPROTEIN		174-910								
L	ISTRUCTURAL POLYPROTEIN	RAINOID		_					1	1	
PPOLO IAEVI	CENONG FOLYPROTEIN		114-24		1794-2023						
PPOLO IAEVI	CENORGE FOR YPROTEIN		П		114.313					1	
PPOLID IMENI	GENORGE FOL YPROTEEN	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAGARS911)		0	2794-2023			1		1	
PPOLID INEWH	GENOME FOLTPROTEDY		П	911-018				1		+	
POLO KUCEN	CENOME FOL YPROTEIN	(5)	60-100				1	1	+	+	Ī
Wall Law	CEDICINE FOLTFROILEIN		+	8		1	+	†	1	\dagger	Ī
THE DESCRIPTION OF THE PERSON	GENORG FOLTING	LAMMAI VIIIUS (SIEMIN TELANI SEV)				1	1	†		\dagger	
TO THE	CENTRAL FOL VACOTEDA	(STEADUSE STA)			T	Ť	T	t		+	
1000	CONTRACT ON VARIOUS IN		Ť	1056.3003	1101.1110	Ì					
A POINT	CENTAGE BOX YPROTEDA	MAIZE DWARF MOSAIC VIRUS	T			Ì	T		-		Ī
PROLG MYRY	GENOAG FOL YPROTEIN	MARKAY VALLEY ENCEMALITIS VIRUS	25.25						ŀ		
Prot 6 Day	GENOME FOL YPROTEIN	ORATTHOGALUM MOSALC VIRUS	Τ	16.93		Ī				l	
PHOLD PEANC	GENOME POLYPROTEIN	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)		36.38	3	120.00	167.1301	1425-1512 17	1767-1814 243	2433.2864	
PICK DICEN	GENORGE FOLYPROTEIN	POLIOVIRUS TYPE I (STRAIN MAJONEY)	2	_	_	Г				Н	
Proto Potis	GENOME FOLVPROTERN	POLIOVIALIS TITE I (STEAM SABIN)		_	1903-1933			H		Н	
Proto Pot 31	GENOME POLYPROTEDI	POLIOVIALIS TYPE 2 (STRAIN LANSING)	_	1501-1931						-	
PPOLIS POLIW	CENOME FOLYPROTEIN	POLIOVIALIS TYPE 2 (STRAIN W.2)	1061-1099	1641-1061	Ī						
Proto Pol.32	GENOME POLYPROTEDI	POLIOVIALIS TYPE I (STRAIN 2)127)	1040-1098	1900-1930						+	
100 PG I	GENOME POLYPROTEIN	AND PALEON (2A) (D)	-1	100					1	+	
POLO PEVD	GOODE POLYPROTEIN	PLUM FOR FOLLY TRUS (STRAIN D)		Ē	E	1	1	+	+	+	1
PIOLO PEVEA	GONDAE POLYMOTEIN	PLUM TOX FULL VIALUS (SIRAINT EL AMARI)	110		1	1	1	1	1	1	7

March Marc	S. C. Carlot	1.02.0120.4	Version (no carried and carrie		ARCAI		1	2016			Ī	
CHOOSE OF THEORIES	27:17			Г	1407-1524					1	!	ļ
CHOOSE PARTORES PARTA REGION WILLS STALL AND COLOUR PARTA REGION WILLS STALL AND COLOUR PARTA REGION PARTA REGION WILLS STALL AND COLOUR PARTA REGION PARTA	TOTAL ST	CONCLETE POLYPROTEIN		Т	1607-1524					:	:	:
CHOOSE POR PROPERTY PARTY REACHO VARIED (TRANS PORTO) THE STATES		CENONE POI VPBOTEIN		5								j
CATONIA PRINCESS PAYATA BERGOD VIRILES (TRANS PORTONIA) 101-101	YALL BY	THE PART OF THE PA			Ī						•	
CHOOSE FOR THE PROPERTY PART OF THE STORY WITH THAT IN COLD	LO PRISMI	CENTRE NO VERNIEN	=									
CHANGE STATEMENT CATABO WILLIAM VILLA DEPORT CHANGE STATEMENT	1	CONTRACTOR OF THE PARTY OF THE	(STRAIN W)			1						
CHANGE OF THE PROPERTY CHANGE WITH STILLING HEACAIDAN CHANGE OF THE PROPERTY CHANGE OF THE PROPERTY CHANGE WITH STILLING HEACAIDAN CHANGE OF THE PROPERTY CHA	. 1	CENCINE FOLITACION	VIRUS (STRAIN DPDI)	7		-						•
CHANGE BY THE PROPERTY OF A TOTAL OF THE PROPERTY OF THE PRO	1	COOPE FOLTER	GIRW	┪			137	1111.1111				
CHANGE BOLD CHANGE BOLD	1	GENOME FOR THEO I EIN		1	3			_	:	: I		
CHANGE ROLYMOTEH TOLYOUTEN VIELDEN TICKNESS TOLYOUTEN 111-111 111-11	L	GENORAL POLYPROTERI			2	1486		:	!	:	:	:
GENERAR DAY PROTECH ALABAT DAY PLEAT VILLAGE (STATE F. 11) 11-11	LO PVINI	GENOME FOLYPROTEIN	MOIATO VIEWS TO THE PARTY OF TH	_	701.735							
GENOME ROLF PROTECH 100.ALGA WALLA WILLIAM STALLY WILLS STALLY STALLY STALLY STALLY STALLY WERN YEARLAND STALLY WILLIAM ST	4 G PVVO	GENOME FOLYPROTEIN	POTATO VIRUS V (STRAIN O)		101.101							
CHANGE OF THE DITABLE STUDATOME MARK VEHICLES VILLES FOR THE DITABLE	TO SOLUTION	CENTRAL POLYPROTEDA	PARSHAP YELLOW FLECK VINUS (150LATE 7-121)	14.13								
CHANGE FOR THE FIRST STANDAR PERCENAL STREAM STOLING STANDAR PERCENAL STANDAR STAN		CONTRACT BOTH VPROTEDA	SUGALCASE MOSAIC VIDUS (STRAIN SC)	024.100			L					
CENSUR FOR THOUSEN FIRE LESS MARKE BECEPIAL CHARLES WILLING	2	STATE OF CHECKEN	SWING VESICULAR DISEASE VIRUS (STRAIN IV) 76)									
CAROAGE FOR TROUTERS THE A BOARD ENCEPTIALITIES VILID (STAINED BEAN STAIN) 100-111 100-1	TAGAIN	CENTRE FOLITAGE ENT	1674,1840			1111111111		Same July	_			
CENOME POLYMOTER TOTAL CONTROL OF STREAM BEAN TOTAL STREAM BEAN TO STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN TOTAL STREAM BEAN T		GENOME FOLTFILLIEUM	TOTAL BOARDS ENCERNAL ITTE VIRITS (STRADS SUITE)	17-128		200		_				
CHANGE OF TYPOTEN TOTAL ALL ALLAND ENCENTLIES WILD STRAIN BEAN BIRD) TOTAL ALLAND ENCENTRAL CONTRILITION WILD STRAIN BEAN BIRD) TOTAL ALLAND ENCENTRAL CONTRILITION WILD STRAIN BEAN BIRD) TOTAL ALLAND ENCENTRAL CONTRILITION WILD STRAIN BEAN BEAN BIRD) TOTAL ALLAND ENCENTRAL CONTRILITION WILD STRAIN BEAN BEAN BEAN BEAN BEAN BEAN BEAN BEA	LO TELVS	GENOME POLYPROTEIN	THE REPORT OF THE CONTRACT OF	1632-1659		_	_					
CHOOSE POLYMOTER TOTAL OF STORY WITH STAND S	A THEW	GENOME FOLYPROTEIN	BORNE BACETACHIS VINCO INCOLUE SCIENCISCI	145-672	1140-1175	1416-1443	1773-1800					
	24.6	CENTRAL POLYPROTEDI	TOBACCO ETCH WIKUS	11.00	100.00			_				
CENORA FOLVENOISH THEILEST MEMBE BLEEPHALOUYELITS VIRIS STRAIN DAN 160-111 160		CONTRACT OF CHAPTER	THEIL ES S MARINE ENCEPHALONINELITIS VIRUS (STRAIM DEAN SINE)									
CENONG FOR THOUGH THERE BY ALRADE BYCEVILLY ONYELLES VARIES TALLED TOTAL ON THE STAND ON	2	Contract of the contract	HIGH ERS LAMBAR ENCEPHALOWYELITIS VIRUS (STRAIN DA)									
CENOME POLYMOTERN	LO THEVO	GENOME POLITICISM	PLET EN LAMINE DACEPILAL OMYELITIS VIRUS (STRAIN GOVII)		1						 	
CENODE POLYMOTERN TOTALOW VALUE OF THE VALUE	LO THEY	CENONG POLYPROTEIN	STATE DARKET WEIN	133-162	B							
CENOME FOR VROOTEN	to Harv	GENOME FOR YPROTEIN	I DIMIT MOSAL VINA	404-433	670-304	2706-2742						
CENOME FOR TPROTEIN WATELDAR THE STATE OF THE STATE O	A PARA	CENTAL POLYPROTEIN	TOBACCO VEIR MOTTERM VINOS	302.230	L							
CENOME FOR TYROTERN VEST FOLE WIND STALEN TOD		CENTAND BOLVEROTSIN	WATERACLON MOSAIC VIRUS II		1							
CENOME POLYMOTERN TELLOW REVER VARU (STAAN FASTEUR TD-104) 114-44 1	7,44,7	With the state of	WEST MILE VIAUS									
CENOME FOL TRODEN VECTOR FELLOW MISSISTAMS ASSECTION 100-101 CENOME FOL TRODEN VECTOR FELLOW MISSISTAMS VALUE CENOME FOL TRODES VECTOR FELLOW MISSISTAMS VALUE CENOME FOL TRODES VECTOR FELLOW MISSISTAMS VALUE CENOME FOL TRODES VECTOR FELLOW MISSISTAMS VALUE CENOME FOL TRODES VECTOR FELLOW MISSISTAMS VALUE VELLOW VECTOR MISSISTAMS VALUE VELLOW VECTOR MISSISTAMS VALUE VELLOW VECTOR MISSISTAMS VALUE VELLOW VECTOR MISSISTAMS VALUE VELLOW VECTOR MISSISTAMS VALUE VELLOW VECTOR MISSISTAMS VALUE VELLOW VECTOR MISSISTAMS VALUE VELLOW VALUE VELLOW VALUE V	K.O. WIN	GENORE POLITICAL	VELLOW FEVER VALUE (STRAIN 170)				\downarrow	-				L
CENOGR POLYMOTH SUCCEED WISHINGTON TOTAL OF THE STAND		GENORE FOLTMUILIN	TATE OF REIGH (YOUR ACTEAN) PASTELLY 170-2041	434-46)								
GENOME POLYMOTERN FOLKMANTERN MALIONEY 1001-1001 1001-101	LO YEAV	GENORGE POL YPROTEIN	TELEGRAPH STATE OF THE PARTY COLUMN	96-69	_							
CENCRE POLYMOTERN VERY PLANTER VERY PLANTER STRAIN TRINIDAD DOWNEY 143-121	LO EMIN	GENOME FOR YPROTEIN	ZUCCHINI TELEVITORIANI MANAGENI	1011-[901	_							
	THE POLITY	GENOME POLYMOTEIN	POLICE LANGE TO SERVICE PROPERTY OF THE PROPER	1403-1467	_							
	TWENT	NONSTRUCTURAL POLYPROTEDY	VENEZULLAN EQUINE ENCEPTIAL IIIS VINOS (2100)	445.472			L					
	AN FONCE	NON-STRUCTURAL POLYPROTECH	FELING CALLETY WALL TO STATE TO THE TOTAL	1014-1041								
	NA PENE	HON-STRUCTURAL FOLYPROTEDY	FELING CALLIVATOR (3) PAGE 179	210.246	146.376		Ļ					
NON-STRUCTURAL POLYPROTEIN IEEAFITIS FYRUS (STAAN PARACA) 110-144 11	THE VALUE	INCHASTRUCTURAL FOLYPROTEIN	DEPATITIS E VINUS (STRAIN BURNIA)	310.344	146.18		L					
H.TRUCTUBAL POLYPROTEIN IERATHINE FYRUS (STAND PARIED) 111.313 141.1	77.7	INCOMETRICATIONAL POLYPROTEIN	HEPATITIS & VILUS (STRAIN NR.AR.C.)	77	140.134							
		TO THE PERSON NOT VORDING	IEPATITIS E VIEUS (STRAIN MYANNIAL)			1				L	L	
NONSTRUCTURAL POLYROTERN ADDOED BIRD VALUE NONSTRUCTURAL POLYROTERN ADDOED BIRD VALUE NONSTRUCTURAL POLYROTERN ADDOED BIRD VALUE NONSTRUCTURAL POLYROTERN ADDOED BIRD VALUE ADDOED BIRD VALU		LOCAL STREET HEALT BOX VORDITED	HEPATHES E VILUS (STILAIN PAKISTAN)			1						L
		PURISING INC. INC. INC. INC. INC.	Action Library Value	237-025		\downarrow	\downarrow					L
MONSTRUCTURAL POLYROTER ALABET RELIGIAL		MONSTRUCTURE POLITICIST	CONTRACT LIVERS OF STRADS CUL.U)	2453-2410	-							L
MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN MONSTRUCTURAL POLYTROTEN AVAILA	ALM CORN'YO	HOMSTRUCTURAL FOLTFRUIERF	A ABUTE LELICATION FACE ASE VIRUS	113.343	163 - 166							
	VON KIK	NON-STRUCTURAL POLYTROTEIN		1037-1084		2410-2445	~					
NONSTRUCTURAL POLYPROTERN ADSISTANCE AND STRAIN TOLE	HARVE NE	NONSTRUCTURAL POLYPROTEIN	ROSS RIVER VILUS (STRAIN REXVI)	1			L		L			
NOWITH LICTUAL POLYPOTEN SUBSTITUTE OF STAND THE SERVICE OF STAND EDSTOYN 13-3) NOWITH LICTUAL POLYPOTEN STANDS VILLS STAND EDSTOYN 13-3) NOWITH LICTUAL POLYPOTEN WESTERN EQUAE BUSSA DISSASE VINUS (STAND AUSTRALIAN POLYPOTEN AVAIN DEFETTIONS BUSSA DISSASE VINUS (STAND AUSTRALIAN POLYPOTEN AVAIN DEFETTIONS BUSSA DISSASE VINUS (STAND AUSTRALIAN POLYPOTEN AVAIN DEFETTIONS BUSSA DISSASE VINUS (STAND BUSA DISSASE DISSASE VINUS (STAND BUSA DISSASE VINUS (STAND BUSA DISSASE DI	47 68 64	NOWSTRUCTURAL FOLYPROTED	ROSS RIVER VILUS (STRAIN 148)	100	1.							
HONSTRUCTURAL FOLTREOTERS HONSTRUCTURAL FOLTREOTERS HONSTRUCTURAL FOLTREOTERS HONSTRUCTURAL FOLTREOTERS HONSTRUCTURAL FOLTREOTERS HONSTRUCTURAL FOLTREOTERS HINDERS HOUSE STATE FOR EAST DISEASE VIRUS (STRAIN SUFFICIAL STRUCTURAL FOLTREOTERS STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BEETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BETTINGS BURSAL VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BETTINGS BURSAL VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BETTINGS BURSAL VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BETTINGS BURSAL DISEASE VIRUS (STRAIN FOLTS) STRUCTURAL FOLTREOTERS AVAN BETTINGS BURSAL VIRUS (STRAIN FOLTS) STRUCTURAL FOLTS		AND THE PARTY OF THE VALUE OF	AUTHOLIA VINUS (STRAIN THE ALEN)			1	L		L	L		
HONSTRUCTURAL FOL TRACTERN HONSTRUCTURAL FOL TRACTERN HONSTRUCTURAL FOL TRACTERN HONSTRUCTURAL FOL TRACTERN HONSTRUCTURAL FOL TRACTERN HONSTRUCTURAL FOL TRACTERN HONSTRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN AUSTRALLAN 00).7)) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN FOL 1) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN FOC 1) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN FOC 1) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN STC) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN STC) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN STC) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN STC) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN STC) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN STC) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL DISEASE VIRUS (STRAIN STC) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL VIRUS (STRAIN EDSOVY 61-5) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL VIRUS (STRAIN EDSOVY 61-5) STRUCTURAL FOL TRACTERN HAVAN BAFETROIS BURGAL VIRUS (STRAIN EDSOVY 61-5)		CONTRACTOR AT BOX YEARTEN	SEPACE FOREST VINUS				-	-				L
MONSTRUCTURAL FOLTROOTER MONSTRUCTURAL FOLTROOTER AVAIN DEFETTION BULLAL DISEASE VIRUS (STRAIN STRUCTURAL FOLTROOTER) STRUCTURAL FOLTROOTER AVAIN DEFETTION BULLAL DISEASE VIRUS (STRAIN CU-1) STRUCTURAL FOLTROOTER AVAIN DEFETTION BULLAL DISEASE VIRUS (STRAIN CU-1) STRUCTURAL FOLTROOTER AVAIN DEFETTION BULLA DISEASE VIRUS (STRAIN STC) STRUCTURAL FOLTROOTER AVAIN DEFETTION BULLA DISEASE VIRUS (STRAIN STC) STRUCTURAL FOLTROOTER AVAIN DEFETTION BULLA DISEASE VIRUS (STRAIN STC) STRUCTURAL FOLTROOTER AVAIN DEFETTION BULLA DISEASE VIRUS (STRAIN STC) STRUCTURAL FOLTROOTER STRUCTURAL	2	MUNICIPAL TO CONTRACT	CONTRACT VIRELS (SUBSTYPE OCKELDO / STRAIN EDSDYN 12-5)	200			-	1				L
HONSTRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN 1270) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN AUSTRALLAN 001-71) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN FOCK) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN FOCK) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN FOCK) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN FOCK) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN STC.) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN STC.) STRUCTUAL POLYMOTER AVUAN BEECHOUS BURSAL DISEASE VIRUS (STRAIN STC.) STRUCTUAL POLYMOTER		MONSTRUCTURAL PACIFICATION	WESTERN BONDER DATE PRIALITIS VIRUS	£3			-	1				
STRUCTUAL NO. THOUSEN AND PARTITIONS SUBJECT STRUCTUAL OF STAIN AUSTRALIAN COLDING STRUCTUAL NO. THOUSEN AND PARTITIONS SUBJECT STRUCTUAL NO. THOUSEN AND PARTITIONS SUBJECT SUBJECT STRUCTUAL NO. THOUSEN AND PARTITIONS SUBJECT SUBJ	OLN WELV	MONESTRUCTURAL POLITICIONE	COLUMN TO THE PROPERTY OF THE	Ī								1
STRUCTURAL FOL TROTEEN AVAN BEECHOUS BURSA. STRUS (STAM CU.1) STRUCTURAL FOL TROTEEN AVAN BEECHOUS BURSA. DISEASE VRUS (STAM E) STRUCTURAL FOL TROTEEN AVAN BEECHOUS BURSA. DISEASE VRUS (STAM BOC.N) STRUCTURAL FOL TROTEEN AVAN BEECHOUS BURSA. DISEASE VRUS (STAM BOC.N) STRUCTURAL FOL TROTEEN AVAN BEECHOUS BURSA. DISEASE VRUS (STAM BOC.N) STRUCTURAL FOL TROTEEN AVAN BEECHOUS BURSA. DISEASE VRUS (STAM BOC.N) STRUCTURAL FOL TROTEEN	OLS BOVS	STRUCTURAL POLYPROTEDI	A TANK DATE INCOME STREAM STRAIN AUSTRALIAN 601-731	Т-	L	L						1
STRUCTURAL FOLVEROTERN AVANA BELLINGUS BURIAL DISEASE VIRGIS (STALIN E) STRUCTURAL FOLVEROTERN AVANA BEECHDUS BURIAL DISEASE VIRGIS (STALIN FOC. 8) STRUCTURAL FOLVEROTERN AVANA BEECHDUS BURIAL DISEASE VIRGIS (STALIN FOC. 8) STRUCTURAL FOLVEROTERN AVANA BEECHDUS BURIAL DISEASE VIRGIS (STALIN STC.) STRUCTURAL FOLVEROTERN AVANA BEECHDUS (STALIN ESSON) STRUCTURAL FOLVEROTERN AVANA FOLVER VIRGIS (STALIN ESSON 8) STRUCTURAL FOLVEROTERN STRUCTURAL FOLVER FOLVE	OLS BLDVA	STRUCTURAL FOLYPROTEDI	A VAN DE LIBOR BUILDING WAS AND LIBOR AND THE IN	7-		L	L					1
STRUCTURAL FOLYBROTERI AVIAN DESCRIDOR BURAL DISEAS VALUS (STALIN SEC.) STRUCTURAL FOLYBROTERI AVIAN DESCRIDOR BURAL DISEAS VALUS (STALIN SEC.) STRUCTURAL FOLYBROTERI AVIAN DESCRIDOR BURAL DISEAS VALUS (STALIN SEC.) STRUCTURAL FOLYBROTERI AVIAN DESCRIDOR STRALM GALU) STRUCTURAL FOLYBROTERI FOLYBROTERI FOLSS INVER VALUS (STRALM SEC.) STRUCTURAL FOLYBROTERI FOLYBROTERI FOLSS VALUS (STRALM SEC.) STRUCTURAL FOLYBROTERI FOLYBROTERI FOLSS VALUS (STRAM FOLSS VALUS FOLSS VALUE FOLSS VALUS FOLSS VALUS FOLSS VALUE FOLSS	of 5 mbVC	SHIUCTURAL FOLYPROTEIN	AVIAN DEECTIONS BUILDING MACANES AND ANALYSIS OF THE COMMENT OF TH	Т			L					
STRUCTURAL FOLYPROTEIN AVIAN BRECT DORS BARTAL DISEASE VALUS (STANIN STO) STRUCTURAL FOLYPROTEIN AVIAN DESCRIBES AVIAN STOLIN STOLIN STRUCTURAL FOLYPROTEIN OVYRONIA VALUS (STANIN GALU) STRUCTURAL FOLYPROTEIN GOSS RIVES VALUS (STANIN NOSON) STRUCTURAL FOLYPROTEIN GOSS RIVES VALUS (STANIN TOLIN STANIN STANIN STRUCTURAL FOLYPROTEIN GOSS RIVES VALUS (STANIN STA	Or & Dabye	STRUCTURAL POLYPROTEIN	AVIAN DESCRIBES SURFACE PROSESSING STANKES	11.516				L				
STRUCTURAL FOLYPROTEIN AVANA BEECHDOIS GRACE VARUS (STRUCTURAL) STRUCTURAL FOLYPROTEIN OPPORALATION OF VIOLES (STRUCTURAL) STRUCTURAL FOLYPROTEIN LOSS RIVEN VEILS (STRUCTURAL) STRUCTURAL FOLYPROTEIN GOSS RIVEN VEILS (STRAIN TOS) STRUCTURAL FOLYPROTEIN STROBEN (STRAIN TOS) STRUCTURAL FOLYPROTEIN STROBEN (STRAIN STRUCTURAL) STRUCTURAL FOLYPROTEIN STROBEN (STRAIN STRUCTURAL) STRUCTURAL FOLYPROTEIN STROBEN (STRUCTURAL) STRUCTURAL FOLYPROTEIN STRUCTURAL FOLYPROTEIN STRUCTURAL FOLYPROTEIN	Was brown	ISTRUCTURAL POLYPROTEIN	AVIAN DEECTIONS BURSAL DISEASE VIRUS (STRAIN FUCTOR		\downarrow	ļ	-	L		Ц		
STRUCTURAL POLYMOTER LOSS ELVEN VELIS (STRAIN POLYMOTER) STRUCTURAL POLYMOTER LOSS ELVEN VELIS (STRAIN TO) STRUCTURAL POLYMOTER LOSS ELVEN VELIS (STRAIN TO) STRUCTURAL POLYMOTER LOSS ELVEN VELIS (STRAIN TO) STRUCTURAL POLYMOTER LOSS ELVEN VELIS (STRAIN TO) STRUCTURAL POLYMOTER LOSS ELVEN VELIS (STRAIN TRAINS PRO AND POLYMOTER)	POLS BOYS	1	AVIAN DEECTROD BUILDE LINEAGE VINOS (STRAIN STATES)	124								1
STRUCTURAL POLYMOTERN GOSS BIVER YOUS (STRUCTURAL POLYMOTERN GOSS BIVER YOUS (STRUCTURAL POLYMOTERN STRUCTURAL	DAY ONO NO	Γ	ONTONCHION VINCE (2) INCH. CO. U.	616.611	L			_				
STRUCTIONAL POLYTROTED ADSS MAREN YOUR STRUCTURAL POLYTROTED STRAIN EDSOYN (1:-5) STRUCTURAL POLYTROTED STROBEN WINS STRUCTURAL POLYTRONE AND AND POLYTRONE AND POLYTRONE AND AND POLYTRONE AND AND POLYTRONE AND AND POLYTRONE AND AND POLYTRONE AND AND POLYTRONE AND PO	PAN S PON	Т	ROSS RIVER VINUS (STRAIN NO 2012)	10.01	ļ				L			
STRUCTURAL POLYROTEIN SACHES VARIS (SUBITTE CLALED) SHOWN ECONTROLS	ACC CAVE	Ī	ROSS RIVER VAUS (STRAIP 141)				-	-	Ŀ			
THE PARTY AND TH	OG S SDOO	STRUCTURAL FOLYPROTEIN	SPORIS VICES (SUBTITE CICALED) STRAIN EUSEN (17.7)	101.10			L					4
STRUCTURAL POLYTROTEIN SALES VEXAS (STRUCTURAL POLYTROTEIN	VOIL LOS	STRUCTURAL FOLYPROTEIN	SPORIS VIII. (STEAMS PROF. AND TALL)	9.86.9		-	L	-				_
STRUCTURAL POLYPROTEIN	VIEW LIN	KTELLETT BAL POLYPROTEIN	WESTERN EXCEPT ENCEPTION - 1503	l	Ŧ							
TABLE PROPERTY OF THE PROPERTY			TEXTEST PROPERTY (VIEITS 151 BAIN)	i i			4	4	-	4		

		All Victorial factorial beautiful	П			$\overline{}$	1				
PCCCME	10717214		I	LHEAL	TYN	4	7	1	Т	┰	9
TO THE PARTY OF TH	POL POLYPROTEIN	CAPIDIE ANTHULTIS ENCEPHALITIS VIRUS (STILATH CORK)	20.00			1001 001			Ì	t	Ī
NAVO POR	PICTATIVE POLYPROTEIN	CONDUCTION MOTTLE VIRUS	_	3		-		T	1	t	
100	POL POL VSBOTEIN		7	2			1	1	Ť	1	Ī
NA PER	POL POL YPROTEDI		Т	10.00			Ì	1	\dagger	\dagger	Ţ
PROLEIAW	POL POLYPROTED ⁴	EQUINE INFECTIOUS ANEMIA VIRUS (ISOLATE WYGAIING)	2	200		T	T	T		T	_
POL PENI	POL POLYPROTED ⁴		201.76			Ì	T	T		 	
PROL BIVIE	Not you vy kottov	FELINE DOGUNODEFICIENCY VIRUS (ISOLATE PETALURIA)				Ì	Ì	T	-	İ	
PPOL PAVO	ENZYMATIC POLYPROTEIN		1					:	:	.	:
A STATE OF THE	POL POLYPROTEIN		П	2			1	Ť	\dagger	t	
PHOL HTLIA	POL POLYPROTEIN	US TYPE I (STRAIN ATK)	27.7				T		Ť	1	
LI EN LOS	POR POR VPROTEDA	HUBIAN F-CELL LEUKEMIA VIRUS TYPE I (CARIDUEAN ISOLATE)	7				İ	Ì		T	
	Not but vecits of	HEALAN DOGUNOEPICIENCY VIRUS TYPE I (ARV2/5/2 ISOLATE)		1400			1	1	1	†	
	No. not vecomen	HIBLAN BOALHODEFICIENCY VIRUS TYPE I (BIIIO ISOLATE)	230-257	(1)-(1)			Ì	Ì	İ		•
	TOP TOP SHOWING		110-157	612-613		1		:	-	•	!
	AL ALTHOUGH	THE AND INCOME FICTERICY VIRUS 19PET HIRU ISOLATE)	230.357	3.63					Ì		1
AND HAIR	FOL FOLTED	CONTACT IN THE INCOME INTERIOR TYPE I LELI ISOLATE	217.344	079-979							
Prot. HVIEL	FOL FOLTFROITER	CONTRACTOR STATEMENT CONTRACTOR TANDED TO THE TOTAL ATEN	Т	194 020	156-176						
Prof. HVIID	POL POLYMOTEEN	THE STATE OF THE PROPERTY OF THE PARTY AND THE PARTY OF T	Г	414-465							
POL HVIR	POL POLYFROTEIN	THE STATE OF THE PARTY OF THE STATE OF THE S	213.344	474.510	099-619						
PPOL HVIMA	POL POLYPROTEIN	HUMAN DOWNOUS KIENCT VIRUS 1 TE 1 (MAL 150CATE)		777		Ī		İ		! !	i
PPOL HVILON	POL POLYPROTEIN	HUMAN INDUMONE MIEME, Y VINUS I TITE I (MIN ISOLATE)	176	177.55			Ť		-		
PPOL HVINS	POL POLYPROTEIN	HENCH DOGDWOODFICENCY VIRUS 17PE I (NEW YORK:) ISUCATE)				1					
PPOL HVIND	POL POLYPROTEDY	HUBLAN DAMINODES ICHENCY VIRUS TYPE I (MDR 150LATE)				T		T	l	İ	
PPOL HVIOY	POL POLYPROTEIN	HUMAN INGRUNODE PICIENCY VIRUS TYPE I (OYI ISOLATE)				Ī					
VAIVE HOLE	POL POLYPROTEDI	HUMAN DOGRODEFICIENCY VIRUS TYPE I (PV2) ISOLATE)	370-237	100			1	Ī	T	İ	
HOLDER POR	POL POLYPROTEIN	INDIAN DOGNODEFICIENCY VIRUS TYPE I (REALAT ISOLATE)		3		1	1		1		
Page Living	POLYPROTEIN	HIBAAN BEADWOOEFICENCY VIRUS TYPE I ISTRAIN UGANDAN ISOLATE U		55.50	919-640			1		Ì	
101	POR BOIL VARIABLE	IRDAAN DAAGNODESICIENCY VIRUS TYPE I (Z2/CDC-234 ISOCATE)		619-440			1			1	
Peri Livia	POS POL VEROTERA	HIDLAN BOALDWOOFFICHENCY VIRUS TYPE I (1501.ATE DEN)	401-582				Ì	Ì		Ì	
1000	Por ton year 1604	INDIAN INDIANOPPICIENCY VIRUS TYPE 2 (ISOLATE CAM2)	431-342					1			
A LINE LAND	POLICE VERNIEN	HRALAN BOADMODEFICIENCY VIRUS TYPE 2 (1504.ATE D194)	309-400								
	Por Pol Veloren	HEDLAN DAGDODICENCY VIRUS 1YPE 2 (ISOLATE D205.7)	28.E								
	NAME OF STREET	IN MAN DAMBRODE ICTENCY VIRUS TYPE 2 (ISOLATE GIIANA-!)	471-542							1	
TOT BASE	POR POR VARIOTEIN	HEALAN BEARWOODS FORMOY VIRUS TYPE 2 (1500, ATE MIH-Z)	431-529								
V 100 100 100 100 100 100 100 100 100 10	TO THE WAY OF THE PARTY OF THE	INDIAN PARAMODEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	472-563							1	
THE HALL	TOT TOT THE STATE OF	INDIAN DACINGDEFICIENCY VIRUS TYPE 2 (150LATE SBLISY)	473-562								
THUE HASS	PAY NOT VINCITED	HUMAN BOATHODE FICTENCY VIRUS TYPE 2 (ISOLATE ST)	491-582								
ALC: NUA	MITATIVE FOL POLYPROTEIN	HAMSTER BYTRACISTERNAL A-PARTICLE	300-127	184-381	461-499					1	
170	PLITATIVE POL POL YPROTEDY	MOUSE INTRACISTERNAL A-PARTICLE	211.236	103-139	400423			1			
AND DES	PROBABLE FOL POLYPROTEIN	MOUSE DYTRACISTERNAL A-PARTICLE	130-157	2 2 2 3					1	1	
Val.	POL POLYPROTEDA	SHEEP PULMONARY ADENOMATOSIS VIRUS	24. 33						1	1	
PPOL MALVAX	POL POLYPHOTEIN	AKR MURDIS LEUKENDA VIRUS	S 48				1		1	1	Ī
PPOL MEVAV	POL POLYPROTEIN	AKV MINDE LEUKENDA VIRUS	103-637				1	1	1	T	
POL MEVED	POL POLYPROTEDI	EADIATION MURDIE LEUKEAGA VIRUS		7 (2)			T	T		Ť	
PPOL MLVIK	FOL FOLYPROTEIN	ILADIATION PURING LEUCEMIA VIRUS (STRAIM RAYLAN)	200	9			T	T			
PPOL NOWY	FOL POLYPROTEIN	SUCAN MASON-FIZER VIRUS	7	107	ma 11.8		T	T		Ī	Ī
PPOL OB/OVS	POL POLYPROTEDI	OVDE LEMIVAUS (STACIN SA OMYV)	25.0	200			T		İ	T	
PPOL BSVP	POL POLYPROTEIN	INDUS SARCTANA VIRUS (STRAIN PRACUE C)	7	10.05	196.301	363.338	(10-01)	41.13	1522.1049	T	
PPOL BTBV	POLYPROTEDI	MICE TURGED BACKLEDORM VIRUS			134.301	Т	Т	۴	623.1049	T	
PPOL RTBVP	POLYPROTEIN	MICE TONGRO BACALLOCOM VIXOS (1904A 1E CHILITTINGS)				Т	Τ	Ť		T	
POL SFVI	POL POLYPROTEIN	SEMINATED AND CONTRACT OF THE LACE AND		75 (7)	417.411		Ī	Ì		T	
PPOL SIVAI	POL POLYPROTEDN	SOUTH BUILDING CONTROL OF THE STANDARD SOUTH STANDARD SOUTH STANDARD SOUTH STANDARD SOUTH SOUTH STANDARD SOUTH SOU	10.15				Ī				
PPOL SIVAL	POL POLYPROTEIN	SUCAN BOUNDARY FLERNING TO INCOME TO CALL TO THE TOTAL TO CALL THE TANK THE						Ī	Ī		
POL SIVA	POL POLYPROTEIN	SOUTH DESCRIPTION OF THE PROPERTY OF THE PROPE		417.716	647.469		T				
PPOL SIVAG	POL POLYPROTEIN	SOUGH DOGGRADES PUBLIC VALUE (ACMINISTRATE)	111.111					Ī			
POL SIVA	POL POLYPROTED	AND THE PROPERTY OF THE PARTY O					Ī				
POL SIVAT	FOLIOL TROUBLE	CHARLE AND SET THE ALCONOMY OF THE CALLED STATE OF THE CONTROL OF	L	20.00							
TAR E	rot rotten										

111 KANK 1102 SIVGS 110 SIVGS 110 SIVGS 110 SIVGS			١			2					
		VIRUS	П	2							
	POL POLYPROTEIN	ATE	33.560								
			3								
		15	133	Ì							Ė
			20.4								
İ											•
		COUNTY MOVER I PLI IN TAKE I VALUE	П	5							
Ī	OTEN		\$78.612	630-603							
T	POLYPROTEDI		15.00	111.010							
Ī			Т	110	616-118						
			L	816-188							
	TOL TOLITHOLEEN		T								
٦	FIN	ACHIEF HALLARY TUROR VIRUS (STRAIN BRO)	,					L			
	PROTECTION	ACTIVE LIANDALA FURACIA VIRUS (STRAIN CIVI)	2						L		_
		CONTRACTOR OF STRAIN CAN	67.20		:	:	:	•	_		
		MUCOS PARAMENTAL STATE TO THE DESCRIPTION OF THE PARAMENTAL STATE	11.11								
Ī	PRECURSOR	SCALD TA MOTH CT 1	11:43								
T		AUTOGRAPHA CALIFORNIA MALLEAN YOU INCOME	14.61	301.328		1	-	1	-	: : 1	-
T		ACROTIS SECETUM NUCLEAR POLYHEDROSIS VIRUS	Ī		i i					1	
ı		BOAGBYX MORI MUCH EAR POL VIICEMOSIS VIRUS									1
MAN OWA	TO THE PARTY OF TH	DUZURA SUPPLESSALIA MUCLEAR POLYHEDROSIS VIRUS	1								
1		HYPHANTELA CUREA MUCLEAL POLYHEDROSIS VIRUS		ĺ							
PAND NAME		I YN ANTHEIR DISPARIMENT FICAPSID MUCLEAR POLYTIEDROSIS VIRUS	1								
TYID WALD		ALL SECTION MAN CONTAIN MICLEAR POLYHEDROSIS VIAUS	7				1				
PAR RAG		SACHA ARE PATERIAL AND TICAPSID POLYINEDROSIS VIAUS						-			Ĺ
AD NOVOP		ORCATA PECUNOTATION A CINCLE CAPCIE NACLE AN POLYTH DATESTS VIRUS	10-43		ļ						ļ
SOA ON COLANS		ORGATA PACINAL SUCKE LANGE TO LANGE FOR APRIL POR VIEW CHANGES VIEWS	_					1	-	ļ	Ļ
SVG LEVE		PANCIES PLANDER MOLITICE TO ENGINEERING COLORIS (CTEAN US)	677								1
Saves on		SPODOPTELA EXICUTA PULLEAR FOR THE LINE AND PROPERTY (1819)	14.41								1
		SPODOFICIA FRUGORIDA MULLEAR POL TIMENASSIS TIMES	17 17								1
1000		SPACE GOODE CERCY VIKUS (110-1130-115)	13-63								1
١		VISMA LEKTIVENS (STICKIN 1914)	1	1111	163.300						1
Į,	MOSTH REDUCT LANGE CHA	ABICAN SWING PEVER VIRUS (ISOLATE RIALAWILLI, 1991)	433.440								
١.	3	HUMAN CYTOACOALOVIRUS (STRAIN ADIEN)	191								
1	13	EQUACE MEDIFICATIONS TYPE I (STRAIN ABAP)						L	L		
- 1	15		170						-		
- 1	i	VACTORIA VILLE ISTILATE COPENIAGEN	107.401						-		L
- 1	1	VACTORIA VIDIS (STRAIN WR)	167-401				1				L
	SI:		167-461							L	L
	ABONAC DONOSTHI REDUCT LAUGE LIN		119-146								ļ
ı	ALBONAC DENOTH REDUCT LATICE CHA		611-06						+	1	1
L	ALBONAC DEHOSPH REDUCT SWALL CHA		77-17	\$13-540					1	1	
1	INA POLASSOC TRANS SPEC PACTOR	VACCINIA VIRUS (STRAIN W.K.)	41.33	3-10	\$13-540						\downarrow
VALVE VALVE	ANA POLASSOC TRANS SPEC FACTOR	VARIOLA VILLS	201.00	313.616	10-01	1961.99			4	1	
ı	DAY DO LETED BUY POL 147 KD	VACCEDIA VELUS (STRAM COPERINGEN)	111.344	31716	100	# 1 · 1 · 1 · 1	1011-1036				4
1.	DAY MARCHED BNA POL 147 KD	VACCIDITA VIAUS (STRAIN WR)	7	11.0	10.0	164-182 184-182		L			
ì	PANA PAREPTED BINA POL 147 KD	VALIDILA VIRUS		17.		L		L			
l	CALL PAREFERS BINA POL 113 KD	CAPADOXVIRUS (STRAIN KS-!)		Ş			L	L			
	THE PERSON AND IN NO.	COWPOX VIDIUS							L		
X ABBOTA	DEA DUCA IN THE BUT IN THE	VACCEDIA VIRUS (STRAIN WR)	2			1		-			
MOS VACEV	DA DUEL ED PAR TAL 111 PA	VARIOTA VIRUS	2			1	\downarrow			-	L
UPOS VARV	DAY DOLECTED LIVA FOL. 13 P.	Paternovonis (STRADERS.)	36.43					1			1
PLPOS CLIVIC	DRIA-DOLECTED LIVA POL. 13 KD	CAPACA VIETE CETEAN WES	16-33	6.5				1	+	1	ļ
APOI VACEV	DNA-DOBCTED BINA POL. 17 KD	VALUE A VOLUE	03-30			4		1	1	1	L
THOU VALV	DNA-DOLECTED RNA POL 17 NU	I EL VEYAN UNLIK	1333-1360	-		_	-	1		-	ļ
PAPOA LELV	ANA DESCRED RNA POLITICANA	E-MINE APPERENT VINES	1111-915	1636-163		4	1	1	1	-	ļ
PRIOR EAV	ANA-DOLECTED RNA POL TAGANSE	INSTITUTE A VILLE (STEATH ANCOREA/1948)	\$75.402			-		4	1	1	ļ
PALED! LAKOR.	RIMA-DOLECTED RIMA POL. SUB 71	HANTIESTE A VIBIL CTRAIN A/ANN ARBORCEGO)	111-146			_		1		1	1
PRINT LAND	ANA DESCRED RNA POL SUB PA	THE THEORY A VISITE TO A PARTICULAR AND COMPANY AND CO	119-146					1		1	1
and who	INA DOLECTED INA POL 543 F2	SENSON A UNITED THE ABS ANOWIL PLACUE VIRUSADS TOCKUSA)	115-106				-	+	-	1	1
MEN WAR	ANA DOLECTED INVA POL. SUR 77	THE PARTY A CHANGE OF THE ANCIET I ALABYT AND YOUTH	116.146	L	٠			-	$\left \cdot \right $		$\frac{1}{1}$

	LACTOR TO THE PROPERTY OF THE	VALUE PRELIGENZA A VIRUS (STRAIN AZEQUINCA ONDOWINIOTI) INSTLÜENZA A VIRUS (STRAIN AZEQUINCTENNI SSI (1910) INSTLÜENZA A VIRUS (STRAIN AZEQUINCTENS)	ARCA!	17387	7477	ABCAL	ARTA	1	7		
	CETED BAN FOL SUB PT CETED BAN		2 2 2					;	:		:
	CTED NAY POLSO PER		914				1	-;	:	:	:
	ETED NAM FOL SUB 72 ETED NAM FOL SUB 73 ETED NAM FOL SUB 74 ETED NAM		1	i	!			•			
	CETED MAY FOL SUB PT CETED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY ESTED MAY FOL IS BY							Ì		Ī	
	CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT CTED INA FOL SID PT		19-146						Ī		Ī
	CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT CETED INA POL SUB PT		914						T		
	CTED INA FOL LID FOL LETED INA FOL LID FO ECTED INA FOL LID FOL ECTED INA FOL ECTED I		9					1	Ť	Ī	
	LETED INA POL 119 P2 ECTED INA POL 119 P3 ECTED INA POL 119 P3 ECTED INA POL 110 P3 ECTED INA POL 110 P3 ECTED INA POL 110 P3 ECTED INA POL 110 P3		92-6-							Ī	1
	ETED BAN POL BLD PE ETED BAN POL BLD PE ETED BAN POL BLD PE ETED BAN POL BLD PE ETED BAN POL BLD PE ETED BAN POL BLD PE ETED BAN POL BLD PE		115.14							1	1
	ETED BAN POL SIGN PS ETED BAN POL SIGN PS ETED BAN POL SIGN PS ETED BAN POL SIGN PS ETED BAN POL SIGN PS ETED BAN POL SIGN PS		119-146					1			
	ECTED MAY FOL SUB PT ECTED MAY FOL SUB PT ECTED MAY FOL SUB PT ECTED MAY FOL SUB PT ECTED MAY FOL SUB PT ECTED MAY FOL SUB PT	FANILY ILESIEVATORS	119.146								
	ICTED INA POL 108 PI ICTED INA POL 108 PI ICTED INA POL 108 PI ICTED INA POL 108 PI ICTED INA POL 108 PI		77.144								
	ETED INA POLSUS PI ETED INA POLSUS PI ECTED INA POLSUS PI			Ī							
	ECTED BAX POL SUP PI ECTED BAX POL SUP PI ECTED BAX POL SUD PI	TA/133/110]	1								
	ECTED ANA POL SUB PT ECTED ANA POL SUD PT		_			Ĭ					
	ECTED ANA POL SUD PT		20141				:				
	ECTED ANA POL SUB PI	201/201	1	Ī	i						
					İ						
		INFLIENZA A VIRUS (STRAIN A/SWINE/HONG KONC/126/17)	2					Ī			
	NA DIRECTED BHA POL SUB PI		9			ĺ					
	BUT SAMERIES BUT AND CITE 93		10.146								
	CALL PROPERTY LOS SIGNEDS	DAPTEDI	157.194								j
	TO THE PARK FOR SUPPLY	PARTY PRINTS A LIMIT OF A PLANT AS BOOK LAKE IWIT D. TVP.	3								
_	INA-DIRECTED RNA POL SUB PI		183.184		į	<u>.</u>		:			
	ANA-DIRECTED BUL POL SUB PI			Ī	-		111		İ		!
Ī	ANA-DORECTED ANA POL SUB PS	ARMOR KALIXVIII)	2								
PAREL LACER BNA. DOM	ANA DIMECHED ENA POL SUB P.		╗								
Ī	EPHER BULL BOX CIES 91		31.X	480-307							
Ī	THE PROPERTY BUT DO STORE OF	(u)	487.514								
Ţ	MA-DOCTION FOR THE BY	DAPTEDII	Ē	432-508							
	ELIED BANK FOL. SUB FI	Ī	3	472.500							
٦	INA DIRECTED RINA POL. SUB P.)		2	Ī							
_	NA DESCRED BNA POL SUM PJ		1								
ì	UA DEFECTED RIVA FOL SUB FI	US (STIAIN CIENT)	Ť	100							
1	LIVA-DINECTED RIVA POL SUB P)		Ť		1031.3000	111111111					
Ī	INA BRECTED ANA POLYNORASE	HUMAN CORONAVEUS (STRAIN 239E)	T			•					
REPA CYMCH RNA-DIR	ANA-DOLECTED RNA POLYMERASE										
Γ	ANA-DOLECTED ANA POLYACEASE		Т	337-384							
3	ANA-DOLECTED RIVA POLYNGRASE		T	20.01							
1976	INA BOLECTED RIVA POLYNGAASE		105-915	20.5							
Ī	ANA DESPETED BNA POLYNGRASE	(STRAM F\$772	ž	353-380	115-412						
Ť	NA PREFITED BNA POLYMORASE	AVIAN DEECTIONS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	1810-1843	1294-2331	1547-1574						
Ī	BWA DOMECTED BWA POL YNG RASE	AVIAN BEECTIOUS BRONCHITIS VIRUS (STRAIN KOH))	165-200	416-443							
Ī,	NA MARCTED RIVA POLYNORASE		S								
T	20 V		100	117.350	1603-1161	1692-1919					
PART BUNTO	TO THE PREMARE	BLIS (STRADY ONDERSTEPOORT)	16.51	ĺ							
Ī,	THE PARTY OF THE ARE		((7-10-	461.510	364.591	136.765	903.946	1993-2020			
۳	MA TOLINGAMO	LABLAND BERBER ATORY CONCYTIAL VIRUS (STRAIN A2)	10)-192	110-237	167.494	718-415	1001-1034	1136-1165	1453-1480	1776-1803	1043-100
Ť	THE THE SAME BEIN SUBJECT TO		8101-164	141.1370	1490-1324		1024-1067	1216-1766			
Ť	ANA-DARK IED ANA I DE VARIO ANE		•	1490-1334	2239-2267						
THE PASSES OF TH	THE PARTY SEED AND THE STREET	NSTON	11176	12.00	2121.3148						
٦	LINGS BEIN AND THE	500	L	710-103	1403-1432						
z	INA FOLTPEAASE BEIA SUBURII	LACACA CT IN PAGE ACT VIDEO COLUMN BE ALBERT TO CALL	Т	43.50	1979.2013						
	ANA POLTNE LAS BE IN SUBURI	NEW CASILE MEANE THE STATE OF THE TOTAL TOTAL STATE OF THE STATE OF TH	۲	161.191	1417.1132	1001					
	KNA POLTBELASE BETA SUBURIT		٢	136.163	9	-	184.2016	2115-21142			
T	INA PALTMERANDE BELA SOCIALI		<u>_</u>	\$37.591	31.75	3	-	1000-197	1994.2025		
Ï	TOTAL SO BEEL COMMENT		Ī	603-433	2066.23		L				
Ĩ	INA POLITICANA DELA SUBURI	19101	T	605-433	2068-2123						
2	MA PALTMEAASE BE LA SUBCINI	Bics bly AB Vinits	Т								
T	EAST-CHECKED BAY BOL WAS BALL	RIST VALLEY PEVER VIRUS (STRATM ZIL:348 MIZ)	134-1361	1453.1407							
PRINT RAPAS	DAY DO VACE ACT BET A CHILDRY		•	1003-1116	26.06.	1720-1754 2105-2180					
T	AND THE STATE OF STATE OF STATE STAT		ı	903-036	1544-1576	1945.3000					

			1	ī	Г						
PCCDNE	107617014	An Virgos (so Distributed C.)	Ī	4		215.2016	200				
THE RAME	PROTLIN	T VALIC (STRAIN 2)	Ť	Ť	36.18	210.108					
HIM SDOZ	ANA POLYMERASE BETA SUBUNIT	190				2					
LH SEOUN	RINA DIRECTED RIVA POL MAERASE	A WE.	3	22.00			1010			ŀ	
THE SYSWIL	RHA FOLYAGRASE BETA SUBURIT		125-059	21	20.00			14.14.1	1431.1488	100	200 11 10
WIND HAR	RHA POLYNGRASE BETA SUBUMT	SONCHOUS TELLUM RELEGIES AS 211 IAM ISOLATE CPINITIBR-01)		_	2						
WASH HAND	NAME - DURECTED INA POLYMERASE	TOWATO SPOTIED WILL VINOS (BINE)	2164-2193 2	_	34.14						•
			143.119	1031.031	2						
PREME UKK	BAIA POLYNGRASE	UST THE SE VALUE AND THE LIGHT OF THE WIE BEEV / STRAIN HAZELIN	1530-1557	100							L
PALENT VSVAH	KHA POLYNERALE BETA SUBURUT	VESICILAR STORATION VIRUS (SCHOOL MEW FIRST Y STRAIN OCDEN)	1365-1333	1005-1136							
DIAM MAD	RNA POLYNGRASK BETA SUBIDAT	VESICILAR SIGNATURS VINUS (SERVITER IN SAN HIAN)	1340-1267	1764-1791							
10000	INA POLYMERASE BETA SUBUNIT	VESICULAR STOMATITES VINDS (STICKLIN SAN SONS)	_	364-591							
	BALL THEREFORD BALL BOIL WAS BASE	APPLE CHECKETIC LEAS SPOT VIRUS	144.383								ļ
ACLAN ACLAN	MA COLOR DE SUA BUILDING	BEEF WESTERN YELLOWS VIRUS (ISOLATE FL-1)	1								
PARIO BUTVE	PUTATIVE REA-GAR POOR TO	BABLEY YELLOW DWARF VINUS (150LATE MAV-PS1)	+	Ī					L	L	
PRESO BYDVI	PUTATIVE BUA DOR BNA POL	EASTE VEIL ON DWARF VIRUS (150LATE PAV)		Ī						Ĺ	
PALLO LYBY	PUTATIVE BHA-DIR RHA POL	BALLEY TELLOW DWANT VIEW AND ATE P. PAVI	171.789								
MOVE OFFICE	PLITATIVE ENA-DIR BNA POL	BABLEY TELLOW DWALE VINDS (1905.	\$1.13	131.304	143.644						ļ
2010	PHITATIVE BNA DIR BNA FOL	CANANTION MOTTLE VIRUS		1000							ļ
2	THE PARTY BUT DOE	CUCUMOER CREEN MOTTLE MOSAIC VIRUS (WATERWELLON STRAINS	Ť	103.410							1
PRINC COMMS	PUINTIVE MAN THE MAN TO	AVIAN DOECTIOUS BURSAL DISEASE VIRUS (STRAIN SUTO)	Т								
PREJO GEDVS	PUTATIVE RIA-DIR RAY FOR	CUANTING PETENDER BURSAL DISEASE VIRUS (STRAIN AUSTRALIAN 002:73)	1							L	
PILLIPO DIDOVA	PUTATIVE RNA-DIR RNA PUL	THE PARTY OF A THE NECHOSIS VIRUS (SEROT VPE JASPER)	23.680								L
PREMO DRIVI	PUTATIVE RNA-DIR RNA POL	INC. INC. TO SECTION OF SECTION O	333.600					\downarrow			L
SAME CARRE	PUTATIVE RNA-DIR RNA POL	INFECTIOUS FAMILIES IN TRANSPORTED AND ANY CERNICAL	311.00	1053-1079							1
	BNA POLYNGRASE	LYAPHOCYTIC CHOROMENDING IIS VINUS (31 INVITED BY	ī	106.736	1073-1079						1
2	ALTERATIVE BMA DIR BMA POL	PEPPER MULD MOTTLE VIRUS (STRAIN SPAIN)	Ť								
PERSONAL PROPERTY.	POINTING MANAGEMENT AND WASHINGTON	INFOVIRUE CHYPE 37 STRAIN DEARING)				<u> </u>					
PRAPO REOVO	ENA-DIRECTED AND TOUR ONES A CE	AFOVIRUS (TYPE 1/ STRAIN LANG)	T	1	9				L		
ı	RINA DIRECTED KINA POLITICANA	EXPORT BOTA WINING (STRADA RE)	1			1				L	L
ı	ANA DE ENA POL SUBURIT VPI	COLUMN TO THE SECTION OF THE SECTION	68-95	2						ļ	
	RMA-DUI RNA POL SUBLANT VPI	BOVINE ROLL VINCE (CONDEX)	3.44	19-103	2	Ž		1			ļ
PREPOR OTPC	RNA DIR RNA POL SUBURGE VP.I	POLCOG ROTAVILLE (CALCATARIES)	\$6.59	103-139	191-616	93.500					1
•	RNA-DOR RNA POL SUBURIT VP1	PORCEAU ROTAVBUS (STRAIN COLLEGE)	5	919:10	975.1002						1
1246	BWA DAR BNA POL SUBURGE VPI	SDAAH 11 ROTAMBUS (STRAIN SATI)	143.181			L	L				4
	THAT THE PER BNA POLYNERASE	SACOLAROM Y CELEVISIAE VIRUS L'A	L	127.152	1103.1134	1971.200					
	Т	TACALIDE VINUS	Т	114.134	-		L				_
7	Т	HOBACCO MILD GALEN MOSAIC VIRUS (TMV STRAIN U2)			_		-	_			
VERTO THEM	Т	BOVING RESPONTORY SYNCYTIAL VIRUS (STRAIN ASIFOL)							L		
VALUE BASVA	MA FOLTBEAMER ALTER STRATE	CANDIG DISTEMBER VIBLUS (STILAD) ONDERSTEPOORT)	27.7			1	ļ			L	
TIPLE COVO	KNA POLTIGIKASE ALTTA SUBSKII	LANGUAGE BECOM A TORY SYNCYTIAL WAVE	14.14							L	L
VIEW 1815	KNA POLYMERASE ALPHA SUBUNIT	THE STATE OF THE PARTY STATE VIEWS (SUBGROUP B / STRAIN 18537)	99-141			1			1	L	L
PERSON HELSVI	RNA POLYNGRASE ALPHA SUBURIT	THE PARTY OF THE CONCOLLABOR (STRADA A.)	99-141					1		1	1
PREP HELVA	ANA POLYNERASE ALPHA SUBURA	THE PROPERTY OF TAXABLE STATES OF THE PROPERTY AND STRAIN LONG.	121-46					-	-	ļ	ļ
PREP HESV.	ANA POLYNERASE ALPHA SUBURIT	MAKAN BESTUAL STREET STREET	115.370		_	_				1	1
STATE OF A	ENA POLYNERASE ALPITA SUBURGE	MEASURES VINUS (SHALM EDMONSHOW)	315.376							1	4
	INA POLYNOLASE ALPHA SUBUNIT	MEASUES VIRUS (STIAM P. J.C.A)	115.116		L	L					1
	ANA MAY TAKE ALL ALPHA SUBURIT	MEASUES VIRUS (STRAIN TANACHAN)	111	234-361	33.416						4
	BEIN DOR YNG BASH ALPHA SUBURGI	HIDGAN PARADH (MICZA I VIXUS (STRAIN C.))		314.34	33.416	L	L				4
27117	ANA POLYMERASIS ALPHA SUBURIL	HENGLAN PARADOLLENZA I VIRUS (STRAIN C.7)	1	237.262	33.416	L					4
9110	ANA POLYNORASE ALPHA SUBURAT	HENDAN PARABOLIENZA I VIRUS (STIAM CL. 27.1)	1	366.231	33.45		L				4
20100	BMA BOL VACEASE ALPHA SUBURIT	HISTORY PARAMETERS 1 VIEWS (STRAIN CHINES)	20.65	231.166			L				4
VILLY MIKE	AND THE WAREAGE AT BUY LIMIDAT	INDIAN PARADOLIENZA 2 VIRUS			1	-	L			Ŀ	
	THE PARTY OF THE ACT AT BUILD STREET	HEBLAN PARADISTLENZA 2 VIRUS (STRAIN TOSHIBA)	K		716.716	-	-		L		L
PERTY PURIT	THE PARTY OF THE PROPERTY OF THE PERSON OF T	INOVINAL PALADOLUTICA 3 VIRUS	1			-	-	-		Ŀ	L
THE PLE		LABLE AND BAR AREST TENZA S VIRUS (STRAIN MIN 47885)	114-144	1		1	1		ļ	L	L
PREP PURA		SATISTICAL PARADITITION AND VIRUS (STRAIN TOSHIBA)	ě.			1	1	1	1	ļ	L
PRINT PARTY		IS A DESCRIPTION OF THE AND POT	91-117			-		+	\downarrow	ļ	-
HER LAW	Ē	SECOND CARLO (SINGE AND PARCET MAIT ANTS)	130-357	139-420		4		-	1	1	ļ
COCK STORY	Γ	SEMINAL VANCE (STANK) AND STANK AND	130-157	179.420			1	4	-	1	\downarrow
PARTY SECON	ANA POLYMERASE ALPHA SUBURAT	SEPTIME VICES (SINCE AND S	136-159	119.420			4	-	1	+	1
PERMIT		TENDAL VICES AND AND MARKET	336-555	379-420			4	4	1	1	+
HORSE STORY	ANA POL'THERASE ALPHA SUBURET	MANAY WILLS (STRAM PANAS)	134.151	374.70		Ц		4	4	4	┨
THE COMP	1	SENDAL VIXUS (31 MAIN 4)						ľ			

		An Virgan (as hatitribable net)					_		П	
T. C. L. L. L. L. L. L. L. L. L. L. L. L. L.			AREAL	OBEA:	77370	ORFA SAFAL	4	7	4	a a
74 LV SVS	ENA POLYNGBASE ALPHA SUBUNIT	SDOLAH VIRUS S (STILAIN W))	2	97.50					\dagger	Ī
PLODE VACEV	DIER	S (STRAIN WR)	£				1		\dagger	Ī
PERSONAL VARV	DIER		12		Т				†	Ī
PAPER ANGERV			91:16	60 161	2	26:380			1	ļ
PSPII MYXM.	Γ	(APPE)	=				1		†	4
PSPIB VACEV			3			1			\dagger	;
PSPIA VACCE		VACCINIA VIRUS (STILADY COPENILAGEN)	2				1		<u> </u>	4
rtica Cimi	Ν		3			-	:	:		_
PIALL VACEV			3						\dagger	Ī
PTAGE FOWPY		FOWLPOX VIAUS	2			+	1		t	T
PIAGI VACCV		VACCINIA VIRUS	٤						\dagger	
PTACE VARV		VARIOLA VIAUS	2					+	\dagger	Ī
PTALA BFDV		BUDGERIGAR FLEDGLING DISEASE VIRUS	= 2					1	İ	
PYALA POVBO	LANGE T ANTIGEN	BOVING POLYOMAVIRUS	3			:	-	•		
PYALA POVILA	I ARON T ANTIOEN		\$17-621			-			1	
PTALA MOVI Y	LARGET ANTIGEN		224-258	616-614			1	1	1	
PTALA BOWE	I ABORT ANTICEN	ACHISE POLYDALA VIRUS (STRADA 3)	913-540						1	
AND AND	A ARCH T ANTIGEN		311-538						1	
7			308-333						1	
TANK PAYER	Ī		407-434	486-533	\$11.559				1	
Name of Assessment	TRANCACT TRANCEROPROTEIN		617-810	494-528	337.564				1	
200	Ī	EDROSIS VIRUS	513:334						1	
Out In the	Ī	EPSTEIN-BALR VIRUS (STRAIN 1995-1)	143-133		1344-1371	1876-1903			1	
PTECH INCOME	T PROTEIN	HILLIN CYTOMEDALOVIRUS (STRAIN AD169)	1381-1381	2201-2229					+	Ì
PTECH LICVII		INTERES SOUND BY VIELDS (TYPE 1 / STRAIN 17)	147.699	1673.1710		П				
PIECE HISTORY	I ARCE TECHNOLOGICAL	HERDES SUNDLEX VIALUS (TYPE 6 / STRAIN GS)	103-134	238.362	119-195	963.093 1081	1008-1181 1661-1688	1884-1911		
П	Ī		226-256	\$64-50)	1305-1333					
Ι.	IT PROTEIN	MERPESVIRLIS SAIMERI (STRAIN II)	134-407	-	337.814	900-000	440-1017	1467-1467	2102-2135	
ŀ		Thath Duniasi	20.00	1579-1609				1	1	
1			3						1	Ī
ŀ		AVIAN MUSCULOAPONEUROTIC FIBROSARCONIA VIRUS AS42	20.20					1	1	Ī
PTOPI SPVICA	DNA TOPOISONEILASE I	SHOPE FIBROALA VIRUS (STRAIN KASZA)	2	97.79					†	Ī
PTOP1 VACCV		VACCINIA VIRUS					+	\downarrow	1	
PTOPI VARV	DNA TOPOISONERASE I	VANOLA VIUIS							\dagger	1
HOM ASTAB		AFRICAN SWINE FRVER VIRUS (ISOLATE MALAW) LIL. (91)	27.70						\dagger	
TYSY HSVAT		PEACES VICES A LELES				1				Ī
PTYSY HSVSA	THE STATE STATES	PERCENSION SALMAN (STRAIN 11)		111.140	43.449	1			1	Ī
Varia EBV	VIJUON PROTEIN BORD	CONTRACTOR EVANOR (1996)	1770						T	
NOOP ISA	VINCE MOTERNICA		40.647						t	
	CONTRACTOR AND TROP	GENERAL SANCTION III	2	302.338	168-402	-			T	
MED HOWA	HYPOTHETICAL PROTEDY LEG	HERAN CYTOREGALDYRUS (STRAIN AD169)	Ī							
JUL 11 15V	HYPOTHETICAL PROTEIN BBLF!	EPSTEEN-BARK VIRUS (STRAIN BY) 1)	13:43						1	
PULL HOWA	INPOTIETICAL PROTEDI ULII	HIDALN CYTOLEGALOVIAUS (STRAIN AD169)	20.52						†	
PULLIA HISVER	HYPOTHETICAL GENE 46 PROTEDY	EQUING HEADESVIAUS TYPE I (STRAIN ABAP)	2				-		1	1
7.12 VZVD	INPOTIETICAL CENE 46 PROTEIN	VANICELLA-ZOSTER YTHUS (STRAIN DURIAS)	2						+	
PLEIS HONYA	HYPOTHETICAL PROTEDI UL 16	HUMAN CYTOMEGALOVIRUS (STRAM AD169)	=						†	Ī
PULN HOPA	HYPOTH PRO ULZO PRECURSOR	HIDAAN CYTOMECALOVIRUS (STRAIN AD149)	=				+		1	
FULLI HEVED	GENE 40 PROTEIN	EQUING HEAPESYTHUS TYPE I (STRAIN ABAP)	-						1	
מעצע וניחה	CENTE 18 PROTEIN	AVIOCETTY-ROSIEV ARAS (STRAIN DURIAS)	9			1		1	\dagger	Ī
PULIS HSVSA	VIDLON GENE IN PROTEIN	HEAVESVERIS SABATU (STRAIN II)	1		20.58	1			\dagger	
MILLI HOWA		HIDAAH CYTONEGALOVINUS (STRAIN AD169)	-	*					1	
PULJE HSVES	MAJOR ENVELOPE CLYCOPROTEIN 100	EQUAR HELVESVAUS TYPE I				1			\dagger	Ī
וואסו זכווי	VIDION PROTEDY UL) 4	HEAPES SOUTEX VINUS (TYPE 1/5TRAIN 17)								Ī
PULLY HEVSA	GDG 47 PROTEIN	DELITE VICTOR SADER (STRAIN II)							t	Ī
22 42 42	VIDION CENE 14 PLOTE IN	VACCELLA-COSTER VINOS (STRAIN DAMAS)								Ī
ML19 HOWA	INTOTICE PROTED ULS	HUMAN CYTOMECALUVINUS (STRAIM ADTON)	317-784						1	

107117814				AMEA S		1				
	AR VERRILL			Τ-	Г					
	CENTRE CACHEST VALUE (TYPE 1/ STRAIN 13)		1017							
	TELESTICAL LANGIN TYPE I (STILA IN ABAP)	٦		1						
	EQUIPMENT STATES AND A 111	Т		776	1001				•	
	HOLDESVILLS AND AND AND DAMASS	Т	T	Т						1
	VARCELLA-LUSTEA VARCE (19 AND MAKAS)	200.5		T						
	VAUCILA-COSTER VENEZIONI STATEMENT S	_								•
	MEDIC SOULE VILLE IN THE STATE OF THE STATE		٦	7	-	İ	:::	i	: i_	
CELLE 15 LANGE AND PROTECT	VALCELLA-ZOSTEL VIAVO PORALITA		648-485	161-740						L
	INTEREST CYTOMEGALOVINUS (STRAIM ADTEN)	111.111			4					L
PROTEIN ULA	LIEBBER GLADLEY VIRILE (TYPE 1/ STRAIM 17)									
VILLON PROTECT U.A.	THE LOST THE ACTUAL PRINCIPLY STRAIN !					L				
	=	180		T						
A DE AL PAIN TO ANS. THOUSE IN	_									
	PRINCIPLE CALOVINUS (STRAIN ADIEN)	Г	707-1111		1		::::	i	:	•
PROJEIN ULA	т	ī	ets.ta							1
1	т	I				L				
ISNA REPLEATION MOTEIN ULS	COUNTY TO LEAVE A PARTY OF THE	100								
THE PROPERTY OF THE PROPERTY	NEAPESVILLS SAMEN DINAR 11)	301-337					ļ		L	L
THE PERSON AND VALUE	VANCELLA-20STER YIRUS (STITAIN DUMAN)	74.101							ļ	L
PROB DWA NEP CAPAS o PROTECT	LESTAN PATOLEGALOVINIS (STRAIN ADIM)									1
HYPOTHETICAL PROTEIN ULS?	THE TAXABLE PARTY (STRAIN ADIO)					L				1
τ	PRINCIPLE COLOR CO	5.73								
Т	HABAN CYTOMEGALOVIEWS 13 I MAIN MAIN	7.5							-	L
PLETS HOW IN THE THE PROPERTY OF THE PARTY O	THE PROVIDE EXPENSION (STRAIN !!)	# 1×								ļ
HYPOTHETICAL CENTS 30 PRUIDES	CALLES CONTRACTOR STRANGE (STRANGA AD169)									1
THE TAX TO THE PROTECT OF 12	MUNICAL LA LANGE COMPANIA COMP	409-436						L		
Ī	EPSTEDLEADE VINUS (STRAIN BY THE STREET STREET STREET	375-363	129.768					1		L
ALCOHOL: SECTION AS	HEADER SINGLES VIRUS (TVPE 6/ STRAM CONTROL	165.450								ļ
HYPOTHELICAL PROJECT AND	LEADER VIEWS SAMON (STRADY !!)	771 671	701 071		L					1
HAPOTHETICAL GENE 24 PROTEIN	CONTRACTOR TABLET AND ROLLIN	100					L	_		
HAVAOTHETICAL PROTEIN BOLF4	EVSTEAMOND VENCE (STORY AND ALL	97-122								
Ī	INCHES VIRUS SADODU (STRAIM 19)	18-38	114-311			1				L
٦	THE LAN EYTONGOAL OWRUS (STRAIN ADIM)									1
	HUBALAN EYTOMEGALOVIRUS (STIVAIN AD 100)	ķ	717.00		L					1
	THE STATE OF WHITE CAST AND UCANDA-1102)						L			
INTOTABLICAL PROTEIN UR	POLICE SUPPLIES VANCOUS ACTOR AND ADDRESS	7	447			1			L	_
THE PARTY OF THE P	HOMAN CTTCMC. LALLO IN CO. L. C. C. C. C. C. C. C. C. C. C. C. C. C.	10:00								L
T	HELLAN CYTOLEGALOVILLE IS INCHED IN THE PARTY AND INCH	251.08	L							ļ
PLES HOW MYTOURS AND A SECOND	HARLAN CYTOMOGALOVINIS (STRAIN ADIM)	791.20				_				1
Г	CENTRAL SAN MARIE (SERVIN)				ļ	-	-	-		-
Γ	PENCES VALVE SETTING SETTING AND A TOTAL	11.113			1	+	-	L	Ļ	_
T	SHOPE FORCEA VINCE (STANDARD)	11311	2 2					1	-	-
THE PERSON AND ADDRESS OF A REST	VACCINITA VINUS (STRAIN COPERMANER)		138-136	_						ļ
PUND VACOE LIBRARATION OF THE	VAPERIOLA VINUS (STRAAN WR)				L					1
	Overve A Visits				L	L			-	4
Ī	CONTRACTOR DATE (STRAIN AD169)	į			-	-	-	L		_
THE LIVEN HAMOTHETICAL PROTECNINGS	MANAGE STATES OF STATES AND A PAINT	327-306					-	-	L	-
Ī	HOMAN CTIONEDALD VANCO (STREET, STATE)	1181-318						-		L
٦	HIBAAN CYTOMEGALOVINIS (STRAIN ADITY)	,		L				4		+
٨	ASSICAN SWINE PEVER VIALIS (STRAIN LISSY)					L				4
VIN ABLA TUS 121-1 PROTEIN	CHARLES LANGUAGE CONTINUES (180LATE LEIDEN)	3			ļ		L	L		
	ALTALA MANAGEMENT (16.10.14 th a 1.14.1)	2.3				1		-		L
T	AS RECAM SWING FOR THE VALUE OF THE PARTY OF	77 55						1		
Ī	TOBACCO RATTLE VIRUS (STICALS IN THE	3	848-973	_					1	-
٦	ALTOGRAPHA CALIFORNICA NUCLEAR PALTITUMOSIS TONO			-	L					+
	TORAND EATTLE VINUS (STRAIN PSG)		1	100		L	_		-	+
	ASSAAN BEAN LANTH & WRUS	K		Т			-	L		4
Γ		25:52 20:00		٦	T	1		-	F	_
A PROTEDI	Brose Moses visco	349-376				1	1	1		l
	COWPEA OLICHOTTILE VIAUS		L	L				1		+
	CHICALDER MOSALC VINUS (STRADM FRY)		177		L	_			1	+
PVIA CAVEN LIA PROTECH	THE TAKE THAT WELL STRAIN (STRAIN C)	*		-	+	+	-			4
T	COCCUPATION VICTOR (STRAIN O)	123	_	\downarrow	$\frac{1}{1}$	+	\mid	Ļ	L	H
Ī	CULUMORAN MONOR VIOLENTIA	÷.	372-377	1	7	1		-		ŀ
1. Section	PEANUT STURT VIXUE (BLIMAIN)	7.1	171-290	176-403	837-634		1	+	+	\mid
TA TROUGH	TOWATO ASPERANT VIRUS	17	-	L	L			1	+	+
	ATHOGRAPHA CALEGRACA NUCLEAR POLYNEDROSIS VIAUS		-			L	_		-	1
WACK NEVAC 13 KD PROTEDN	THE PART OF PRINCIPLES VIETS	-		1	+	-	-	-	-	
Se & P.D. PROTED!	PLA CALL DATA THE CALL THE CAL	126-191			-	1	-	$\left\{ \right.$		

POCENE	107m17ftx4	AB Variet (no occurrence)	ABFAI	ARTA 2	AREA 3 1/	ARIA	3	000	٦		
TILE HAME	PROTEIN	VRUS	Г	Г						_	
VZHK TRVTC	29 KD PROTEIN	TOBACCO RATTLE VIRUS (STACHIN ICAN)	20.10			!	:	_			•
PV2A DEMV	2A PROTEIN	BROAD BEAM MOTILLY VIRIA	. SQ. 22.	: :	: :				+	- 1	١
PVZA COAV	2A PROTEIN	CONTEA CILIDADIA MOTOR STRANDING	192.419						-	1	ļ
PVZA CHIVEN	2A PROTEIN	CUCCHEEK MOSKIC VINOS (STORIN)	335-352	113.751				1	+	†	╡
PV2A PSVI	ZA PROTEIN	SOURCE ASSESSAY VIBUS	313-340	723-756					+	†	ŀ
PV2A TAV	SA PROTEIN	HIDMAN CYTOMEGALOWRUS (STRAIN EISENIARI))	184-221					+	t	+	-
PVJOK HCJAVE	SOLUTION EXAMENTED	TOBACCO BATTLE VIRUS (STRAIN TCAI)	130-160	;	!			;	-	_	
PV NOR THAT	STATE OF THE PROPERTY OF THE PA	IIIIMAN ADEMOVIRUS TYPE 41	15.42				Ì	+	1	\dagger	
LATE ADCS	STAN THOUSENED	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	75-102					1	\dagger	\dagger	
PAN AND	A John Tanana	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	3.30	2				1	+	T	
A PARTY	ST PROPERTY.	BROME MOSALC VIAUS	-38						\dagger	\dagger	
AND YOU	SA PROTEIN	CUCIAMER MOSAIC VALUS (STRAIN FNY)	111-152					T	+	Ť	1
2000	TA DECISE	CUCLAMBER MOSAIC VIRUS (STRAIN M)	217-252					Ť	+	-	!
W. C.	1 4 84 0 TEN	CUCLACRER MOSAIC VIRUS (STRAIN O)	111.11)					+	+	Ť	
200	14 PEOTEON	CUCUMBER MOSAIC VIRUS (STRAIN Y)	222-253					\dagger	t	T	
W 455	1A PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN HEACIN: 171.)	25:57							T	
NIVE VINE	NA PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN UNITUGE)	79.30					İ			
ave eve	12 PROTEIN	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	G.						-	İ	
ANGKE BADAS	SO KD PROTEIN	BANLEY YELLOW DWALF VIRUS (ISOLATE PAV)	2				T			İ	į
PAYIN BUTAN	SI KD PROTEIN	BEET WESTERN YELLOWS VIRUS (ISOLATE PL-1)	13:61							İ	İ
DALLE MANAGE	SI KD PROTED	BEET WESTERN YELLOWS VIRUS (ISOLATE GRI)						T			
174	K KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	124-131						 	İ	
200	A KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	134-155						t	Ť	١
AVE AND	SEED PROTEDA	BALLEY STRUPE MOSAIC VIRUS	128-155						t	T	
IN THE PROPERTY.	AA 1 KD PROTEIN	POTATO LEAFACIL VIRUS (STRAIN I)	10-140						Ť	Ì	İ
	Т	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	10-140						T	T	l
TANK VIVIE	Т	ALFALFA MOSAIC VIRUS (STRAIN 433 / ISOLATE LEIDEN)	10.0		91,110	200					
PVAGE VACEC	Т	VACCINIA VIÂUS (STRAIN COPENHAGEN)	137-218	2	207.700				Ì		
WASS VACCV	Г	VACCINIA VIRUS (STRAIN WR)	200	2 2		1					
PVACE VARV	PROTEDY A4	VARIOLA VIRUS	70. 70								
PVADE VACCE	PROTEIN AS	VACCINIA VIRUS (STRAIN COPENHAGEN)	30.00								
PVACE VARV	PROTEDIAS	VARIOLA VIRUS	30.00								
PVACS VARV	PROTEIN AS	VALUE VICES	219.283								
PVAIL VACCE	PROTECN A11	VACCINA VINOS (STAMP CONTINUEN)	230-234								1
PVAIL VARV	PROTEDI ALI	VACCULA VIXOS	440-467								
PVAIR VARV	54 KD ADORTIVE LATE PROTEIN	VACCEDIA VIBILIA PER ANI COPENHACEN	19	130-157		L					١
VAN VACC	٦	UABING A VIBILE	19-8	330-357						1	
7VA20 VARV	٦	VACTINIA VILIS (STRAIN COPENHAGEN)	45-73						1		
AAL VACE	PROJECT ALS	VARIOLA VIRUS	26-83								
	PROTEIN A31	VACCIPILA VIRUS (STEAD) COPENHAGEN)	95-144			1			Ť		١
VAN VARV	Т	VALIOLA VIRUS	3-16			\downarrow	1		1		١
PVA28 VACCV	T	VACCINIA VIDUS (STRAIN WR.)	A							Ī	
PVAZE VARV	PROTEDY A28	VALUELA VIRUS	A			1			T	Ī	
PVANG VACCV	PROTEDI A30	VACCINIA VIRUS (STRAIN WR)			\downarrow	\downarrow	1		T		
PVAJI VACCC	PROTEIN A31	VACCDIA VIAUS (STRAIN COPENHAUEN)			\downarrow	1	1				
PVAUL VARV	PROTEDI AJI	VARIOLA VIRUS		1	1	1	1		T		
PVAJA VACCC	PROTEIN A34	VACCINIA VIXUS (STRAIN COPENHAGEN)			\downarrow	1	-				
PVAJA VAČEV	PROTEIN AJ4	VACCORIA VIRUS (STRAIN WR)		1	1	1	\downarrow		T		
PVAM VARV	PROTEDI A34	VARIOLA VOLUS	1 2 2	\downarrow	\downarrow	1	\downarrow		T		
PVAJ4 VACCV	PROTEIN A34 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	61-671	\downarrow	\downarrow	\downarrow	1		Ī		Ì
WASH VARV	PROTEIN A36 PRECURSOR	VALULA VILUS	-				ļ				
PVAJI VAČEC	PROTEIN ASS	VACCINIA YINUN CUPERTANCEN	1	1	-		ļ				
PVAJS VACEV		VACCERIA YELDS (STEAMS WIN)	2		L	L					
WASE VARV		VACOUS VICTOR	17.71	155-102	-	L	-				
1	0. V (N) 24-0-0-0										

T.CLME		All Victoria (no una company)		- VIIV	9					
THE WANT		YIRUS		193-220			1	+	1	<u> </u>
VAN VACOV	62	VACCINIA VIRUS (STRAIN WR)	145-172						1	
		VACCINIA VIRUS (STRAIN COPENIIAGA:N)	21.5				-			+
		VACCINIA VIRUS (STRAIN WR)	146-173							+
VALUE VALUE		VALIDLA VIRUS	143.164						1	+
TO THE PARTY OF TH		VACCINGA VIRUS (STRAIN COPEMHAUEN)	14).[24	Ī					1	+
200		VACCINIA VIRUS (STRAIN WR)	71.57							٩
VI VO EVAN		VAUGLA VIIUS	16:19					!		:
PVAN VACOR		VACCINIA VIRUS (STRAIN COPEMIAGEN)	10:10						<u>!</u>	!
AND THE		VACCIMIA VIRUS (STRAIN WR)	100		i					-
		VALIDLA VIRUS	T	201.00	675.467					
TVA OVAT		VACCINIA VIRUS (STILAIN COPENHAGEN)	T	Т	697.567					
PVA35 VACC		VACCINIA VIGILS (STILAD) WR)	T	R.	200.66		+	-		-
WASS WACEV		REET CHRLY TOP VIRUS	47.72				+			-
TVAL! BCTV		FACCAVA LATENT VIRUS (STRAIN WEST KENYAN 144)	79-106					\mid		\mid
WALD CLVK		CASSAVA LATENT VIRUS (STRAIN INGERIAN)	79-106				1		-	+
אאם נדאא	AL3 PROTEIN	PONIA CHILL VIRUS	101-138				†	$\frac{1}{1}$		H
אאנו מכי	AL 3 PROTEIN	PANATO VELLOW LEAF CURL VIRUS						1	-	\vdash
IVAL) TALCV	ALI PROTEIN	CALIFIC OWER MOSAIC VIRUS (STRAIN CM-1941)		93.129			†		-	H
PVAT CAMPC	APHID TRANSMISSION PROTEIN	CACILLIA AWER LANGALE VIRUS (STRAIN DAI)					†			ł
PVAT CAMPO	APHED TRANSMISSION PROTEIN	CALL THE AWER LOCKLE VIRUS (STRAIN BBC)		2 2 2			†		1	ł
PVAT CAMPE	APIED TILANSMISSION PROTEIN	CALLE IN CALLE MOSAIC VIRUS (STRAIN NYSIS)	Į	21.0			+		+	\mid
PVAT CUMM	APPED TRANSMISSION PROTEIN	CALIFIED MOSAIC VIRUS (STRAIN PVIAT)	,	2			1	1	-	+
	APHED TRANSMISSION PROTEIN			93.130				\dagger	+	t
	AMED TRANSMISSION PROTEIN	THE PARTY WAS ALC VIETE STRAIN WISO	36-70					+	$\frac{1}{1}$	\dagger
ı	APPED TRANSMISSION PROTEIN	CAULIFLOWER MOSAN TANDS (3) TO THE STATE OF	102-138				1	1	+	+
VAT CERV	APHED TRANSMESSION PROTEIN	CARATION BICKED MIND VINUS	52-83	103-130					1	+
1	AHID TRANSMISSION PROTEIN	FIGURE MONEY VIANGE (SERVICE)	104-135					1		+
1	PROTEIN B3	VACCIDIA VILLA (STINAIN WA)	93.133	112:211	206-313	324-361			1	1
PVPAN VACOR	PROTEIN	VACCINIA VIRUS (3) INJIN COFERINACES	23.123	112-211	286-313	134-361		-	1	†
VACCV	PADITEN B4	VACCINIA VILUS (STIVAIN W.K.)	189-127	187-31	206-313	124.361	L		1	+
VALVE VALVE	PLOTEIN B4	VALIOLA VIRUS	254-284						1	1
VACO VACO	PLACUE SIZE / HOST PANCE PRO PREC	VACCINIA VILUS (STRAIM LLISMO)	234-214			L			-	1
PVRM VACOC	PLAQUE SIZE / HOST RANGE PRO PREC	VACCINIA VIRUS (318AM COTEMBACE)	234.284						1	†
PVBOS VACCL	MAQUE SIZE / HOST RANCE PRO PREC	VACCINIA VICOS (3 INVITA LIST LA)	354-284					1		\dagger
PVBOS VACEV	PLAQUE, SIZE / HOST PLANCE PRO PREC	VACCORIA VIRUS (STRAIN WR.)	28-62						1	+
PVBOY VACCV	PROTEIN BY PRECURSOR	VACCOUR VIXUS (STRAIN WA)	36.53					1	$\frac{1}{1}$	\dagger
PVNG VACCC	PROTEIN BS PRECURSOR	VACCINIA VIRUS (STICAL) CONTENTIALES	26-53		L				1	†
PVIDOR VACCV	PROTEIN BS PRECURSOR	VACCIMIA VIRUS (31 MAY WAY)	¥.12					1		\dagger
PVBII VACCC	PROTEINBIL	VACCING VINOS (STRAIN CO. C.	5.38	L						†
PVBII VACCY	PROTEIN BIL	VACUIND VINOS (31 MON WA)	13:140							+
ryais courx	IL. I BIND PRO PRECURSOR	COMPON VACO	258-285			Ц		1		1
PVBIS VACCC	PROTEIN B17	VACCATA VIEW (AVAILABLE)	151-215							1
PVRITY VACCV	PROTED [®] B13	VACCINIA VICES (STRAIN WA)	333.375	L	_			1		1
PVB19 VACCC	PROTEDUBIO	VACLING VALUE (1) A TO WE.	337.375					1	+	1
PVB18 VACCV	PROTEDUBLE	VACUAL VACUATION	337.338						1	1
PVB18 VARV	Profession	VALUE VALUE VALUE AND COPENNACEN	102:313					1		1
PVB19 VACCC	SURFACE ANTIGEN'S PRECURSOR	VACCINIA VINOS (STANIA COL ESCACIO)	160-210						1	†
PVRII VACCO	SURFACE ANTIGEN S PRECURSOR	VACUALA VIACO (STANINO)	180-210							1
VALUE VACCV	SURFACE ANTIGEN S PRECURSOR	VACCINIA VINUS (STANIA WA)	180-210							1
PVBIS VARV	SURFACE ANTIGEN & PRECURSOR	VARIOLA VIGUS	48-42	L					+	1
PVR20 VACCC	PROTECN B20	VACCINA VINUS (3) INAMA CONTINUACA)	2.0	L		L				1
Wall VACCV	PROTEIN B21	VACCING (STRAIN W.T.)	120-147	348.275		L				7
Will how	BL1 PROTEIN	BEAN COLDEN MOSAIC VIRUS	118.145							
AVE LINE	BL! PROTED!	CASSAVA LATENT VIRUS (SITAIN WEST RENTAN 1974)	13-14							
N. C.	BLI PROTECH	CASSAVA LATENT VIXUS (STRUM MICENAM)	130.147			L				
PVRI. I PYLOV	BLI PROTEDI	POTATO YELLOW MOSAL, VIRUS (ISOLATE VENEZUELA)	405.432	L		-				
VACOC	PROTEDICS	VACCINIA VIRUS (STRAIN CUPENHAVEN)	15:15	(F)07		L				
	DAUTED CO	VACCINIA VIRUS (STRAIN WIL)								ĺ

	4.00	All Vicence (so besteriophages)	П		Н	1 1 1 1 1	3 7 4 8 7	ABFA ABFA?	A 7 AREAB	VIIIV
2000	PECTE (1)	VIRUS	I	J.		_	7-	Т		_
7,000	PROTEIN CA	SHOPE FIBROMA VIRUS (STRAIN KASZA)	Ţ							L
ANN VACO	PROTENCA	VACCINIA VIALIS (STRAIN COPENHAGEN)	•							
2000	SECTION CA	VACCINIA VIRUS (STRAD) WR)	9	1						L
ANY ANA	PERMIT NA	VALOLA VRUS	1					-		-
PACOS COVEA	HAYOTHOTHEAL PROTEDY CS	SHOPE FIBROWA VIDUS (STRAIN KASZA)	1							
POPEL VAPOR	RECORDING.	VACCINIA VILUS (STIVADA COPENHAGEM)	?						-	١
PWON VACEV	PROTEBYCS	VACCINIA VIRUS (STRAIN WR)	S S						-	1
PVCDS VALIV	PROTEINCS	VARIOLA VIRUS	8					!	-	<u> </u>
PVCS/ VACEV	PROTEINCT	VACCINIA VIRLIS (STRAIN WR)								L
PACES VALV	PROTEIN C7	VAUGLA VIRUS			, 55	01.5.10	100	107761		
PWDS VACOE	PROTEINCY	VACCINIA VIKUS (STILADI COPENHAGEN)	1		27:47		310.333	104.763		L
PWOS VACOV	PROTEINCS	VACCOUN VIRUS (STRAIN WR)	Т	2						ļ
PVC16 VACTO	PROTEIN C10	VACCINIA VIILUS (STRAIN COPENHAGEN)	136-180						<u> </u> 	ļ
PVPIO VACTO	PROTEDUCIO	VACCINIA VIRUS (STRAIN WR)	36.		:		:	<u>.</u>	:	_
PVC16 VARV	PROTEIN CLO		136-163							1
PUCIT COVE	PROTEIN C13	SHOPE FIREOMA VIRUS (STRAIN KASZA)	3.30	39-66	27.12	200-740				1
7476	PROTEIN C17/823	VACCINIA VIRUS (STRAIN COPENHACEN)	22							1
A COLUMN	PROTEIN CIVILIA	VACCINIA VIRUS (STRAIN COPENHAGEN)	40-74							-
PUCIO SEVICA	PROTEIN C19	SHOPE FIBROMA VIRUS (STRAIN KASZA)	56-97						<u> </u>	i
PACTO VACO	PAOTEIN CYORIS	VACCINIA VIRUS (STRAIN COPENIACIEN)	72.99							-
Valva White	NECTEDA PROMIS MOMOLOG	VARIOLA VIRUS	299-326							4
DOLLAR PROPERTY.	MANOR PAREN PROTEIN	EPSTEIN-BAUR VIRUS (STRAIN B95-8)	847-874							+
SUCA BENEFIT	MAKE CAPSID PROTEIN	HEAPES SINGLEX VIRUS (TYPE 6/ STRAIN UGANDA-1102)	136-170	355.382					1	1
AND DEVE	SALION CAPSID PROTEIN	HERPESVIRUS SAIMIRI (STRAIN !!)	169-199							1
Jenes Book	DNA-ROUDAG PROTEDA	AUTOCRAPHA CALIFORNICA MUCLEAR POLYMEDROSIS VIRUS	133-165	199-248					+	1
WOOD ADOUG	MINOR CORE PROTEIN	HUDGAN ADENOVIRUS TYPE 2	18-115						1	1
A PROPERTY AND A PROP	MONOR CORE PROTEIN	KINAAN ADENOVIRUS TYPE 5	87-114							1
PVDOS FOWP	92.6 KD PROTED ^N	FOWLPOX VIRUS (STRAIN FF.1)	6.3		2					1
PVD03 VACCC	PROTEIN DS	VACCINIA VIRUS (STRAIN COPENHAGEN)	240-267	3						1
PVD05 VACCV	PROTECH DS	VACCINGA VIRUS (STRAIN WR)	740-707						 	1
PVDOS VARV	PROTEIN DS	VARIOLA VIRUS	1							ļ
PVD09 VACCC	PROTEIN D9	VACCINIA VIRUS (STRAIN COPENHAGEN)	20.07							ļ
PVD09 VACCV	PROTEIN D9	VACCINIA VILUS (STRAIN WR.)	971.65						-	
PVDOS VARV	PROTEIN D9	VAROLA VILUS	18.53							
PVD10 SFVKA	PROTEIN DIO	SHUTE PERCENT TO (31 MAIN MASES)	î						-	
WEB CEAV	DNA-BRODNG PROTEIN	CANALIAN BILLIAN TANA TIMOS	282-323							
PVEED VAILY	MOTEURE	VACTORIA VIBITE (STRAIN COPENHAGEN)	89-116	437-464	L	L				
TAKE WALLE	TAULTON CO	VACCINGA VIBLIS (STRAIN WR)	39-116	437-464						4
PVEDS VACE	TAULUM EA	VARIOUA VIRIUS	11-68	367-394	437-464		Ц			4
TARIO VALLE	RI PROTEIN	HIDALN PAPEL COLON TYPE 18	60-87							\downarrow
PVEL PVZA	EI PROTEIN	HUMAN PAPILL OMAVIRUS TYPE 1A	7							\downarrow
PVE! MPV33	EI PROTEIN	HUNAN PAPELIDMAVIRUS TYPE 33	2				\downarrow			1
PVEI HOVJ9	BI PROTEIN	HUMAN PAPEL DMAVEUS TYPE 19	103-130	\downarrow		\downarrow	\downarrow			ļ
PVEJ HPV41	EI PROTEIN	HUMAN PARTICULATORS 177E.	À	\downarrow		\downarrow	\downarrow			
PVEL HPV42	EI PROTEIN	HUMAN PAPELOMAVIRUS TYPE 42				1			 -	-
PVEI HDV47	EI PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 47			1	-			<u> </u>	-
PVEI HOVS?	EI PROTEIN	MIDAN PARLLOMAVIRUS TYPE 57								+
PVE24 NOVAC	EARLY 15.9 KD PROTEIN	AUTOCRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS				\downarrow				+
PVE2 CRVK	PROBABLE E2 PROTEIN	COTTONTALL BABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANNAS)				\downarrow	-			-
PVE2 HPV05	PROBABLE E2 PROTEIN	HIGALN PAPILIOMAVRUS TYPE S		191.71	1				-	+
PVE2 HPVI)	E1 PROTEDI	HUMAN PAPILLOMAVIRUS TYPE II			ļ	1	1			ļ
PVE3 HPV16	E2 PROTEIN	HUMAN PARLUMAVIRUS ITPE 10	97.10				ļ		<u> </u>	L
PVEZ HPV18	E2 PROTEIN	HUMAN PAPILLOMAVIRUS LITE II	201.00		1	1				ŀ
PVE2 HPVIA	E2 PROTEIN	HOMAN PAPELOMANUOS ITTE IA	100	\downarrow		1	-			ļ
PVE2 HDV2A	E2 PROTEIN	RUMAN PALLUMANIUS ITTE IA	11.		1	1	1	+		ļ
PVE3 IOV33	E2 MOTEIN	PROMAN PAPELCHAN VINCS 1 TPE 33								

10.00.00.00.00.00.00.00.00.00.00.00.00.0	E PROTEIN E PROTEIN	RUS TYPE 1	13.14 13.14	337-361 337-361 337-361	276-303		╂╂╂╂	11111		
	Z	INUS TYPE 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		76.303	 	++++		<u> </u>	
27 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2		AIRUS TYPE 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		7(6.10)		+++			
		MRUS TYPE 1		37.361			+	$\frac{1}{1}$	11111	
	X X X W W X X X X X X X X X X X X X X X	JANUS TYPE 1 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		31.361			+	H		1
	X X M V X X X X X X X X X X X X X X X X	IRUS TYPE I		37-361 37-361		++++	_	+		
	X X W X X X X X X X X X X X X X X X X X			1974		+++	+		\prod	•
	<u> </u>			197:41		+	+		-	L
							+			
			2002-229 (61-10) (61-10) (61-10) (61-97) (61-9				+			
		VRUS TYPE I	11.103 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16 19.16			+	+			Ц
		VRUS TYPE I	00-93 19-16 13-17 101-17 101-10 10-00 11-41 11-41 11-41 11-41 11-41 11-41 11-41 11-41			+	-			
		VRUS TVPE I	202-103 61-97 202-329 202-329 30-00 10-00 11-41 11-41 11-41 11-41 11-41 11-41 11-41			+	+			Ц
		WING TYPE I	75-102 103-279 103-279 10-60 10-60 11-41 11-41 11-102 11-102			-	-			
		IRUS TYPE I	203-27 203-279 30-00 30-00 31-34 11-41 31-62 66-86 11-102			-	-			-;
1111111		IRUS TYPE I	20-11/2 20-00 20-00 27-14 27-103 21-103 19-140				+	<u> </u> 		
		IRUS TYPE I	30-46 31-46 31-46 31-46 31-46 31-46 31-46				+		Ц	4
		/RUS TYPE !	10.00 17.54 11.41 15.63 17.102 19.103			+	-	-	_	
_[,]		IRUS TYPE I	27.54 11.41 13.62 73.102 66.90 71.102		_	:	-	1		ļ
111111		IRUS TYPE I	11.41 35.62 75.102 50.96 71.102 119.146		-				1	1
111111		INUS TYPE I	35-63 75-102 69-96 71-102 119-146					-	<u> </u>	!
	I PROTEIN	NOS INTE	75-102 60-96 71-102 119-146						+	+
			71-102 119-146					1	+	1
\prod			71-102			!		1	<u> </u>	<u> </u>
		HIGHAN PAPILLOMAVINUS TYPE 41	119-146				-		1	+
П		HUMAAN PAPILLOMAVINUS I TPE 41					+	1	1	+
T			75-102			1		1	+	<u> </u>
		MONTAL PARTICIPATION OF THE STATE OF THE STA	72.90			+	+	+	+	╀
PVEA HOVS! EA PROTEIN		HUBINAT PATELOMA THOSE AND THE BOOK TO THE	71.102			1	+	1		-
		ATHOCOLOGICA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	620-047		1	+	+		-	
	Т	THE ICHOPOLISMA IN CACAMOLOSIS VINUS			1	+		-		
٦	L	DHONI VIRUS (STRAIN INDIAN(1)(1)(4))						-		
PADA DIANI	THE VIEW BY WATER OF PROTECT	EQUINE ARTENTIS VIRUS								+
Ţ		THOGOTO VINUS	91	105.213						+
HAN CAPE PROTECTED	П	VACCINIA VINUS (STRAIN COPENHALLEN)	31.110	165-213				1	+	+
T			8				+	1	1	+
SUPER VACO	A MEMBRANE PRO PRECURSO	VACCINIA VINUS (STRAIN L-1 **)	3.40				+		+	\downarrow
Г	MENDIANE PRO PLECURSO		10.			+		-		\mid
Г		VACCINA VIETE (STRAIN COPENHAGEN)	374-331				+		-	H
		VACCINIA VIDUS (STRAIN L-1VP)	20.2				\dagger		-	-
		VARIOLA VIRUS								-
PYFII VARV MOTERAFII	N. D.	VACCINTA VIDUS (STRAIN COPENHAGEN)			184.581			-		
PVF11 VACE	71,213	VACCORA VIRUS (STRADA L-IVP)		302.236	Т		T			-
T	7.00	VALIDLA VIRUS	3	152.179	Т					$\frac{1}{1}$
PVF11 VARV	MEIG	VACCORA VIRUS (STRAIN COPENHAGEN)	3	152.179						+
Ţ	914.00	VACCINIA VIRUS (STRAIN L-IVP)	12	149-170						+
T	27.614	VANOLA VIBUS	144-13							+
Т	200	FOWLPOX VRUS	20.50						-	+
PACTIC CHESTS 10 KD F	IS KD FUSION PROTEIN	ORF VIRUS (STIMM PAZZ)	25						1	+
T	4 KD FUSION PROTEIN	VACCINIA VINUS (STRAIN COFFERNACES)	13.62				1	1	1	+
Γ	KD FUSION PROTEIN	VACCINIA VIKUS (STRAIN WA)	225-252	301-335			1		1	+
П	ואַ פו	VACCING VINIS (STACK WR)	161-191	240-374	1		+	+	1	ł
Н	ENG!	VARIORA VIRUS	23,23	Š	\prod		1			+
	PROTEING	VACCEDEA VIBUS (STRAIN WR)			-		1		-	-
	A.B. TSC DEF PROTEIN	VARIOR A VIRUS	86-123		1		1			

PCGENE	107117814	All Viruses (as becertaphages)	П	т	17					
FILE MANIE	PROTEIN	VINIE	\Box	7	S TOWN	TO TOTAL	A810 . CARO	Torres	- dua	O BELOT
PVCO) HSVED	GENE 3 PROTEIN	EQUINE HEAPESVIAUS TYPE I (STRAIN ABAP)	16-176	-	- - 		:	:	:	:
PVQ03_IISVEK	GENE 3 PROTEIN	EQUING HEAPESVIAUS TYPE I (STRAIN KENTUCKY A)	١	7	✝			1		
PVG65 VACCC	PROTEIN GS	VACCINIA VIRUS (STRAIN COPENHAGEN)	T	Т	1	335-386			ŀ	
PVOOS VARV	PROTEIN GS	VARIOLA VIRUS	T	101-17		137-764	1	-		Ī
PVGOT HEVII	HYPOTH GENE 7 MEMB PRO	ICTALURED MERPES VIRUS I			1	+	1			
PVCOP VACCC	PROTEIN FI	VACCINIA VIRUS (STRAIN COPEMIAGEN)	301.338	Ì	<u> </u>		:		_	
PVOOP VACEV	PROTEINFI	VACCINIA VIRIIS (STRAIN WR)	10.17					-		
PYCO VAIV	PROTEINFI	VARIOLA VIRUS		T	1	T				
PVG13 SPVIA	GENE 13 PROTEIN	SPROPLASMA VIRUS SEVI-MAZ B		1				ļ		
PVGIT HEVII	HYPOTHETICAL GENE 17 PROTEIN	ICTALUMD PENESVIKUS I	30.77	1		+		1		
PVG18 HGVI1	HYPOTHETICAL GENE 18 PROTEIN	ICTAL CAUD PERUPS VIRUS 1		1	†	+				
PVOI SPVIR	CAPSID PROTEIN	SPIROPLASMA VIRUS SPVI-RIAZ B	1		1	1			-	i
PVGI SPV4	CAPSID PROTEIN	SPIROPLASMA VIRUS 4	1	T	Ť					
PVG11 HSVII	HYPOTHETICAL GENE 22 PROTEIN	ICTALUMO HEAPES VIRUS I	R	781-077	200	***	1	1	-	
PVG24 HSVII	HYPOTHETICAL GENE 24 PROTEIN	ICTALUNIO WEAPESVILUS I	T				$\frac{1}{1}$	1		
PVGZB HSVII	HYPOTHETICAL CENE 28 PROTEIN	ICTALUALD HEAPES VIRUS I	8	825-760	1		1	1	\downarrow	
PVGIR ALCEPY	HYPOTHETICAL GIR PROTEIN	AMSACTA MOOREI ENTOMOPOXVIRUS	Т				+	1		
PVG3 SPVIR	GENE 2 PROTEIN	SPIROPLASMA VIRUS SPVI-RIAZ B	٦	┪						
PVQ SPV4	GENE 2 PROTEIN	SHROPLASMA VIRUS 4	٦	25.20	262.310		1			
PVG34 HSV31	HYPOTHETICAL GENE 34 PROTEIN	ICTALUND HENDESVIRUS I	95-122					1		
PVC37 HSVII	HYPOTHETICAL GENE 37 PROTEIN	ICTALUND HEAPESVIXUS I	442-460							
PVG39 HSVII	HYPOTIGHTICAL GENE 39 PROTEIN	ICTALURUD HEAPESVIRUS I	870-159	1088-1115						
VOTAL ANTERV	HAPOTHETICAL GIL PROTEIN	AMSACTA MOORE! ENTOMOPOXVIRUS	1.29							
BIAGI EDAG	CENT 1 PROTEIN	SPIROPLASMA VIRIUS SPVI-RSA2 B	15-49							
1000 CO/Ve	CENTINENTEN	SPILOPLASMA VIXIUS 4	18-52	87.78		-				
ALVALO TRUET	LAVADARACTICAL ACTUAL ACTUAL	HERPESVIRITS SAIMUR (STRAIN !!)	138-165	Ī		_				
1500	MINISTER MAIOR CLYCOPROTEIN	ICTALLINID HEAPESVIRUS I	L	146-373	107.034	913-1007				
PACAS HRWA	HYPOTHETICAL GENE 48 PROTEIN	HENDESVAUS SALIMIN (STRAIN !!)	360-394							
PVG-ALGENY	OAR PROTEIN	ADASACTA MODREI ENTOMOPOXVIRUS	4-31							
PVQ4 SPVIR	75	SPIROPLASMA VIRUS SPVI-REAZ B	9			-	1			
PVOSI HSVII	HYPOTH OENE SI MEMORANE PROTEIN	ICTALUND HEAVESVAUS I	٦	<u> </u>	1			1		
PYCH HEVY	HYPOTHETICAL GENE 32 PROTEIN	HERPESVRUS SADKIN (STRAIN !!)	47-74		1					
PVOSE HSVII	HYPOTHETICAL GENE 36 PROTEIN	ICTALUND HENDESVIAUS 1	382-609	1	1	+		+		
PVOS SPVIR	CENTE 5 PROTEIN	SPROPLASMA VIXILIS SPVI-RIAZ B	26.0	1	1	-	1	+	_	
PVQ3 SPV4	GENE 5 PROTEIN	SAROPLASAA VOLUS 4	2000		1	\dagger		+		
PVOED HEVEL	HYPOTHETICAL GENE 6) PROTEIN	ICTALUMB PRICES VICES I	2000		1	1	1			
PVCAN HSVII	HYPOTHETICAL CENE 64 PROTEIN	ICTALUND HERPESYTAUS I	,			+	+	+	1	
PVG63 HSVII	HYPOTHESICAL GENER 65 PROTEIN	KTALUAID MEMBESVIKUS I	× 2				$\frac{1}{1}$			
PVC46 HSVII	HYPOTHETICAL CENE 66 PROTEIN	ICTALUMD PEAPESVIRUS I	On-zer				+		-	
PVG67 HSVII	HYPOTHETICAL GENES 67 PROTEIN	ICTALURID REPRESVIAUS I	1000			1		-	1	
WCM HSWI	HYPOTHE INCAL GENE OF PROJECT	ICIALUM MACENTANA		Ī	Ī			 	\downarrow	
PVG72 HSWII	HYPOTHETICAL GENE 72 PROTEIN	W. CALUMID RESPECTABLE		Ī	T	$\frac{1}{2}$				
PVG75 HSVI	HYPOTHETRAL GENE 12 TROTEIN	Increase the property of the second s	700-227	T						
TWO!	MITCHEST AND ACTOR	CONTROL A CALLA VIETE A	3					-	L	
	Et benteld	AVAN INFECTIOUS BROWCHITS VIRUS	8	2404-2435		ŀ			L	
	ES OF VOYAGE PERSON	BOVDGE CORONA VIRUS (STRAIN F15)		642.676	1022-1064 1278-1305	1278-1305	ļ		L	
	E) CI VONECTIEN PRECINCOL	BOVINE CORDINAVILLS (STRAIN L9)	Τ		1022-1084 1278-1309	1378-1305	-			
A 100	IE3 CE VOOPROTEDI PRECIDIOR	BOVING CORONAVILUS (STRAIN LY-138)	355-426	642-676	1022-1084 1278-1305	1278-1305	-			
AND CAME	E2 GLYCOPROTEIN PRECURSOR	BOVING CONCONAVILUS (STRAIN MEBUS)	399-426	642-676	1022-1084 1278-1305	1278-1305				
PVGL 2 CVBO	E2 GLYCOPROTEDI PRECURSOR	BOVINE CORONAVILUS (STRAIN QUEBEC)	199-426	642-676		1378-1305	Н	Н	Ц	
VOL 2 CVIIV	E2 GLYCOPROTEIN PLECURSOR	BOVING CORONAVIRUS (STRAIN VACCINE)	199-426	969-209	1022-1084	50(1-142)	L			
PVIR J CVIDS	E2 GLYCOPROTEIN PRECUISOR	HUMAN CORONA VIRUS (STRAIN 229E)	770-767	609-675	1056-1112					
PVG1 CVM	E3 GLYCOPROTEIN PRECURSOR	MUNDE CORONAVILUS MAY (STRAIN WILD TYPE 4)	z				Ŀ	H		
PVCL2 CYMAS	E2 OLYCOPROTEIN PRECURSOR	MUNIDAE CORONAVIRUS NOV (STRAIN AS9)		501-632	978-1040		1	1		
PVGE3 CVNUC	E2 CLYCOPIOTED PRECURSOR	MARING COROMAVIRUS MAY (STRAIN MARY / VARIANT CL.2)	- [1030-109Z	1	+	+	+	\downarrow	
PVCL2 CYMUH	E2 GLYCOPROTEIN PRECURSOR	MURLINE CORONAVIRUS MIFV (STRAIN FRM)	502-543	2		4	1	-		

	/	All Viruse (se berierbehalm)	AREAL	ř	AHEAL	1	3	1	9		
CGENE		AND THE PRINTER CONTONING (STRAIN FS112	Г	Н	5	133.1369					\downarrow
CHANGE COME	PROTEIN PRECURSOR	PORCINE TRANSMISSIBLE GASTROEM EALLS CORONAVILLE (STRAIN MILLES	Γ	F	069-1145	1353-1369				1	
		PORCING TRANSMISSIBLE GASTROEMTERLIS CONCAS VIRUS (STRAIN PURA)	Г	166-009	1067-1147 1351-1387	351-1387					1
TANK CANADA		PORCINE TRANSMISSIBLE GASTROEMTER IIS CORDINA VIKIS (STRAIN PURD) 69-107	Γ	Г	1067-1143	131-1311					Ï
TANKE OF THE		PORCINE TRANSMISSING CASTACENTIANIES CONC. BRITISH ISOLAT 46		1 126-508	1179-1165						-
VOL 5 CYPES		PORCINE RESPIRATORY CONCORATIONS (STRAIN RAM)		Π					1		ŀ
VCE 2 CVPEM		PORCONE RESPIRATORY COMMANDER THE CONOMAVIRUS (STRAIN NED 7 64-107		166-099	1007-143					1	1
Vota 2 Cymes		POSCING TRANSPOSICION CONTRACTOR	102		┪				1	-	· -
VALLS ENV	ROTEIN	EPSTEDLEALE VOICE (STRAIN DOZIN)		Ë	_	1073-1141	3				_
Adia S Pon	ES OL YCOPROTEIN PRECURSOR		Π	=	1027-1071		_		1		<u> </u>
WOLS DW	113 GLYCOPROTEIN PRECURSOR		200-03	173.902	1056-1000					1	+
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ES AL VEOPROTEIN PRECURSOR	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	109-836 87	Г	1001-1001						1
TOTAL DE LANGE	ES CU VACABOTED MECURSOR		T	175-902	056-1090					4	1
	ES CE VOOPBOTEDA PRECURSOR.		Т	Ē	056-1090					4	<u> </u>
100	CO CO SCORE STEP PRECINGOR	IRUS (STRAIN MAI)	Т	t	•		L				4
	C. Consocreted Carto Paricin SOR		Т	Ţ	440-467	151.470	L				
WOLD EBY	CLTCOTAGE TO THE PERSON		T	Т	T	813.839		L	L		
VCLB HOAVA	G. YCOPKUTEIN B PACCOMOUN		Т	Т	Т				L		
PVGLB HOW	CLYCOPILOTEIN B PRELUACION		¥77.7	1			ļ	-		-	L
PVCLD HSVBI	GLYCOPROTEIN I PRECUISOR		٦	1			\downarrow	1	ļ		L
	GLYCOPROTEIN B-1 PRECURSOR	(V)	_	100-50			1	1	-	-	
PVCLA MSVEI	GLYCOPADTED B PRECUISOR		486-513 6	616-643			\downarrow	1	+	-	L
L	GLYCOPROTEIN IN PRECURSOR	EXPLINE PROPERTY VALUE (ACT A TEL ART)	413.470	434-961			1	1		1	-
	GLYCOPROTEIN B PRECURSOR		443-470 9	196766				-	\downarrow	\downarrow	+
	CH VCOPEDITIN B PRECUASOR		Т	933-960						+	+
	CL VCOPROTEIN B PRECURSOR		Т	352.379			Ц		1	-	+
	TO: VICTORIOTEIN IN PRECURSOR		L	441-479		L				_	+
1	CONTROL DESCRIPTION		Т							-	-
۰	C. LOCKED TENT DESCRIPTION		017 077					L			-
- 1	CLICATOLEIN CINESCONO	8	2				-				
PVGLC MSVIK	GLICOTOLEIN CINECOS						-			Ц	
- 1	C. T. Constant Cav.		100.130	T				L	Ц		4
ı	C3 VCOREGIFIER GPV		111.148			L			4	4	1
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	C VONDENTEN & PRECURSOR		T	134-201	16-243	442-409	416-531			-	1
4 1 20 00	FINITION OF YCOPROTEDY PRECURSOR		T	24.20	216.243	773	411-333			4	+
1	THE WOOD VOODS OF THE CLASOR	UMUEN)	T	\$4.702	216-243	444471	486.533				$\frac{1}{1}$
Water Bassie	ELECTRICAL OF VACABLE PRECURSOR		1	140.167				L	H		-
A PROPERTY OF	HIGH OF VOOROTEIN PRECURSOR	100000	T	16,301	442.472	486-515	-			Ц	$\frac{1}{2}$
אפר פאס	TOSTON OF TOTAL PARTIES OF	B/STIMIN 1837/)	T		100	411-511	-	-	-		
HESS.	TOSOTA OF TOTAL PRINCIPLE CONTRACTOR	T	T			1444	488.53		-	L	Н
VOL HOSV	TOSULA CANADA MANA PRECIDENT	A / STRAIN LONG)	T		1	462.43	T		H	_	Ц
E POR	POSICION CE LOCATION DE COMPANI	T	Ť				T	l	-	L	
WOLF HOSVIA	PUSION OL TOURNILLE PARCHASON		7			\downarrow	1	+	-	ŀ	\vdash
VOLUMENSE	FUSION OLI CONTROLLIN PARCHEON		2				1	-	-	L	\vdash
TYCH MEASI	POSICIA CLICOTROLLES Y MINISTRA	ATA-1)				1	-	-	-	L	H
No.	FUNCTION OF TOWNS IN THE PARTY BOTH TOWN		T			1		-	-	L	H
NG MON	1	IAJIA VACCINE)	T			\downarrow	1	1	-	-	\vdash
VOL. MONON	FUSION OF YOUR DISTRICT BY BOTH TO THE COR		T			1	+	+	-	-	-
NOT NOTION	PUSSON OF TOTAL PARTY IN TOTAL		Т			1	-	-	-	L	L
VCLF MUDDES	PUSICING OF TOWN PERCHASOR	NEWCASTLE DISEASE VILUS (STRAIN AUSTRALIA-VICTORIAA)				1	+	-	-		ŀ
VOL DOV	PUSICAL OF TOUR AND LESS THE STATE OF THE ST	NEWCASTLE DISBASE VIXUS (STIVAIN BEAUDETTE C/45)		10.00	\downarrow	1	1	-	-	-	-
NOT NOVE	PUNCH OF TOTAL OF THE PRECITE OF	NEWCASTLE DISEASE VIRUS (STRAIN HERO))		2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		1	+	+	-	-	L
NG VO	CONTROL OF VONEBOTERN PRECIDENCE	NEWCASTLE DISEASE VINUS (STRAIN BI-HITCHNEW47)		1	\downarrow	1	-		-		
VOL BONE	FUSION OF COMPANIES PRECINCOR	NEWCASTLE DISEASE VINUS (STRAIN IT ALENAS)		916	13.76.7	1	+	ŀ	-		H
VOL. NOV	PUSION OF TOWNSHIPS AND PRECINEDA	NEWCASTLE DISEASE VIRUS (STRAIN LAS/46)		4		1	+	ŀ	-	-	H
NOT TON	THE PRINT OF VICTOR OFFICE PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN MOYADERAS))			1	1	+	-		H	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	INTERNAL PROPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STTAIN QUEENSLANDON)		715-969	1	L	-	L	Н		+
7	STREET, OF VICTORITY PRECURSOR	NEWCASTLE DISEASE VIXUS (STRAIN TEXAS)			1	-	-	-	-		_
						_		_	-		

FILE NAME		A SE VALUATION AND INCOMPARISONS	•			7				
PVCI F NDVU		AN VINE OF STATE OF S		ABCAZ	AREAZ	AREA	AREA A	TAMES LAND	TVIEV 7	AREAs
	FUSION OLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIAUS (STAAIN ULSTERAS)	121-178	_			 	:	· •	
VOLT MIDOV	FUSION OLYCOPROTEIN PRECURSOR	PROCINE DISTEMPER VINUS	7	П	309-336		1		_	
PVG. PIEC	PUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAING LIENZA I VIRUS (STRAIN C19)	╗	╗			1	+		\prod
MOL PON	FUSION GLYCOPROTEIN PRECURSOR	HIDGAN PARADOLUENZA 2 VIRUS	٦	┑	238-766		1	1		I
IVGL! PERSO	FUSION GLYCOPROTEIN PRECURSOR	HEDICAN PARAMPLUENZA 2 VIRUS (STRAIN GREER)	T	Т	207-100			+		4
PVGLY PERH	FUSION OLYCOPROTEIN PRECURSOR	INDICAN PARADITUDICA 2 VIRUS (STRAIN TOSHIBA)	2	Т	997-162	276-763	1		-	•
PVGLT PUB	FUSION GLYCOPROTEIN PRECURSOR	BOVDG PALADOLUEICA JATRUS		207-241	457.403		Ì	1		
7GF 23	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PAKAIN LUGACA J VIACO (SI AAIN MIII 47813)	374.744	Т			\dagger			
YOU SENDY	FUSION GLYCOPROTEIN PRECUISOR	MADERTES VINUS (SINAIR KABELE U)	1	3			T			
707 EPO	FUSION GLYCOPROTEIN PRECUISOR	MINDEAPEST VIALE (STANDE)	97.	Т	180.503		l			
VOLY SENES	FUSION CLYCOPROTEDN PRECURSOR	SENDAL VILLE (STEAM 27 HOST MULANTS)	201	Τ	2 2		T	-	-	
TVGT EDGE	FUSION OF YCOPROTEIN PRECURSOR	SENDAL VILLE (STRAIN PUSHING)	133.140	Т	10, 01		\dagger		-	
NG PROPE	FUSION GLYCUPROTEIN PRELUCION	SENUAL VIEWS (STEWART DOWNS)	97.	Т	9					
	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIII. (3 I MAIR III V.)		Т					-	
PVGLF SENDZ	FUSION OLYCOPROTEIN PRECURSOR	SENDAL VICUS (STRAIM Z)		Т	707 037		\dagger	1	1	
PVCL SV4	FUSION OLYCOPROTEIN PRECURSOR	SBUAR VIXUS 41							-	
rval svs	FUSION GLYCOPHOTEIN PRECURSOR	SURLAN VICEO 3 (SIRVAN W.)	134.16	101-200	457.424		ŀ	-	L	
PVG. TRIV	FUSION OF TOOPROTEIN PRECURSOR	TOWARD FOUND TOWARD VISITE	531.557				T		-	
TVC DECY	NAME OF THE PARTY OF VIOLENTIED OF	POWER PERPEATORY SYNCYTIAL VIRIUS (STRAIN COPENHAGEN)	92.133							
TO STATE OF THE PARTY OF THE PA	MANNE GIBEACH OF VICTORIOTEIN O	HIDAAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 18537)	63.63							
TAN DE DA	MAIOR GIRFACE (IL VCOPROTEIN G	HIDAAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSDSSSS)	66-107							
PVGLO HRSVS	MAJOR SIRFACE OF YCOPROTEIN O	HIDAAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSB6190)	243-273							
PVCI O IOSVI	MAJOR SURFACE GLYCOPROTEDY G	HUMAN RESPONATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 240)	66-93							
PVCLO HSVEA	GLYCOPROTEIN G PRECURSOR	EQUINE HEAVESVIRUS TYPE 4	271-298							
PVCLO HSVEB	GLYCOPROTEIN O PRECURSOR	EQUINE HEAVESVIRUS TYPE I (STRAIN ABAP)	383-410				1		-	
WELD ENEW	SPIXE GLYCOPROTEIN PRECURSOR	RABIES VIRUS (STRAIN STREET)	489-519						1	
PVOLO VSVIO	SPICE OLYCOPROTEIN PRECURSOR	VESICULAR STORATITIS VIRUS (SEROTYPE INDIANA / STRAIN GLASGOW)	477.49				\dagger	1	1	
FVOLH EBV	GLYCOPROTEDI GP65 PRECURSOR	EPSTEN-BARK VINUS (STRAIN BYS.4)	2	019-048			1			
WOLK HOW	CL YCOPROTEIN H PRECUISOR	HUNGAR CYTCHOLOGIALUVIKUS (STRAIN AUTOWNE)	104.135	1						
TANKE IN THE PARK	OLICONARDIEM II PRECIENCE	HERES SILVE EX VIRIS TYPE 6 / STRAIN GS	63.69	360-403			T	-	-	
PUTE IL BEVEA	CHANGE HE HELLINGS	HERPESVINUS SAIMIN (STRAIN !!)	388-415					_		
WOLL HOWA	IE CLYCOPROTEIN PRECURSOR	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47.111							
PVOLV BUNGS	M POLYPROTEIN PRECURSOR	BUNYAVBUS GEAKISTON	912-546	914.941	\$\$21-9211				-	
PVOLM BUNE.	M POLYPROTEIN PRECUMSOR	BUNYAVBUS LA CROSSE (ISOLATE L'14)	913.950							
PYCEN BUNNA	IM POLYPROTEIN PRECURSOR	BUNY AMWEKA VIRUS	740.374	ŝ	25.700		1		+	
PVCLM DUGBV	M POLYPROTEDN PRECURSOR	DUGGE VINUS	276-68	916 107						
PYCIN HANTE	M POLYFROTEN PRECURSOR	HANTAAN VIKUS (STRAIN B-1)	2017	077-160					+	
THE PARTY OF THE P	M FOLTPROTEIN PACTORSON	HANTAAN VIII IS STRAIN LESS	75.102				T			
A STATE OF THE PARTY OF THE PAR	M COLLEGE PROCESSOR	HANTAAN VIDIS (STRAD) 76-113)	25:102				T			
ANU PLAN	M POL VPROTEIN PRECIESCOS	INPATIENS NECROTIC SPOT VIRUS	628-655	1011-6901					-	
AM IT FLAG	M HOL VPROTEIN PRECIDISOR	PROSPECT HILL VIXUS	8.8					-	_	
PVCL IN MIRBOR	M POLYPROTEDN PRECURSOR	PUDALLA VILUS (STRAIN HALLMAS BI)	72-110							
PYCLM PUBMS	Т	PUUMALA VIRUS (STRAIN SOTICANO)	72-110							
PVCLM SEOUS	Г	SECUL. VIRUS (STRAIN 80-39)	\$13.540	693-720						
PYGLM SEOUR	П	SEOUL VIRUS (STIAM R22)	73-100	313-540	694-731					
PVCLM SEOUS			 8	513-540	694-721			-		
PVGLM BEFV	NONSTRUCT GLYCOPRO GNS PRECURSOR	ľ	ž						-	
PVGLP BEV			2	145:179	1145-1179 1184-1211	1505-1532		1	4	
PVCLY JUNDA		CIUNDI ARENAVIRUS	7						$\frac{1}{1}$	Ī
PVGLY LASSO	GLYCOPROTEIN POLYPROTEIN PRECURSO	QLASSA VIRUS (STRAIN GA191)	199						-	
PVGLY MOPE	GLYCOPROTEIN POLYPROTEIN PRECURSO	DMOPELA VIRUS	9	316-346				1		
PVCLY PLARY		ASCIPICATION ALENAVIRUS	34.33	,,,			1	+	1	
PVGLY TACV		A SQ TACALDE VIXUS	6	115-130			1		$\frac{1}{1}$	
PVGLY TACVS	GLYCOPROTEIN POLYPROTEIN PRECURS	GTACARUBE VIRUS (3 FACIN V.)	107				1		$\frac{1}{1}$	

								Γ	_		
	7	All Virgins (no besteriophages)	ABEAL	AREA?	AREAL	AREA 4	AREAS	ARCAL	AREA?	TYNT	1414
NCCINE.	т			Г							
THAM.	DECLERATION OF THE PRESENCE OF			Ī							
PVCLY TACVI	т	/L 11590)		1	Ī						
WOLY TACYT		IN bG)			Ī						
PYCHOL CPSMV	Τ		3	Ī							
	PROBABLE MEMBERSON ANTINERS CONT.		Т		T						
	STRUCTURAL CLYCUPROJEIN PRECURSO	THE (STRAIN MUSOKE)	П	0							•
	STRUCTURAL CLYCOPROFELY PRELIMENT		┪	0100							
	STRUCTURAL CLYCOPICOI EIN PRELONSO	NIAGEN	20 20								
PVN65 VACCC			132-166								
PVIES VACCV			16.19	20.05							
PVINS VARV			30-160								
PVACE ISV	PROBABLE HELICASE		241-275								
WAYN THE	HOST RANGE PROTEIN	ENHAGEN)	241.235			L					
ALL ALL	ALCOHOL & ALCOHOLD TO A PERSON			401.00							
WISE VACEV	HUS I KANDE TRASICEAN	ENHAGEN)									
PVIBI VACC	PROTEIN II		8-117	133-180							
VIDI VARV	PROTECTION	EVETEATIN COPENHAGEN	160.190								
VIOS VACCC	PROTEIN IS		8199								
VACYV 199V	PROTEINU		160-190								
VAAV VAN	PROTEIN IS		200-317	\$48-575	163-633						
	MITATIVE BNA HELICASE IS	Christin	111	541.575	593-632	L		į			
AND AND	THE PAYMENT WAS UPS BOASE IN	(STRAIN WR)		267.575	617-103	L	L				
AND ANTE	CONTINUE NOW THE PARTY IN		1 6-447							L	
VIDE VARV	PUTATIVE MAN HELE ASS IS	AND THE PAYMANETIAL DATE IS (STRAIN SMITH)	192-192								L
VIE! MON	DOMEDIATE EARLY PROTEIN !	YHEDROSIS VIRUS	355-385							1	
VIES NOVOP	DOGEDIATE EAST Y PROTEDY IB-3		217-325	343-400							
TANA LINE	IN REG PROTEDNISAN		08-69			L	L				
	WEIGHT INTECTIVITY FACTOR	HIDLAN DAGGROOFFICENCY VIRUS TYPE I (NUMA I SULATE)									
VI RVING	A PART OF THE PROPERTY BACTOR	ISDAIAN DOADNODEFICIENCY VIRUS (ISOLATE AGM / CLUNE UN-1)									
VID SIVAI	VILLON DO ELLIVII I PALION	ECHING HELDESYTHUS TYPE I (STRAIN AB4P)									
VOO HEVER	PROB INTEGRAL MEMBRANE INC.	HERPESVIRITS SAIMER (STRAIN !!)	90.10						L		
VDO HSVSA	INTEGRAL MEMBRANE PROTEIN	GREWARING THE PARTICLE SSVI	2. 80				1				L
עסת צגעו	PROBABLE DITECRASE	SACTION OF INTERNATIONAL COPENSIAGEN	22.56						1	-	
VIDI VACCE	PROTEDNJI	THE COURT CASE AND CASE	22.56								
VIDI VACEV	PROTEIN JI	A CALL CALL CALL CALL CALL CALL CALL CA	23-56						\downarrow		
VIO. VARV	PROTEIN 11	VALUE A VINUS	331-383	L			_				
XX C	PROBABLE LI PROTECH	COTTONIAL KABBI (Serve) PARTICIONI	18-45	L							
M	PROBABLE LI PROTEIN	AVIAN PAPILICACAVIRUS PPV-L	14.101		L		_				
	PECCE AND RILL PROTEIN	HUMAN PAPALOMAVINUS TYPE 6						L			
	CANADA STATE OF THE STATE OF	HUMAN PAPELDMA VIRUS TYPE 18				-		L			
	PRUBABLE LI PROTECI	HAIMAN PAPALOMAVIBUS TYPE 33	9			1	1	1			L
VE PASS	PRUBABLE LI PROTESSI	HIBLAN PAPEL COLAVIDUS TYPE 41	2			1	\downarrow			-	L
W.I. HOVE	PROBABLE LI PROTESS	TURBLAND PAPELL CALAVIRUS TYPE SI	976					1			
VLI HPVSI	PROBABLE LI PROTEIN	THE SAME OF A VALUE TYPE SE	43.72			4				-	
W.I. HOVSI	PROBABLE LI PROTEIN	LINE AND PART COMAVEUS TYPE IA	407.445			1		1	\downarrow	-	ļ
VL2 HDVIA	PROBABLE L2 PROTEIN	LANAL BANK I PALAURING TVPR 41	3					1	}		1
W.2 HPV41	PROBABLE 1.2 PROTEIN	DOLLAR SANGE COMPANY OF BRIDE	130-357						$\frac{1}{1}$	\downarrow	1
VLJ REOVD	MONTH OF THE PROTEIN LANGEDA 3	ACCOUNTS AND AND AND	130-357								
VL) REDVI.	MONOR CORE PROTEIN LAMBOA 3	PECULIAR INSTANCED VIOLE	146-150	625-652							1
VLS6 DAVI	L96 PROTEDA		200.313						1		1
PVMI REDVI.	MONOR VIDION STRITCTURAL PROTEIN A		625-662								
OVOT BEOVO	MAJOR VIRION STRUC PROTEIN MIL-1/MIL-		19979			L	L	L			4
CACHE BANK	LANDA VIDION STRUC PROTEIN MU-1/MI	AGE REOVINUS (TYPE 37 STRAIN DEALING)		ļ		L	L	L	L		
	LA SOR WIRTH STRUC PROTECN MU-104			1	100	18715	-	-	-	Ŀ	_
AND THAN	ALCON MANCETE INTERNAL PROTEIN MOL						-	-	-	-	L
	TALLED OF COMMENTS OF THE PARTY		76-175	\downarrow	\downarrow		+	-	-	-	L
PWAS BESVA	MAINTA GLICATION AND	HIDLAN REPUBLICATIONY SYNCYTIAL VINUS (STRAIN A2)	5 2 2		1	1	\downarrow	1	+	-	
PWAZ HILSVA	Ť	BOVING RESPIRATORY SYNCYTIAL VIRUS (STRAIN AS1904)	2		1		1	\downarrow	-	-	L
PWAT BESVA	T	HIBAAN RESPECTORY SYNCYTIAL VIRUS (STRAIN A2)	200	1		1	+	-	-		Ļ
YACK TANK	T	DATLUDICA C VIRUS (STRAIN C/1/50)				1	1	1	L		
NAME OF	THE PROPERTY	NEWCASTLE DISBASE VIRUS (STRAIN AUSTRALIA-VICTORIA/)	77.77	1	1	\downarrow	1	1			
	Mary services	HUMAN PARAMPLUENZA 1 VIRUS (STRAIN TOSHBA)	2			$\left \cdot \right $	-				
PVMAT PIZHT	MAINATHUEST										

PCCENE	107s178s4	All Viraces (no hosterfoghages)	AREAI	AREAZ	AREAS	AREA	AREA S AR	AREA 4 AREA 2	AREA 8	AREA?
FILENAME	PROTEIN	POYANG PARATHELIENZA 3 VIRUS	201-231	T				_		
PVANT PUB	MAIRIX PROTEIN	MI BAAN PARADAT UENZA) VIRUS (STRAIN NIII 47885)	101-231							
100 TANA	MATRIX PROTEIN	SDARAN VINUS 41	133-153				+			
Many Com	MILLION CONTROL	DOVINE CORONAVIRUS (STRAIN NEBUS)	175-209	Ì		1	1			Ţ
PWGE CVTKE	EI GLYCOPROTEIN	TURKEY ENTERIC COROMAVIRUS	175.209		1	1	\dagger	-		1
PVACE 19V6	EI GLYCOPROTEIN	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN 642)	-			+	+			
PVACE EBVB	EI GLYCOPROTEIN	AVAN BRECTIOUS BRONCHITIS VIRUS (STRAIN REAUDI: 111:)		14.3	1	+	+			1
PVACE IBVIES	EI GLYCOPROTEIN	AVIAN DE EL TRUS BRUMENTOS VINOS (STRAIN DEALINGTE ANT.)					-			
PVACE! IBVK	EI OLYCOPROTEIN	AVIAN DECINOS SKUMETITIS VIKOS (STRAIN KIRSO)	34.46	19.18						
PWD CANC	MOVEMENT PROTEIN	CAUDIOWER MUSAR VIRUS (STRAIN CAPITAL)	2	;		:	:-	-		
PVAC CAMVO	MOVEMENT PROTEIN	CALL BY CORER MUSAN, VINUS (STRAIN DOL)	22.34	1			<u>:</u>			
PAG CAINE	MOVEMENT PROTEIN	CAUCH LUMER MOARL VIALS (STRAIN BOL)	3,0,0			-	\dagger			i
PWD CANN	MOVEMENT PROTEIN	CAULIFORER MOSALE VIALLS (STEAM PROFILE)	370.344	27.176		ļ		-		i
PYNO CUNVS	MOVEMENT PROTEIN	CALLIFICATES BUDALL VIAUS (STRAIN STRASDOUN)	200	20.116	Ī	-				
PVIO CUMM	MOVEMENT PROTEIN	CAULD LOWER MUSAAL VIRUS (STRAIN WAW)		601 001			<u>i</u>	! !	:	
PVIO CERV	MOVEMENT PROTEIN	CAUVATION ETUTED KING VIRUS				-	!	-	-	:
PMP SOON	MOVELENT PROTEIN	SOTECAL CILCROTT, PROTICE VINOS	30. 330			<u> </u>	-	╀	╀	
PYNCSA HEBNE	MAJOR SUIU ACE ANTIGEN PRECURSOR	REMON TREATMENT OF THE STATE OF	10.61	117.364		<u> </u>	<u> </u> -		:	-
PVACTI DHIVII	MATRIX PROTEIN I	DHON VIKUS (STRAIN INDIANCE)	2				 			
PUNCTE MYXVI.	IL-TS PROTEIN	MYXOMA VIXUS (STRAIN LAUSAMME)	446 463				1			Ī
PUNTS MYXVL	MT-9 PROTEIN	MYXOMA VIRUS (STRAIN LAUSANNE)	207-736		1	1	+	1 1	-	-
PYYON ROTH	NONSTRUCTURAL PROTEIN NS34	PORCINE MOTAVIRUS (GROUP C./ STRAIN COWDEN)			1	1	1		1	
PVNCA PAVBO	PROBABLE MONCAPSID PROTEIN NPI	BOVING PARVOVIRUS	149-170		1	+	+			
PWC Abvo	MONCAPSID PROTEIN NS-1	ALEUTIAN MINIC DISEASE PARVOVIRUS (STRAIN G)	10-14	┪	T	Т	Т		1	
PVWC3 AEDEV	NONCAPSID PROTEIN NS-1	AEDES DENSONUCLEOSIS VIRUS (STRAIN GKV 002 002)	7	╗	417.517	313-612	760-817 82	851-848		
TVNCS MORES	NONCAPSID PROTEIN NS-1	MUNUME MONUTE VIRUS (STRAIN MYNI)	2	682-292		+				
PYNCS MUMOV	NONCAPSID PROTEIN MS-1	MUNIOR MENUTE VINUS	35-62	262-289			+			
PANCE PANCE	MONCAPSID PROTEIN NS-1	HISTAN PARVOVINUS B19	2,70			+	\dagger		1	Ī
PANCS PAVIE	NONCAMED PROTEIN NS-1	HALKSTER PARVOVINUS HI	200	7		1	1	1	1	Ī
PANCE DAVIN	NONCAPSID PROTEIN NS-1	POXCINE PARVOYIRUS (STRAIN NADL-2)	2	9	2	+	\dagger		1	
PANSI BADVI	MOMSTRUCTURAL PROTEIN NS!	EPIZOOTIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 27 STRAIN ALITERTA				\dagger	\dagger			Ī
PVNSI DALA	NONSTRUCTURAL PROTEIN MS:	DETLIENZA A VIRUS (STRAIN A/ALASKAM77)	261-1/1			+	\dagger		1	I
PYNS! LANON	NONSTRUCTURAL PROTEIN NSI	DELLENZA A VIRUS (STRADY AVANN AUBORGMO)	K .			+	+	1	1	T
PYNSI IACHE	NOWSTRUCTURAL PROTEIN MSI	INTLUDIZA A VIRUS (STRAIN ACHILLEIGE)				1	+		1	T
PYRSI IACKO	HONSTRUCTURAL PROTEIN NSI	DOLLDOZA A VIXIS (STRAIN ACHUCAENGANA)	201			+	\dagger		1	
PANSI LACKU	NONSTRUCTURAL PROTEIN NSI	INTEREST A VALUE (STRAIN ACTURATION AND A				+	+	1	1	
PVNSI LADAZ	MONSTRUCTURAL PROTEIN NSI	INTELLEGIZA A VILLE (SINCH AUCHANDER) MOSTO	131			+	\dagger		-	
PVISI INCOM	NONSTRUCTURAL PROTEIN MS	INTUCACA A VIDA (SI MAIN MICA)	101			\mid	\dagger			
PASS MOV	NOMSTRUCTURAL PROTEIN ASI	INTLIENCE A UNITED STRUCTURE AND A STRUCTURE A				+	\dagger			
WAS IN E	NOWSTRUCTURAL PROTEIN NS	INTELLIGENCE A VIDER (CTRADI ANALI LARIVA) BERTARIOS	13:16			-	-			
TVRSI MACA	MONETHING IN A PROTECT NO.	MELLINGA A VIRIS (STRAIN APINTALL/ALBERTA/121/79)	171-198			-	\vdash			
TAKE TO SELECT	POWER PROPERTY AS BEOTERN NO.	DELIENZA A VIRUS (STRAIN APONTALI/ALBERTA/)SU/9)	171-194				-			
	CONSTRUCTION AT PROTECT NO.	INSTITEMEN A VIRUS (STRAIN ATURKEY BETHLEHEM-GLILIT/1492-B/82)	13:18				+			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AVACEDITED IN ALL PROTEIN NSI	INSTITEMENT A VIRUS (STRAIN A/TURKEY/CANADAKI)	171-198			-	-			
PACKE IN THE	MANAGERICAL MAIL PROTEDUNS!	DIFFLENCE A VIBUS (STRAIN ATERNATURKAGENIA/1972)	171-198			-	-			
PVNS: IAIDO	HONSTRUCTURAL PROTEDY NS!	DETLEDEA A VIDUS (STRAIN AUDORN/101/72)	171-191				H			
PVNS: TAIRS	HONSTRUCTURAL PROTEIN NS!	DELUENZA A VIKUŠ (STLAIN AKISSK9077)	191-198							
PVAKI DOLPA	NONSTRUCTURAL PROTEIN NS!	DEFLUENCA B YOU'S (STRAIN B/PA/79)	131-168							
PANCE LATER	NONSTRUCTURAL PROTEIN NS2	DIFLUENCA A VIRUS (STRAIN A/TURICE Y/OREGON/TI)	87-114							
PANSE DOLLE	HONSTRUCTURAL PROTEIN NS2	DYFLUENCA B VIXUS (STYAIN BALEE/40)	21-38 21-38							
PVNS DOVA	HONSTRUCTURAL PROTEIN NS2	INTELENCA B VOLUS (STRAIN BY AMAGATA/1/7)	5				+]	
PVNS1 Decid	NONSTRUCTURAL PROTEIN NS2	INSTITUTOREA C VIRUS (STRAIN CIIVSO)	. B				-	-		
PWISS CVPFS	HONSTRUCTURAL PROTEDY 3-1	PORCOG TRANSAGSSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN FS772	29-36			1	+			
PVNSA CVIDS	NONSTRUCTURAL PROTEIN 4	HUMAN COLONAVIRUS (STRAIN 279%)	2 5		1	1	\dagger		1	
אנו אנו	NONSTRUCTURAL PROTEIN MA	COLUMN CAPTURE CONTRACTOR AND VISES					+			
PWS) CYCLE	INCHASTRUCTURAL PROTEEN	CANAGE ENTENC CONOIN TROS (STANTE AS A								

╒╕╒╒╒╒╒┍┍ ┼┾┼┼┼	HOTEIN 7 HOTEIN 7 HOTEIN 7 HOTEIN 7 HOTEIN 15	PELINE ENTELIC CORGNAVIRUS (STALIN 79-164) PELINE ENTELIC CORGNAVIRUS (STALIN 79-164) PELINE IN STANIANISSIBLE GASTROGETERITIS CORGNAVIRUS (STRAIN FURI) 14-61 PORCINE TLANSMISSIBLE GASTROGETERITIS CORGNAVIRUS (STRAIN FURI) 14-61 PORCINE TLANSMISSIBLE GASTROGETERITIS CORGNAVIRUS (STRAIN FURI) 14-61 PELINE INVECTIOUS PERITORITIS VIRUS (STRAIN MIL 1784) 14-73 PERALDA PARABELLERIZA 1 VIRUS (STRAIN MIL 1784) 14-73 PERALDA PARABELLERIZA 1 VIRUS (STRAIN MIL 1784) 14-73 PERALDE AND STRAIN MIL 1784 14-74 PERALDE AND VIRUS (STRAIN AND STRAIN MIL 1784) 171-4 PERLIEGIZA A VIRUS (STRAIN AND STRAIN MIL 1784) 171-4 PERLIEGI	14-43 14-61 14-61 14-13 14-13 14-13 14-13 11-13 111-403 1					
	HOTEIN 7 HOTEIN 7 HOTEIN 7 HOTEIN 7 HOTEIN 7 HOTEIN 84 HOTEIN 184 HOTEIN 185	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		╵╶┊ ┧ ╏┋┇┊╸╏╏╏┩╏╏╏			
	HOTEIN 7 HOTEIN 7 HOTEIN 7 HOTEIN 7 HOTEIN 8 HOTEIN 84 HOTEIN RAS	7:213 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		╶┊ ┨ ╏┇┇ ╌┈┼╂╀┦┼┼┼╁╂╂┪			
	MOTEIN 7 MOTEIN 7 MOTEIN 8-4 MOTEIN RE-4 MOTEIN RE-3 MOTEIN RE-3 MOTEIN RE-3	217 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	13 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		┆ ╂╀╄╂╬╾┼╂╂╃╂┼┼┼╁╂╂╅			
	HOTEIN 7 HOTEIN C HOTEIN C HOTEIN NS H HOTEIN NS H HOTEIN NS S	((STIKAIN 79-1146)) 4 AIN CI-1401) 4 AIN CI-1401) 5 AIN CI-1401) 5 AIN CI-1401) 6 AIN CI-1401) 7 BEOGRAPH 7001/71) 7 BEOGRAPH 7001/71) 7 BEUNGENIAN 7001/71) 7 BEUNGENIAN 7001/71) 7 BEUNGENIAN 7001/71 7 BEUNGENIAN 7001/71 7 BEUNGENIAN 7001/71 7 BEUNGENIAN 7001/71 7 BEUNGENIAN 7001/71 7 BENGENIAN 7001/71 7	13.5 14.03 14.			┞┩┩┋┈╏ ┼┼┼┼┼┼┼┼┼┼		 - :
	NOTEIN C NOTEIN C NOTEIN NA H NOTEIN NA H NOTEIN NA S	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3.5799 3.5799			╏╏╏┊╸╏╏╏╏╏		• :
	MOTEN C NOTEN 834 MOTEN NS.3 MOTEN NS.3	1000(17) 100	1-05 1-05			╏╏┊╸╏╏╏┩ ╅┼┼┼┼┼┼		
	MOTERN 1844 MOTERN 1853 MOTERN 1853	11/695/76) 10/10/21/77) 11/20/21/77) 11/20/21/77) 11/20/21/77) 11/20/21/77) 11/20/21/77)	84			┊╸╎╎╎ ┪┪┪┪		: []]]] ;]]]]]
	FOTEN 18-3	AS ACUTAFRINORINGSTO) TABORANO ARIOLAND DGERGANANORI LIFORNIANORI GERGERIANORI GERGERIANORI GERGERIANORI CELAUSTRALLATORI CELAUST	1-103 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403			┊╸╎┤┤┩ ┆┼┼┼┼┼		
	MOTERIARS.	AIN AANAS ACUTAFRIAORIEVOSTO) AIN AANNA ARBORGEO AIN AARIN ARBORGEO AIN ARBUDGERIGANINONIO AIN ARBUDGERIGANINONIO AIN ARBUDGERIGANINONIO AIN ARBUDGERIGANINONIO AIN ACUTEREPRISTALIATIONIO AIN	1-100 1-100					
	MOTERA 18-3	VRUS (STRAIN AJANAS ACUTAFRINORIDOSTA) VRUS (STRAIN AJANA REBOROM) VRUS (STRAIN AJANA REBOROM) VRUS (STRAIN AGUILITION VRUS (STRAIN AGUILITION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATION VRUS (STRAIN AGUILITONINATIONINA	1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403					
		VIRUS (STRAIN ANANAS ACUTAPRINORIEVOSTO) VIRUS (STRAIN ANANAS ACUTAPRINORIEVOSTO) VIRUS (STRAIN ANANAS ACUTAPRINORIEVOSTO) VIRUS (STRAIN ANANAS ACUTAPRINORIEVOSTO) VIRUS (STRAIN ANAUGERAGANINORIE) VIRUS (STRAIN ACHICKENGERISTANIATI) VIRUS (STRAIN ACHICKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATI) VIRUS (STRAIN ANDUCKENGERISTANIATIATIATIATIATIATIATIATIATIATIATIATIATI	1-63 1-63					
			1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403					
		#KAIDOUTT) INTERNATI INTERNATI ATEMATIS OVAKIASIS INTERNATIS OVAKIASIS INTERNATIS INTERNATIS INTERNATIS INTERNATIS INTERNATIS	1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403					
			1-03 1-03 1-03 1-03 1-03 1-03 1-03 1-03					
			1-403 1-403 1-403 1-403 1-403 1-403 1-403					;
			1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403 1-403					
		(1/0.) (36)	\$0+1 \$0+1 \$0+1 \$0+1 \$0+3 \$0+3					
		36)	1-405 1-405 1-405 1-405 1-405					
			1-03 1-03 1-03					
			1-405 1-405 1-405 1-405					
			1-405 1-405 1-405					
			1-403					
		2) 1773) 74)	1-405					Ш
			8-408					
						_		
			200-075					
			500-1			-		
		76)	178-405		1	+		L
	EIN		378-405		+	-		L
			378-403	1		+		L
	EUN		371-403	+		-		L
	W13		378-403			+		L
	- E	rcirati	378-405	+		1		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	- N	ļ	178.405	1		+		
	ECA		178-405	-		+		L
1	TEIN		178-405			+		
	ED.		378-405		1	+		L
	KIN		374-405	-		+		
	TED		378-405			+		
	TEDN		378-405			+		ļ
	LED.	740)	378-405			+		1
	TEDA		378-405		-	+		\downarrow
	Man		378-405				1	1
\sqcap	TEIN	DW1/1191	378-405				1	ļ
П	TEIN	1673)	378-405			+	-	1
	TED		378-405			1		1
F	TEN		378-405			+		\downarrow
Γ	TED	INCLUSION A CORP (CTE AND MONO KONCAST)	378-40S			+		1
	Mari	(36)	178-405		1	+		1
Ī	TED	46)	178-405		-	+	1	\downarrow
Γ	TEL		378-405				1	\downarrow
Γ	TED	DYSVII	178-405			+		1
PUNIC INITIAL INICIEDRIOTED	TEIN	KHAN/144/62)	378-405			+		1
٦	DITEIN		378-405			+		
	STEIN		378-405			+		
T	STEIN	DELUENZA A VIKUA (SI KALI APRIANO SI ELECTO)	178-405					1
T	OTEN		376-405			-		1
	DTED	DETUBLY A VILLE (STRAIN AND INCOME)	378-405			-	-	
Τ	OTEN					İ		

	200		A REAL A	ABFA? AG	AREA 3 AR	AREA I AR	AREA S AR	AKIA LIONIO I		
FILENAME	PROTEIN	VIRUS	Г	П	П	Т				\dashv
PRIC INPAR	NUCLEOPROTEIN		178.405	+	\vdash	-	-	H		Ц
PVNUC JAPUE	NUCLEOPROTED	DOLLENZA A VRUS (STRADA APUERTO RUCOVA)	11.40		+	-	-			H
AUC IARUD	MUCLEOPHOTEN	T	504.05	-	-					
PVNUC IASED	NUCLEOPROTEIN	١	378-405	\mid	-					-
NUC IASH2	NUCLEOPROTEIN		378-405							-
VINUC LASIN	NUCLEOPROTEIN	9,0001	178-405		-	-	H			+
WALL LATE!	NUCLEOPROTEIN	11661/813	378-405		-	-	\mid	Н		-
PVALIC TATION	NUCLEOPROTEIN		37-46 503-46				H			
ACC IATEO	MUCLEOFROTEIN		207-02	-	-					_
AUC IATAS	MUCLEOPROTEIN		378-405	<u>:</u> 	:	:		_		
VRUC LATRE	NUCLEOPROTEIN		178.405	l	1					
PVAUC LATX	NUCLEOPROTEIN	INTLUENCA A VIRUS (3) FAMILY A LEAST (177)	200 000	t	+	I	\mid	\vdash		-
WILE IAUDO	NUCLEOPROTEIN	BALLENZA A VRUS (STRAIM AUDUMANO)//1/	100	+		+	+	l		L
ANC IAUSS	NUCLEOPROTEIN	DIFLUENZA A VIXUS (STIAIN AUSSILABIT!)	100		+		+		-	٠.
WRUE LAVIE	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AMICTORIA/961)		1	+	1	<u> </u>	<u>:</u>	-	<u>:</u> :
WALLE LAWIN	NUCL EOPROTEIN	INSTLUENZA A VIRUS (STRAIN AMILAI EMAINEDIMA)	S S	†	+	†	1	t	-	+
VALLE LAWIE	NUCL EOPROTEIN	INFLUENZA A VIXUS (STRAIN AWITALEPACIFIC OCEANISMS)	S I	\dagger	†	\dagger	1	\dagger		ł
WALE TAWA	NICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AWILSON-SMITHO))	378-405	1	\dagger		1	$\frac{1}{1}$	+	1
VALLE TAWAS	NACT EDPROTEIN	INFLUENCA A VIRUS (STRAIN AMISCONSINVISIVE)	378-405		1	+	+	$\frac{1}{1}$		ł
WHILE IATE	NAMES EXPROTEIN	DIGLUENZA A VIRUS (STRAIN A/SWING/29/37)	378-405		+	1	+	\dagger	1	+
VARIE 1AZ41	NUCLEOPROTEIN	INFLIENZA A VIRUS (STRAIN A/SWINE/41/49)	378-403		1	1	i	1	<u> </u>	:
WALLE LAZEA	NAICL FOR LOTEIN	INFLUENZA A VIRUS (STICAIN ASWINEXCAMBRIDGE/1/35)	378-405	1	1	+	+	1	+	\dagger
WHIT IAZDA	MICHEOPROTEIN	DOLUENZA A VIRUS (STRAIN ASWINE/DANDONC/9/1)	378-405			1		\dagger		t
Walter TAYOR	MICL FORESTEDA	INTLUENZA A VIRUS (STRAIN ASWINE/GERMANY/2/81)	178-405			+	1	1	$\frac{1}{1}$	\dagger
PARTY TANK	NAICH EOPROTEIN	INFLUENZA A VIRUS (STRAIN A/SWINE/HONG KONC/6/76)	25.405		+	\dagger	+	$\frac{1}{1}$	1	\dagger
WEST IN THE	NUCLEOPEDITON	DOFLUENZA A VIRUS (STIAIN A/SWING/HONG KONC/126/12)	378-403	1	+	+	1			t
PUNIT TATAL	AUCI EGRADIEM	DOLUBRIZA A VIRUS (STRAIN ASWINERIONG KONG/12//82)	378-405	1	+	1	+		1	\dagger
MARIE IAZII	NUCL FOR OTHER	DOLUENZA A YTRUS (STRAIN ASWINGAOWA! \$70)	335-405		+	+		\dagger	1	\dagger
WALLE LAYED	NUCL EOPTOTEIN	INFLIENZA A VIRUS (STRAIN ASWINGMOWALIFIENZ)	31403	1	+	†	1	\dagger		\dagger
PVNUC IAZO	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ASWINEROWAM)	200	1	\dagger	+	+	\dagger	+	t
WALC IAZII	MUCL EOPROTEDA	INTLUENZA A VIRUS (STRAIN ASWINEITALY/4)7/76)		†	1		\dagger		+	t
PVNUC IAZZ	NUCLEOPROTEIN	INFLUENCEA A VIRUS (STRAIN A/SWINE/ITAL Y/1/19)	378-403		1	1	1	\dagger		\dagger
PVNUC IAZII	NUCLEOPROTEIN	DIFLUENZA A VIRUS (STRAIN A/SWINE/ITAL Y/141/81)	276-403	1	1	1	+	\dagger		\dagger
PVAUC JAZIA	MUCLEOPROTEIN	DEFLIENZA A VIRUS (STRAIN ASWINEITAL YRIWTY)		1	\dagger	\dagger	†	\dagger		t
PVNUC_LAZIA	NUCLEOPROTEIN	BATLIENZA A VIRUS (STRAIN ASWINE)/AMESBURG42)	707 11.	Ì	t	†	-	\mid	-	1
PVNUC IAZMA	NUCL EGMOTED	INTLIENZA A VIKUS (STRAIN ASSWINGPRATICS)	107 111	\dagger		T	l	l	-	\vdash
PYNEC LAZNE	NUCL EOPROTEIN	MATCHARA A WALL CATA AN A KINGTONION	378.405		T		T		-	-
WALC IAZOH	NUCL EOPROTEIN	INTEREST A VINUE (CTA A PARAMETER)	200	T	T			-	_	H
WINC INZON	NUCLEOPROTEIN	INTELLEGIZA A VIDER (CTEAN AND INTELLEGIZATION	200			T				Н
PVNUC IAZTE	NUCLEOFICIEN	INTELLIGIAL A VIDER (STRAIN ASWINGALISCONSINUS)	275.405				T			Н
PWRUC IAZWI	MUCLEOFROIEIN	DATIEDICA A VIRLIS (STRAIN A/SWINE/WISCONSIN/I/A!)	178-405							1
PVACE LACKS	NOTICE ECONOTION	INFLUENZA C VINUS (STRAIN CYCALIFORMIAM)	Г	416-44) 4	451-478					+
WATER WATER	MAINT FORGITEDA	MAJEGRO VIRUS (STRAIN MUSOKE)	166-407						1	1
SALA MANA	MICHEOPROTEIN	IMARBURG VIRUS (STRAIN POPP)	166-407	П				1	+	+
VACOL	PROTEINO	VACCINIA VIRUS (STRAIN COPENHAGEN)	Ę	⊣	SB -608	1	1	1	1	\dagger
VAN ION	PROTEINO	VALUOLA VIRUS		2 2 8	8	1	+	1	+	\dagger
PVOR FXDAY	153 KD PROTEIN	FOXTAIL MOSAIC VIRUS	- 1		1		†	\dagger	1	\dagger
VOR 1 NAV	186 KD PROTEIN	NANCISSUS MOSAIC VIRUS	_1	127.130	+		1	1		\dagger
PVOR! PACY	1% KD PROTEIN	PAPAYA MOSAIC POTEXVIRUS	941.978	1272	1	1	1	†	+	\dagger
PVOR I PVACE	22) KD PROTEIN	POTATO VIRUS M (STRAIN RUSSIAN)	207-627			1	1	1	1	\dagger
PVOR1 PVX	165 KD PROTEIN	POTATO VIRUS X	£ 72	017.04	1	1	1	1	+	t
PVOR! PYXXX	165 KD PROTEIN	POTATO VIRUS X (STRAIN X2)			1	1	1	1		t
PVORI SATTEA	150 KD PROTEIN	STRAWBELLY MILD YELLOW EINCE-ASSACIATED VIRUS			1	\dagger	T	+	-	ŀ
PVP10 NPVAC	P16 PROTEIN	AUTOMATIA CALPONALA ROCLEAR POLITICANOSIS VIRGIS	7	T			İ	T	-	-
ADADE OI AA	PIO PLOTEIN	URUTIA PAEUDOI SOUALA FIOLITICA SIO FOLITICOROSIIS FINES								

CORNE	107217324	All Variets (no bacterioping to)	AREAL	ARCAL	7	1	4				
200			Г							Ī	
COLUMN TO SERVICE STATE OF THE PERSON STATE OF			Г	227-254						Ī	
		03	33.60								
			101-108								1
			100								1
1000			1.10	Ī							ŀ
MAIN MIAN								L			•
PVP19 AUCY		CHERRY)									
PVP19 TBSVC	1000	LEBBERGVIRES SATMIRE (STRAIN 11)									
WPJ HEWSA	OTELIN VEZO	SALING THE PART OF THE LATERALY ADAPT	16-61								
VP26 HSVES			48-75								
ALVEN MEYEA		HERPESVIKUS SAMINU (STRAIN OF THE ACCINE)	277-304	410-437	632-662	907.934					
10504	A VP.	AFRICAN HORSE SICKNESS VINUS (SCAULTICAL SICKNESS)	811.846								1
		BLUETONOUE VIRUS (SENOTYPE 13 / ISOLATE USA)	350 000								
11/12		HI (IETONOLE VIRUS (SEROTYPE 1 / ISOLATE AUSTRALIA)					:				
VP2 BTVIA		THE POWER WINDS (SEROTYPH: 1 / ISONATE SONTILL ALINEA)	9 :								_
VP2 BTV15		THE PARTY OF THE P	72-103	415-451						<u> </u>	i i
WATER BOOK		ENZOCIAL HEMORITARIA CITATA	7.6	\$23-553	_						1
1		BOVINE ROTAVIRUS (STRAIM RV)	20.02	\$24.554	L						
		BOVING ROTAVIRUS (STRAIN UK)	101.02	19.10							
Ver ROTEU	ANA BUREAU PROPERTY OF	HILMAN ROTAVIAUS (SEROTYPE 1 / STRAIN WA)			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	704.746	-		L		
PVP1 ROTHW		POSCING BOTAVIETS (CROKIP C / STRAIN CONDI.N)	37.44	061-107			-	!	:	:	
PVP1 KOTPC			9					_			_
VP1 KOTSI	74.	MINISTER OF THE PROPERTY AND A STATE OF THE PA	39.75								
Care Arees		AFLICAN SWINE PEVER VINCE (STRAIN 1973)	10.91		L						1
		AFRICAN SWINE FEVER VIRUS (STRAIN BATIN)	911								
100	CV PROTECN VP31	EBOLA VIRUS		936 755			-				
S EBOV	Т	MARRIED VIRUS (STRADA MUSOKE)	100			1					L
PARTY SEAM	Т	CONTRACTOR AND PROPER	10-101	231-238							
WATS MABY	X PROTEIN VP35	MANAGORIO VIRGO (STREET FOR THE BOX VIRGO CIS VIRGO	270-297								
200		AUTOGRAPHA CALIFORNICA POCLEZA POCENCIO	101			L					4
		BOARYX MONI MUCLEAR POLYTEDROSIS VINUS	300				_	L			
		VACCINGA VIRUS (STRAIN WR)		100			-	L	L		
PVP35 VACEV	DOMINION CAN THE SECOND	ALITICICALAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS								L	L
NAVE 20		ONG TIA PSEUDOTSUGATA MALTICAPSID POL MIEDROSIS VIRUS	207		\downarrow	\downarrow		-		L	L
10 M	MACHINE CANADA T	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)	75-134				+	-	-		L
WE AND LAN	VP) COSE PLOTEDY	THE PROPERTY OF THE PARTY PE TO / ISOLATE USA)	214-252				$\frac{1}{4}$				L
WP3 BTV10	VP) CORE PROTEIN	THE CONTROL WAS IN THE BOTTY PE 17 / ISOLATE USA)	214-252								
VAN ARVIS	IVP) CORE PROTEIN	BLUELOTTO THE TANK THE PARTY AND A PRINTED IN THE ALICTICAL IA.	214-252						$\frac{1}{4}$		1
Ver BIVIA	VP3 CORE PROTEIN	ELUETOWGOE VINOS (SEACOL IN CASA CASA CASA CASA CASA CASA CASA CAS	204-243	700-077		L					1
10000	VP1 CORR PROTEIN	EPIZOOTIC HEMOREKAGIC DISEASE VIRUS (SENOTITE 1)					L				4
	MAN POOR PROTEIN	EPIZOOTIC HEMORINACIC DISEASE VIRUS (SERU) TEE A STRAIN ACCOUNT						L			
WI DOWA	VI) COMB TROITE	CALPEVINE FANCEAS VIXUS			\downarrow		-	ļ	L		L
WIN GREV	P) PROTEIN	PORCHER ROTA VIRUS (GROUP C / STRAÍN COWDEN)				1		-			L
PVP3 ROTIC	DOKE COME PROTEIN VI	CONTRACTOR STRAIN SAIL	<u>2</u>	330-337	100	100	-				1
PVP3 ROTS!	INVEX CORE PLOTEIN VP3	SUMLANT IN A CITY OF A CITY AND MANUAL TO A CITY AND A	440-470				-				1
Van oran	CANSO PROTEDY PAG	EPSTEIN-LANCE VICTOR (1910-1910)	203-232	344-372	-	-	_				4
SUPER BROKE	CANSID PROTEDY PRO	MEMPES VIRUS SAUMANI (STRANGE 11)	3.5			_					4
1	CARGO PROTEDUPAD	DOTECTIOUS LARYNCOTIKACHELITS VINUS (3) INAIR TITORILE TOTAL	196	404.433	-	-	L	L	_		
	CABETTE DE CATETO PED	VARICELLA-ZOSTER VILUS (STRAIN DUNIAS)		917 985	-	-	ļ	 -		L	
200	AND THE PERSON NAMED AND ADDRESS OF THE PERSON NAMED AND ADDRE	CONDAN 11 ROTAVIRUS (STRAIN SA11)			1	-	+	-			Ļ
PVP41 ROTS!	With Committee in the	SELECTANTI POTAVILLE (STRADI SAII)	î	770			1				L
WP42 ROTS!	OUTER CASE PROTEIN VA	TO COMMA VINITA STRAIN COPENDAGEN	48.75					$\frac{1}{4}$		1	ļ
WALK VACCE	MAJOR CORE PROTEDY PAR PRELUESUR	A CALL CONTRACT A DATE OF CALL CONTRACT	48-75				4				4
VACA VACCV	MAJOR CORE PROTEIN PAA PRECURSOR	VALLER VENOS (3 : 100)	46-75								4
VALV VA	MAJOR CORE PROTEIN MA PRECURSOR	VARIOLA VIRUS	92					L			-
Vental Reserve	LALIOR CORE PROTEIN PAB PRECURSOR	FOWLAOX VIXUS	133	L		L	L	_			
	LANDS CORE PROTEIN PAR PRECURSOR	VACCINIA VILUS (STRAIN CUPENMANEM)					-	Ì			
	ALL LAB CORE DECITEIN PAR PRECURSOR	VACCINIA VIRUS (STRAIN WR)		1	+	1				L	L
	STATE OF THE PRECIES OF	VALIDIA VIIUS			+	-	-	-	-		L
VP4B VARV	MAJOR CORE PROTEIN THE PRECORDS	BIT INTOMODIA VIBUS (SENOTYPE 10 / ISOLATE USA)	200	2000		\downarrow	-	1		ļ	ļ
PVP4 BTV10	VPA CORE PROTECT	IN THE POWER VIBILS (SEROTYPE 1) / ISOLATE USA)	34-61	<u>§</u>	4	-	$\left \right $	1	+		-
PVP4 BIVII	VIN CORE PROTEDY	SCHENNING VIBIR (CERCITYPE 2 / ISOLATE USA)	19-40	194-903		_	-	-	-		\downarrow
VIN BTVI	VIN CORE PROTEDY	BLUETOWOOD VENCE VIEW OF IN STRAIN MCDV-LINCOLM	553-622					4			4
ATAMA BANA	CANADA CANADA PROTEIN VPA	NEBRASIA CAL MAGNES TAKES (STORES						-	-		_
		CENTRAL PARTY OF THE ACT OF THE A	23	_	-			_			-

27.400.4	7.000	Att Vicence for harterleshaper)				П		П	1	П
FILE NAME		YIRUS	4	ABEA1	AREA AR	AREA! AREA!	AREAS	AREA? AREA	41 AREA	न्
TVN ROTA	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STILAD) C486)	- 1	14.622	1		1		+	T
TVP4 ROTEC	OUTER CAPSID PROTEIN VP4	BOVING ROTAVIRUS (STRAIN UK)	П	╗			1		+	T
PVP4 ROTHU	OUTER CAPSID PROTEDY VP4	EQUINE ROTAVÍRUS (STRAIN H-3)	ş	235-269	923-629			1	-	Ī
PVP4 ROTEH	OUTER CAPSID PROTEDY VP4							1	1]
PVN ROTGE	OUTER CAPSID PROTEIN VP4				1				7	Ţ
PVP4 ROTH!	OUTER CASID PROTEDY VP4	HUMAN KOTAVIKUS (SEKOTYPE 2 / STRAIN RV-S)			363-621					
PVP4 ROTHS	OUTER CAPSID PROTEDY VPA	HUMAN ROTAVIRUS (SERO) YPE I / STRAIN 69M)	1.35		584-629		-			j
l	OUTER CAPSID PROTEIN VP4		ļ	-	\$65-621					
L	OUTER CAPSID PROTEIN VP4	I/STRAIN DSI)		_	7	:				
L					╗				-	
L.		HILLAN ROTAVINUS (STIALIN KU)	1-35			577-621		1		
l			1.35	900-648	168-621					1
L		HIGGAN ROTAVIRUS (SEROTYPE 1 / STRAIN M37)		233-610						Ī
1	COTTER CAPGID PROTEIN VPA	HILLAN ROTAVIRUS (SEROTYPE 3 / STRAIN MCN1)	1.35	573-628					_	
ALL BOTTO	CATER CAPED PROTEIN VPA		8:35	17.621					: !	
l	OUTER CAREST PROTEIN VPA	1	1	105-135	235-262				L	Γ
	CATTER CANEED BECTEEN VPA	MIDGAN BOTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3)	52.9	173-527	-				\vdash	Γ
	CATTER CANCEL PROTTED UNA	HERAAN BOTAVIRUS (SEROTYPE 4 / STRAIN VA70)	Π	١.	390-617					Γ
L	CATTER CARETY DECITED VEA	MANAN BOTAVIRUS (SEROTVPE 1/STRAIN WA)	Π	537-621						
	CARCO CARCO BEOTEN VIEW	POPUNE BOTAVIRIS (SEROTYPE S / STRAIN OSL)	112.146	\$14-625				_		
	CHES CASES BROTES VOL	POPUNE BOTAVIALIS (CROSS C. STRAIN COWDEN)	Т	Т	293.320	-			L	
TION LANGE	COLEA CARGIN TROUGHANT	PORCHAG ROTA VIRGIS (STRADS COTTERED)	ĺ	1				-	ŀ	
2104	COLUMN TO SECULIAR SECU	PORCHAR ROTAVIRUS (STRADA YAS)	Ī	Т	\$84-625					Γ
TATA MOINT	COLEA CASID TROITER VIV	SURFIX SOLANDER	Τ	Т		-				Ī
AN ROLL	COTEX CAPILIFICATION OF	PRINCE IN BOTH A UNBITLE AND RATEL FRAN	Ţ	919-915	1				-	Γ
TANK ROISE	COTER CASID PROTEIN VP	STREAM IN BOTH VIBILE COP AND CALL CRUS	Ī	7	\$14-622					Ī
200	COLEA CASILIFACIEM VIN	STATE OF THE COLUMN AND THE COLUMN A		T						Γ
A 1 A 1 A 1	COLUMN TO THE PROPERTY OF THE	APPLIANTORS SICKNESS WRITE (SEROTYPE 4 / STRAIN VACCINE)		161-218						Γ
STATE STATE	CONTRACTOR DESCRIPTION OF THE PROPERTY OF THE	RI INTONOME VIRIS (SEROTYPE 10 / ISOLATE USA)	Τ	85.126				-	-	Γ
	CHAPTER PARTY BACTER VO	RUTETOWOUR VIRIUS (SEROTYPE 11 / ISOLATE USA)	Γ	92:136	\mid					Γ
PVPS BTV13	OUTER CAPSID PROTEIN VPS	BLUETONOUR VIRUS (SEROTYPE 137 ISOLATE USA)	53-60			L				П
PVP5 BTV1A	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIXUS (SEROTYPE I / ISOLATE AUSTRALIA)	23-60	921-68						
PVP5 BTV15	OUTER CAPSID PROTEIN VPS	BLUETOWOUR VINUS (SENOTYPE I / ISOLATE SOUTH AFILICA)			148-182					
PWP BTWA	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE 1/ISOLATE USA)		19-126						
PVPS ENEDV!	OUTER CAPSED PROTEIN VPS	EPIZOOTIC HEMONULAGIC DISEASE VIRUS (SEROTYPE I)	31-80	101.218	199-426					
WPS WIV	OUTER COAT PROTEIN PS	WOUND TUNOR VIRUS	648-675		-				-	Ī
PVP61 BTV10	VP6 PROTEIN	BLUETONGUE VDUS (SEROTYPE 10/15OLATE USA)	161-193						1	٦
PVP61 LOLDV	PROB NONSTRUCT 41.0 KD PRO	MAIZE ROUGH DWARF VINUS	151-202						+	T
PVP61 NPVAC	61 KD PROTEIN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	1				1		+	T
PVP62 BTV10	VPS PROTEIN	BLUETOWGUE VIRUS (SEROTYPE 10/150LATE USA)	137-189						+	T
ACAMA MANOR	MAJOR ENV CE YCOPHO PRECURSOR	CACATA PSEUDOISOCATA MULTICAZSIO POLTREDACISIS VIKUS	77.		1	+	1		+	T
PVP67 NOVAC	MACOR ENVIOL TOURS PRECORDE	AUTOMOBILE VINES (SEROTVE 11 / IGO) ATE (JCA)	163					+	1	Ī
10.00	VAN PROTEIN	ALTERONOLIE VIRUS (SEROTYPE II / ISOLATE USA)	137.189		\dagger	-			+	Τ
PVP BTV17	VPS PROTED	BLUETONGUE VIRUS (SENOTYPE 17/1SOLATE USA)	57.189						-	Γ
PVW BTVIS	VIN PROTEIN	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	161.193						L	
PVP6 BTVZA	VP6 PROTEIN	BLUETONGUE VIRUS (SELOTYPE 2 / ISOLATE USA)	133-172					_		
PVPK MDV	STRUCTURAL PROTEIN P6	ILCE DWAJE VILLS	П	154-381						
PVP74 NPVAC	P74 PROTED4	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	П						+	
PVP75 HSVSA	PROBABLE MEMBRANE ANTIGEN 19	HELPESVIKUS SADADI (STRAIN !!)	g	429-977						
PVP79 NOVAC	79 KD PROTEIN	AUTOCIAMA CALIFORNICA MUCLEAR MA VIEDROSIS VIRUS	2.7	370-397		-		+	1	Ī
PVP) EOV	VP7 CORE PROTEIN	EFICULIA TRACE VIEW		T	1	1	1		+	T
PVP VIV	CAREER BOOTERS BOO	ATTOCA APPLA CALIFORNICA MICTEAR POLYHEDROSIS VIRLIS	101:10	340.304	\dagger				1	T
SUPER MANAGE	CAPACID PROTEIN PAT	ORGYTA PSEIDOTSUGATA MULTICAPSID POLYMEDROSIS VIRUS	132-159			-			<u> </u>	T
PVPL BTV10	MONSTRUCTURAL PROTEIN PO	BEURTONOUR VIRUS (SEROTYPE 10/150LATE USA)	105-132						L	Γ
VWW FOWPV	STRUCTURAL PROTEIN VP8 PRÉCURSOR	FOWLI-OX VIRUS	211-230		-	-			L	Γ

PROTEIN NORTHEAN PAINTEN PAIN	19-34 113-143 113-143 113-144 113-144 113-144 13-144
MASTILCTURAL PROTEIN PASSINGS MASTILCTURAL PROTEIN PASSINGS MASTILCTURAL PROTEIN PASSINGS PAS	19-234 19-234 19-234 19-234 19-234 19-231 1
MUMERILLETURAL PROTEIN PHS STRUCTURAL PROTEIN PH STRUCTURAL PROTEIN PH STRUCTURAL PROTEIN PH STRUCTURAL PROTEIN PH STRUCTURAL PROTEIN PH STRUCTURAL PROTEIN PH WELL PROTEIN PHO	23-49 24-49 24-49 196-231 15 137-186 218-285 167-194 1501.AT(53) 5-48 15-48 15-48 15-48 15-48 15-48 15-48 15-48 15-49 15
STRUCTUAL PROTEEN POSTEIN POSTEIN PROTEIN POSTEIN PROTEIN POSTEIN PROTEIN POSTEIN PROT	13 11-49 11-104
STRUCTURAL PROTEIN PO STRUCTURAL PROTEIN PO STRUCTURAL PROTEIN PO STRUCTURAL PROTEIN PO STRUCTURAL PROTEIN PO STRUCTURAL PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN PO VEU PROTEIN VEU CLYCOPROTEIN VEU	15 11-186 118-255 167-186 118-255 167-184 118-255 167-184 118-255 11-48 11-48 11-48 11-48 11-49 11-48
STRUCTUAL MOTERN 13 ED POLYTEDIAL ENVELORE MOTERN 13 ED POLYTEDIAL ENVELORE PROTEIN PURDIEIN WHO PROTEIN	15 (17-186 218-285) (E) 167-184 (18-285) (E) 1-194 (18-184) (E) 1-24 (18-184) (E) 1-
13 ED POLYREDAL ENVELOR MOTERN 13 ED POLYREDAL ENVELOR MOTERN 13 ED POLYREDAL ENVELOR MOTERN 14 PROTEIN 15 PROTEIN 16 PROTEIN 16 PROTEIN 16 PROTEIN 16 PROTEIN 17 PROTEIN 18 PRO	13 12.146 218-285 167-194 1-285 1-11 1-48 1-285 1-14 1-48 1-285 1-14 1-28 1-28 1-28 1-29 1-29 1-28 1-28 1-29 1-29 1-28 1-28 1-29 1-28 1-28 1-28 1-28 1-28 1-28 1-28 1-28
13 KD POLYNEDRAL ENVELORE MODERN PROPRIED NATERIAL WALPROTEIN WALPROTEIN NATERIAL WALPROTEIN WALPROTEIN NATERIAL WALPROTEIN NATERIAL WALPROTEIN NATERIAL WALPROTEIN WA	167.194 167.194 1.31 1.31 1.41 1.30 1
PROOPAGITASS WHY MOTERN WHY MOTERN WHY PROTEIN WHY PR	1.31 1.41 1.40 1.50 1.50 1.50 1.50 1.50 1.40 1.50
WOU PROTEIN WHO PR	1.71i:3) 5-4f 11-48 1-48 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49 1-49
WHO PROTEIN WHO PR	
WHO MOTEIN WHO WHO WORNOTEIN WHO WHO WOOMOTEIN WHO WHO WHO WHO WHO WHO WHO WHO WHO WHO	
WOUNDERN IN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY WAY CONNOTEIN WAY WAY CONNOTEIN WAY WAY CONNOTEIN WAY WAY CONNOTEIN WAY WAY WAY WAY WAY WAY WAY WAY WAY WAY	8 6 6 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
WU PROTEIN WU PROTEIN	A A S S A A A A A A A A A A A A A A A A
WU PROTEIN WU PROTEIN	
WHO MOTERN WHO PROTEIN WHO PRO	
WAU MOTEIN WAU PROTEIN WAY PRO	
VPU PROTEIN RI	
WAU PROTEIN WAY WOOTHIN WAY GLYCOPHOTEIN WAY GLYCOP	
VYU PROTEIN WE WAN PROTEIN WE WAN PROTEIN WE WANTHLICTIALL PROTEIN WE W	
VAU PROTEIN WAU PROTEIN WAU PROTEIN WAU PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY GAYCOPRO	
VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W VPU PROFEIN W W VPU PROFEIN W W VPU PROFEIN W W W W W W W W W	
VYU PROTEIN WE WIND THE WAY PROTEIN WE WIND THE WAY PROTEIN WE WIND THE WAY PROTEIN WE WIND THE WAY PROTEIN WE WIND THE WAY PROTEIN WE WIND THE WAY PROTEIN WE WIND THE WAY PROTEIN WE WIND THE WAY WE WAY WE WIND THE WAY WAY WAY	
WYU PROTEIN WYU PROTEIN WYU PROTEIN WYU PROTEIN WYU PROTEIN WYU PROTEIN WYW PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY WORMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY GLYCOMOTEIN WY	
WIND PROTEIN WIND	
VVV MOTEN VV MOTEN VV M	
WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY PROTEIN WY WY PROTEIN GUYCOPROTEIN WY	
VAV PAGTEDN VAV PAGTEDN VAV PAGTEDN LAPALS LAPA	
WAY PROTEIN ALPHAA, PROTEIN ALPHAA, PROTEIN WA PROTEIN WA PROTEIN WA PROTEIN WAS PROTEIN	101.1078
WW MOTED WW W GLYCOMOTED W GLYCOMOTED W GLYCO	1201,1001
ALPRA, NOTEDN W MOTEDN W MOTEDN W M MOTEDN W M M M M M M M M M M M M M M M M M M M	
WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW PROTEDN WW W W W W PRECURSON G W W W W W PRECURSON G W W W W W PRECURSON G W W W W W W PRECURSON G W W W W W W W PRECURSON G W W W W W W W W W W W W W W W W W W W	
WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN WW PROTEIN W PROTEIN W PROTEIN W W W W PROTEIN W P	117.14
WW PROTECH WW PROTECH WW PROTECH WW PROTECH GAYCOPHOTELN WYT MOMSTILLCTURAL PROTECH WAYT MOMSTILLCTURAL PROTECH WAYT MOMSTILLCTURAL PROTECH WAYT GAYCOPHOTEN W	
WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY PROTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY WAY GLYCOPHOTEIN WAY GLYCOPHOTEIN WAY WAY WAY WAY WAY WAY WAY WA	
WAY MOTERN WAY PROTEIN GLYCOPHOTELN WAY) MONSTHILCTURAL PROTEIN NCV7) MONSTHILCTURAL PROTEIN NCV7) MONSTHILCTURAL PROTEIN NCV7) MONSTHILCTURAL PROTEIN NCV7 MONSTHILCTURAL PROTEIN NCV7 GLYCOPHOTEIN W7	4775
WW PROTEIN WY GLYCOPROTEIN WOYD GLYCOPROTEIN WOYD GLYCOPROTEIN WY	
CAYCOPROTER VP7 CAYCOPROTER VP7 NONSTRUCTURAL PROTER NCV7 NONSTRUCTURAL PROTER NCV7 NONSTRUCTURAL PROTER NSV79 NONSTRUCTURAL PROTER NSV79 CAYCOPROTER VP7	3.39
MONTHLETTIAAL PROTEBN WCV7) MONSTHLETTIAAL PROTEBN WCV7) MONSTHLETTIAAL PROTEBN WCV7) MONSTHLETTIAAL PROTEBN WCV7) MONSTHLETTIAAL PROTEBN WCV7) GLYCOPROTEBN W7 GLYCOPROTEBN W	91-146 199-236
NOWSTRUCTURAL PROTESS NEW? NOWSTRUCTURAL PROTESS NEW? NOWSTRUCTURAL PROTESS NEW? GLYCOPHOTESS VF GLYCOPH	91:146 202-236
MONTHLETIAL PROTEIN NEV?) NONSTRUCTURAL PROTEIN NESVYP NONSTRUCTURAL PROTEIN NESVYP GLYCOROTEIN V??	T
MONSTILLCTURAL PROTEIN NEW MONSTILLCTURAL PROTEIN NEW MONSTILLCTURAL PROTEIN NEW GAYCOMOTEIN NY	Ţ
MOMERTIAL THAT FROM THE STATE OF THE STATE O	Т
GLYCOROTERN VP7 GLYCOROTERN VP	164-201 [217-23]
GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7 GLYCOROTEIN VP7	3.29
GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7 GLYCOMOTEIN VY7	9.30
G. YOSPOTEN V7 MECURSON G. YOSPOTEN V7 MECURSON G. YOSPOTEN V7 C. G. YOSPOTEN V7 C. G. YOSPOTEN V7 C. G. YOSPOTEN V7 C. G. YOSPOTEN V7 C. G. YOSPOTEN V7 C. G. YOSPOTEN V7 C. G. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. YOSPOTEN V7 C. G. G. YOSPOTEN V7 C. G. YOSPOTEN V7 C.	C)
GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7	4.7
GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7 GLYCOPROTES VP7	210-27/
GLYCOPHOTEN VP7 GLYCOPHOTEN VP7 GLYCOPHOTEN VP7 GLYCOPHOTEN VP7 GLYCOPHOTEN VP7 GLYCOPHOTEN VP7 GLYCOPHOTEN VP7 GLYCOPHOTEN VP7 GLYCOPHOTEN VP7	13-29
GLYCOPROTEIN VP7 GLYCOPROTEIN VP7 GLYCOPROTEIN VP7 GLYCOPROTEIN VP7 GLYCOPROTEIN VP7 GLYCOPROTEIN VP7 GLYCOPROTEIN VP7	3.39
GLYCOMOTEIN VP7 GLYCOMOTEIN VP7 GLYCOMOTEIN VP7 GLYCOMOTEIN VP7 GLYCOMOTEIN VP7	GF 6
GLYCOPROTED VF7 GLYCOPROTED VF7 GLYCOPROTED VF7 GLYCOPROTED VF7	
GLYCOPROTEIN VY7 GLYCOPROTEIN VY7 GLYCOPROTEIN VY7 GLYCOPROTEIN VY7	5.75
GLYCOMOTEN V77 GLYCOMOTEN V77	2.29
GLYCOROTEN V7	2.2
GLYCOPROTEIN VY7 GLYCOPROTEIN VY7 GLYCOPROTEIN VY7 GLYCOPROTEIN VY7 GLYCOPROTEIN VY7 GLYCOPROTEIN VY7	STRAIN DI
GLYCOFROTEN VP7 GLYCOFROTEN VP7 GLYCOFROTEN VP7 GLYCOFROTEN VP7 GLYCOFROTEN VP7	
GLYCOPROTEIN VP7 GLYCOPROTEIN VP7 GLYCOPROTEIN VP7 GLYCOPROTEIN VP7	
GLYCOPIOTEN YTT GLYCOPIOTEN YTT GLYCOPIOTEN YTT GLYCOPIOTEN YTT	7.77
GLYCOPROTEN V77 GLYCOPROTEN V77 GLYCOPROTEN V77	2:29
GLYCOPROTEIN VP7	3-29
GLYCOPROTEDI VP?	2.29
	3:39
GR.YCOPROTEIN VP7	125-153
ATTACK CATTER CAPSED PROTEIN	
MONATHUCHUNAL CLYCOPROTEIN NCVPS	11.40
SANCE WITTER CAPSED PROTEIN	
MOTOR CALLS CALLS BOOTEN	2
	INHEA ROTAVIRUS) (11-60

200000	7	All Virgan (to bestrateghenn)	П	$\overline{}$		_	П		П	
FU F NAME			7	J	7 7 7 7	AKYA AKYA	2	ARCA & AREA /	T ONLY	2
PVS11 ROTHS	UTER CAPSID PROTEIN	N ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	1	2			1			
PVS11 ROTHO			T	2		1	T		<u> </u>	-
PVS11 ROTHW		NWA)	9			İ	İ	1		
PVS11 ROTEA		(A)				Ì	İ	-		-
PVS11 ROTS1	MINOR OUTER CAPSID PROTEIN	SIMIAN II ROTAVIRUS (STRAIN SAII)	2				1		-	1
PVSH MUSOU			2	1			1			ŀ
PVSH MONDA	SMALL HYDROPHOBIC PROTEIN	(ISUYAMA)	2			1	1			1
PVSH MAGE			7			1	1		 -	ļ
PVSH MADE			2			1		1	+	1
PVSH LAND		MIDAPS VIRUS (STRAIN JERYL-LYNN)	9			-		_		
PUCH LINEVER			9-46						-	4
The state of the s	Ī		97-0							
TYSH MUSIC		VACCINE	1741							
PVSH MUMOR	SMALL HTURUTHURK TRUIEUN		3						L	
PVSH MOROR	SMALL HYDROPHOBIC PROTEIN					1			-	-
PVSH MUMOU	SMALL HYDROPHOBIC PROTEIN	(E. AMY)	T		17. 16.	333,360	Ţ			L
PVSII REOVD	SIGMA I PROTEIN PRECURSOR		Ī	27.1	1		Ì		<u> </u>	İ
PVSII REOVI	ISIGMA I PROTEIN PRECURSOR	res)]	rain i						\downarrow
PVSII REOVE	SIGMA I PROTEIN PRECURSOR		٦	2016	75.100				+	
DVCD BEOVE	SIGMA 2 PROTEIN		150-384						1	
PUCIT REDVI	SIGMA 1 PROTEIN		219-316						$\frac{1}{1}$	1
200	SIGNAL S DECISION		211-06							_
rysis neuvo	SIGHT IN THOUSAN		50-77						L	L
PYSES REDW.	SIGMA I-9 PROJECT		134.150				İ		-	: -
PVTJA CAVI	PROTEIN TJA									L
PVTS SPVKA	PROTEIN 75	(A)	17-00				1		 	+
PVTER EBV	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-BAUR VIRUS (STRAIN B95-1)	234-290							!
AVAILE MOLEVA	PROBABLE DNA PACKAGING PROTEIN		17.451	**		;			-	_
SCHED HEVEL	PRODUCED BY DACK ACING PROTEIN	INCHES SIMPLEX VIRUS (TYPE 6 / STRAIN DEANITY-11:12)	176-201							
POTER MENT	PROBABLE DNA PACKAGING PROTEIN		710-737							4
W.C.	PROBABLE THAT PACE AGING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	394-421							
ALC: LANCE	MAN AN PROTECTION TOX	THERMOPROTEUS TENAX VIRUS I (STRAIN VT.)	961.691							
1011	VIEWS BECTERNATOR	6	961.691							_
AUV. 11/104	V PROTEIN	(IBA)	1:38							
PVIOI CEVI	HYPOTHETICAL 18 I KD PROTEIN		13-65							<u> </u>
1000 00100	HAPOTHEY MAL 16 & KD PROTEIN		19-1							
20110	LIVECTURETICAL 11 9 KD PROTEIN		30-38							
100 M	LONG THE THE ALL IN SIN PROTEIN	N AUSTRALIA)	53-67							
200	MILETING OF THE COLUMN	VIRUS	\$11.58					_		
TY JA REAL	ANTONIA IN TANABOTED		55.55 56.55							L
	THE STATE OF THE PROPERTY.		\$:39							
MAK SSVI	HATOIHEILAL IS A MOTALIER	N VIJEDROSIS VIRUS	\$0.107							L
PY ION NOVAC	REPORT OF THE PROJECT OF THE PROPERTY.		33.111							
	ALTOING TO THE PROPERTY		67.6	119-153						
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HTPUMBIECAL IVENOTABLES	F1	14-61							
PVIEW MSVN	HYPOTHETICAL 11.7 KD TROILER	N A TEN	14.61						 -	
PYIEK MSVS	HYPOTHETICAL 172 KD PAOLEIN		34.161				Ī		-	
PYZOK SSVI	HYPOTHETICAL 28.4 K.D PKU I ELIV		77. 19						-	ļ
IV22 XACY1	INPOTRETICAL 24.5 KD PROTEDY) VI	N - 10					+		
773 SOOK	HYPOTHETICAL PROTEIN?	SOYBEAN CHLOROTIC MOTTLE VIXUS	118-148				1			
PYDIK SSVI	HYPOTHETICAL 31.5 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	2.5					1	$\frac{1}{1}$	
IVSZ XCV4	HYPOTHETICAL 31.7 KD PROTEIN	SULFOLOBUS VIRUS-LINE PARTICLE SSVI	233-267							_
PVISK NOVAC	HYPOTHETICAL 31.7 KD PROTEDA	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	133-184						-	
200	HYPOTHETICAL PROTEIN 3	SOYBEAN CHLOROTIC MOTTLE VIRUS	133-149							
	SVENTINETICAL PROTEIN 2	SOYBEAN CHEOROTIC MOTTLE VIRUS	56-94							
1	A CONTRACTOR AND PROTECTION	SURFOLOBUS VINUS-LIKE PARTICLE SSVI	<u>===</u>	\$46.573	651.700					L
200	LOND THE THE PROTEIN B	SOYBEAN CHLONOTIC MOTTLE VIRUS	9					-		
THE PORTS	HYPOTHETICAL BANGILORF! PROTEIN	FOWLDOX VIRUS (ISOLATE HP-A) S[MUNICH])	74-108	153-179	184-218					
THE POST	AVPOTTER TO A SANGOLORYS PROTEIN	FOWLPOX VIXUS (ISOLATE HP-4)8[MUNICH])	67-79							
MANUA COUNTY	HYPOTHETICAL BANGO ORF 10 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-4)8(MONICH))	2	214-241						
Tiplo Coult										

201	1107217124	All Viruso (se beciertophages)	AREAL	AREAL	ARIAZ	ABEA4	1030	प उप्राप्त	PEAT ABEA	┪	AREA
200	PROTEIN	WRUS	11-38					1	1	-	Ī
THE PARTY	LONG THE RANGE ON 12 PROTEDU	FOWL POX VIXUS (ISOLATE HE 431 HUMANI)	128-167					1	$\frac{1}{1}$	1	T
100	AND THE PROTECT BANGO CAPIS PROTECT	FOWLYOX VISUS (ISOLATE HP-434) MUNICALL	17.336							\dagger	T
TAGE COLUMN	PER 1 00 CTEPA	HUMAN SPUMARETROVIRUS	161-188							+]
	MONOGET BY IN IN IN INCHES THE PORTON	TELVESVALUS SAIMADU (STRADA 484-77)							-	1	
POH HSVS	MINDIN ALL MANAGER SELECTION	LER PREVIILIS SADORI (SUBGROUP C / STRAIN 441)							_		1
PYDHI HSVSC	HYPOTH ZE, TO SK DROK J FESTIVE	LIKE BETOTE IN TAINORI (SUBGROUP C / STRAIN 488)	2							_	-
PYDHA HSVSC	HYPOTH 9.9 KD IN DIGIT TREGION	SAME BOY WITH (CTRAIN PELL)	ŝ							\vdash	
PYT26 FOURT	HYPOTHETICAL 15.9 KD PROTEIN	POWLFOA VANCE (STREET)	170-204					Ì		ŀ	
SWITH LAUDI	HAYDOTHETICAL 30.9 KD PROTEIN	FOWLYOX VIKUS (STRAME 17-1)	33-64	95-136	144-171			1	1	+	l
	TUVERMENT ST 5 KTD MINIORI C. PRO	VACCINIA VIRUS (STRAIN WR)	13.12	179-206						1	T
A 100 A	THE PARTY IN THE P	VACCINIA VIRUS (STRAIN WR)								-	
THE VACT	HYPOTH MOST MANUEL AT A MANUEL	CONTRACTOR VIRILS (STRAIN 895-4)	2								
PYKKZ EBV	HYPOTHETICAL BKR72 PROTEIN	PARTITION OF THE PARTY (CTEAN BOLE)	19.53								
PYKUA EBV	HYPOTHETICAL BKR54 PROTEIN	EVEL PROPERTY OF THE PARK AT	47.86						-	H	Ī
BY 14 ADEA!	HYPOTH 12.4 KD IN 33 KD REGION	HUMAN ALBENDA 1175 41	27.54							+	
	GOSCINETICAL BURES PROTEON	EPSTEIN-BANK VINUS (STRAIM BUY-1)	26.143							1	Ī
1	THE CONTRACT OF THE PARTY OF TH	CONDUCTION YELLOW MOTTLE VIRUS								-	
PYOR! COYNEY	MYPOTHETICAL DESCRIPTION OF	CONTRACT THAT VIELL MAY MOTTLE VIRUS	٤						-		
PYORE COVIAN	HYPOTHETICAL IS NO PROTEIN	WATER OF AVER APPRAIN VIRIES (STRAIN M)	2						-	-	
PACKET WOME	HAYPOTHETICAL IS KD PROTEIN	WILLIAM COLOR MAN WE CAN AND CO.	65.93							-	
CAVON 180A	HAYPOTHETICAL 13 KD PROTEIN	WHITE CLOVER MUSAK VINUS (2) WHITE CLOVER MUSAK VINUS	92-119		L				+	+	I
	MATORIA 11 CKO PROTEIN	AVIAN ADENOVIRUS GAL! (STRAIN PIELL'S)				L					I
YOU ADED!	HINDER STORY OF THE PROPERTY	THE ELECTRONS TENAX VIRUS I (STRAIN KIA!)									
PYORA TTVI	HYPOTHETICAL S.I ALV PROTEIN	THE BLANSE OFFICE TENAX VIELS 1 (STRAIN KRAI)	Ž								
PYORT TTVI	HYPOTHETICAL 26.8 KD PROTEIN	THE STATE OF THE PARTY OF THE PARTY (TAILS)	1.1						-	1	Γ
PYORO TTVI	HYPOTHETICAL 7.3 KD PROTEIN	TREADMOND LEGIS AND }{1}$	+								
INTE MICHE	INTROPPETICAL 13.1 KD PROTEIN	THE ENCORPOREUS I BLACK VILLES I (3) FAMILY ROOM	17.3	L						†	Ī
	GONDOTTORICAL PIZ PROTEIN	NCE TUNGRO EACELLIFORM VIEWS	44.71							+	Ī
	LICENTURY PARTIES	NCE TUNGED PACELLIFORM VINUS (ISOLATE PRINCE)	101.03	104.157		L	L				T
PYPIZ KIBVE	THE SAME TO SECULD IN SECULDS	RICE TUNCALO BACTILIBORIA VIRUS		101	ļ				Ц		
PYTZA RTBV	HYPOTHETICAL PACEDICAL	PROFESTINGED BACHLIFORM VIRUS (ISOLATE PHILIPPINES)	101-101								
PYP24 RTBVP	KYPOTHETICAL PA PROJECT	PACE HANDED BANTIL ISOBAL VIRUS	26-107	17:74							
PYPE RIBY	HYPOTRIETICAL P44 PROTEIN	THE WALL BY THE PARTY (ISOLATE PALLIPINES)	\$8-107	187-201							
PVPAL RTRVP	HYPOTHETICAL PM PROTEIN	RICE LUMBER SALES OF THE EAR BOY WEDERS VALUE	14-11							+	
PVPA1 NOVAC	HYPOTH PLO PLS STEGION	AUTOGRAFIA CALIFORNIA PO POR VIETBOSIS VIRUS	335-352							\dagger	
STATE OF THE PERSONS	EGION	ORGYIA PSEUDOISUUALA MULLICAS SUST CALIFORNIA VIENE VIENE	116-133		L					†	
200	HAPPOTH 23 4 KD IN POLYMEDSUN STEGSO	SAUTOGRAPHA CALIDONICA PULLCAA PALITEOANSIS	253		L	L				1	
			5	80.05	156-183	_	L				
100	STATES OF THE PROPERTY OF THE STREET			-							
YOU AND				1							
PAIN HSV80	HINDER STORY IN	HERPHES SIMPLEX VIRUS (TYPE 6/ STRAIN GS)			-	-					
PYRU1 HSV60	HYPOTHE ILANGER TO	HERPER RIAM EX VIBUS (TYPE 6 / STRAIN US)	2		$\frac{1}{4}$						
PYNY HSV60	KYPOTHETICAL PROJECT IN	LEGISTER EXCEPT BY VIRUS (TYPE 6/ STRAIN US)	40440				-				
PYRF4 HSV60	HYPOTHETICAL PROTEIN AT	Ann State Creat Visits	1013	_						T	
PYRET DAVE	DEPETITIVE PROTECN ORUT	COLLO CARROLL AFTER A TO COMPANY A CHEM	7.34							t	
PWAG VACCE	٢	VACCINIA VIII.S (81 MAIN CONTRACTOR)	1113	L						1	
PYVAH VACCE	Γ	VACUNIA VIEWS (3) INAMA CONTRACTOR	19.71	L	L					1	
2000	T	VACCINIA VINOS (STIVAIN CUPEATANCEA)	144.33	-	-	Ŀ				1	
TANK AND	1	VACCINIA VIXUS (STRAIN WR.)				-	-	-			
PYNDS VACEV	1	VACCORIA VIDUS (STRAIN WR)	2	1	-	ļ	-				
PYVDH VACCV	1	VACCOMIA VIRUS (STRADA COPENHAGEN)	į		1	1	-	-			
PYYCE VACOC		CROTENARA VIRUS (STRAIN B95-1)	152-179	_		_					
PY21.3 EDV	Γ	EZIEMPOWAN 1									

TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

PROTECT PROT	# M. T.	7	All Virues (as becteriophs fre)	T	APEAL	AREAS	ABEASIL	ABEAS	ABEAL	AREAL	AREAL	48132
V. C. CATACHER ACCOUNTS CONTRIBUTION CONTRI	17.17				ī			Ì	j	Ì		
NEW REYMENTED NEW REYMENTED NEW REYMENTED NEW REYMENTED NEW REAL PROPERTY	N.			125.61	İ						Ī	
The Company of the	VAVA			105.031								1
The Theory Decay Profile Avian will control to the profile A	247			ī	3						•	
THE TANGED SHORTER AVAILA PART LOC TO AN 1919 WILL BY THE CONTRACT OF THE	1			1	197							
TOTAL COLORED TOTAL COLORE				ī	100 7	Ī						
CONTROLLE PROPERTY CONTROLLE CONTR	Y.		2	1					Ī			•
ACCESSION OF THE COLUMN CO	AVE.								Ī	İ	İ	i I
ACCOUNT OF THE PROPERTY OF THE STATE OF TH	TAK.									Ī		
A	LE HSVBI	100	TANN 145		1							i
Characteristic Corporation	UIRMI			461.434								
DATE OF THE PROPERTY 100 PROPERT	IL HSVD	CLYCOPAGIEIN 6-1 PARCUASOR		1	ī	631-603						
STATE OF THE PROPERTY IN COMPANIES AND ALLES	20010		DOVING DARWOOFFICERCY VIRUS (1904-ALE 199)	Ī	7	100.334						
Dev Control Everal Eve	l		DOVING INCLUDED CREMEY VIRUS (ISOLATE 177)	į.				Ī				
Dev On The Color Experiment	١		GANGE (BIRGING VALUS (ALGENCAM ISOLATE FLX)									İ
DAY OR THOUGH DAY OR THOUG			SALAR TRIBERIAL CHELL JAMERICAN ISOLATE VOND	Š							1	
DEV POLYTOLIEN DOVING LIBERTAN FOR THE STATE			CONTROL CANADA C	18.31								
DEVICE CHEEN DOVAGE LEAR LAND WILLIAMS DOVAGE LEAR LAND DOVAGE	N BLVAU		DAME LEUKENER VIII ON INCHES AND INCHES	11.313			•					į
SECTION OF THE PROPERTY SECTION OF THE P			SOVE CELECATA VALUS (BELCEMA ISOLATE LESUS)		1					İ		
VAN PACTIFICIES VAN PACTIFICATION VAN PA			BOVDOR (EURENDA VIRUS (BELGIUM ISOLATE LOSS)									1
DEV NOT PROTECT INCREMENTAL AND SHAPE AND			COLUMN TRIBETOR CONTRACTOR AND AND ALL W. 13	2.5			İ			!!!	:	
INTERCENTATION 1990	CV BLV			5.45							-	i
UNIVERSITED PROPRETED PR	ELA PINO	EURAMINIDASE	BOVING PARAMINING A VINCE	16.0	111.202	13.314						
		175	DOVING PARAZNELUENZA J VIRUS		1	440.401						
		152	BOVING PARAING LIENZA I VIRUS									<u> </u>
MAY DAY PROCESSED MAY DAY DAY PROCESSED MAY DAY PROCESSED MAY DAY PROCESSED MAY DAY DAY PROCESSED MAY DAY PROCESSED MAY DAY PROCESSED MAY DAY DAY PROCESSED MAY DAY DAY PROCESSED MAY DAY DAY PROCESSED MAY DAY DAY PROCESSED MAY DAY DAY PROCESSED MAY DAY DAY DAY DAY PROCESSED MAY DAY DAY DAY DAY DAY DAY DAY DAY DAY D	CA. P. P. S.	1	STANDED TO BE A STANDARD OF THE STANDARD OF TH	361-331								
UNIT DOUGHEST A PRINCIPATION 100000000000000000000000000000000000	M 120		TANKS CONTRACTOR OF THE PARTY OF THE ACT AND A CHANGE	3							-	ļ
UNION GLYCOPROTERM 100000 111-101 111-	AVER 961	INA POLYMETASE ALPIN SUBURIT	BOVING RESPIRATORY STREET THAT THE STREET	10.04	707	2	102-505	416.331				
MATINE G. VCOPOTERING GOVER BLIFER DE PRECINCA MINO) 115-101		CONTRACTOR VIOLENTE BY PRECUESOR	BOVING RESPONATIONY SYNCYTIAL WINUS (STRATIN ASSEMBLE									
MAINTERFORD 1000000 1000000 1000000 1000000 100000 100000 100000 1000000 100000 100000 100000	3	CHINATOR CONTRACTOR IN	BOVDE RESPIRATORY SYNCYTIAL VIRUS (STRAIN AS1904)				İ					
MAINAY CONTRIBUTE OF CUSTOM MAINAY CONTRIBUTED	AV BESVA	MAINA W. I. COT POLICIO PAR	SACKER BEGINNERS TO THE VIEWS (STRAIN ASIMA)	316.766								ļ
	MAT BRSVA	MATRIX PROTEDI	THE REPORT OF THE VALUE OF THE PROPERTY OF THE	10-65	15+ 2n3	116.243	1000					
Line Line	GLF BRSWC	FUSION OF YCOPROTEDY PRECUESOR:	SOVER TEST AND THE SOURCE SOURCE STATE OF THE PROPERTY OF THE	61:13								1
THICK CAPORETER CLEECARD LEAVES	CLO BASVC	MAJOR SURVACE CLYCOPROTEIN O	DOVER LEAVEN LAND THE COMMENT OF THE	1	134.702	116-310	115.47	11.13				
EWY POLYMOTER CLASA & MADRA LLEGAL VALUE 11-110 1	2000 250	FINGON CLYCOPROTED! PASCURSOR ,	BOVING RESPONDED SYNCYTIAL VIRUS (SINAIN ROPE)	1								
It POLYPROTER CHREWARDS INCRECKY VALUE 17-15 11-15 1			CAS BAS BAURDA LEUKENIIA VIRUS			4	116.464	417.416				
VIV. FACITIES CINDA AND EL SACINOCIS (CENCY VIRUE) 13.70 141-411			CHAPANZEE INMODEFICIENCY VIAUS									
MOLINIA MOLINIA CONTONTIA LABIN GIOCENTA MOLINIA MOL	Z A		CHALPANTER DIRACHODESICIENCY VIRUS	-								!
CONOMINE COTTONIAL LABIN (NIONE) PARL COLAVRUS (FIZAMELS) 13.1 15.1 1	ביונים		CHANNER BANDADE MIEWY VIEWS (SIVICPZII)	143.200	579.512							
REGEAL EL PROTECH REGEAL OF THE COTTON ALL MANIET STATES STATES 111-111 111-11	SVC2		THE PARTY AND PARTY OF THE PART	-			_					
CENCRE FOR THE PROPERTY COTTON A A A A A A A A A A A A A A A A A A A	T) Chrys	_	COTOMIAL MASIC (SIGNE) A CALLOTT MASON SIGNATURE AND A CALLOTT MAS									
	200		COTTONIAL RABBIT (SHOPE) FAULUMA HAD STRING TO THE STRING THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO THE STRING TO			÷						_
CENCRE FOR TREOTER DESCRIPTION DESCRIP	1		DENGLE VISIUS TYTE I (STRAIN SONCAPORE STRING)				2001 1001	1111				
CENOCA FOLTROTTEN DESCRIVED 1976 [STACK IMPACA] 144 111 144			DENGLE VOLUS TYPE 3 (STRAM 1668))			***		***	36.01			_
CENOCIE CENO			DENCINE VILLE TYPE S (STRAIN 1444) POX 53)			7.	-	-	<u> </u>			
CENCOR FOLTROITEN DESCRIVENCE FOR STATES PRISESTED	5000		PREMILIE VINITE 1 (SINAIN JAMANCA)	2		-	-					ļ
Choose Rolling	OLG DENU		PACIFIC COLOR I VPE 1/51BADI PRISONEIS	1944-1973		-	10.00		-			
CENCRET OF TROUGHS DESCRIPTION DESCRIP	OLO DENIE		SECURITY FOR STREET TONGS 19741	1	=			_	-			1
CENCAR POLYTROINEN DESCRIPTION 1911-1911-	OLG DENT			133.164	1843-1561		1464-1521	1940-1014	1			1
Chocket Por Tradition Duck teration Duck	OLO DEN	GENOME POLYPROTEIN		3865-3910	=	1341.3361						
DEATH OF THE STATE DUCK REATHER VALUE DUCK RE	OLG DEN	GENOME FOR YPROTEIN	DESCRIPTION TITLES	1 2								_
DEAT FOLYMEANT DUCK REPARTITE WINNERS CHARAL BUCK STOCKES	Sect to bob	DHA POL MERASE	DOCK HOLD B VIACO (DROWN SHAMESON DOCK 1997)	15								
UAGE TECHNICAL PROTECT UAGE TECHNICAL PROT	Sect 10 hor	DNA POL TABANSE	DUCK IEPATHIS B VIRUT (STRAIN CIENA)		١	ļ		<u> </u>			<u> </u>	<u> </u>
CARGE TECHNORISM ESTEDNIAM YOUR STRAIN BIT	1	THE POST WOLLASS	DUCK HEPATTIS & WRUS PARTIE SILANGIAI DUCK ISOLATE 311)				1					<u> </u>
VOLUM PROTED BAD		TOTED	EPSTEIN DARA VIRUS (STILATIN BPS II)		_		-		1			<u> </u>
MYPOTRETECAL MOTERN SALF EFFETN SALE VILUS (STAND SSF 1) 11-71	100		EPSTEIN BARR VILLE (STRAIN B95-6)	=	2							<u> </u>
	ILOS EDV	VOUCH PROTECT AND ADDRESS OF	COCTEDA BARE VIRUS (STRADA 093.0)	?	_							1
MATORIE MALL PROTEIN BLATA VEGUS (STAIN 1851) INTO THE WALL PROTEIN BLATA VEGUS (STAIN 1851) INTO THE WALL PROTEIN BLATA VEGUS (STAIN 1851) INTO THE WALL RELIGIATION BY STAIN BLATA VEGUS (STAIN 1851) INTO THE WALL RELIGIATION BY STAIN BLATA VEGUS (STAIN 1851) INTO THE WALL WALL WALL WALL WALL WALL STAIN WALL STAIN WALL STAIN WALL STAIN WALL STAIN WALL STAIN WALL STAIN WALL WALL WALL WALL WALL WALL WALL WAL	ULII EDV	MATORIE INCL. PROIEST SECTIONS	SPECTED BARE VARIS (STRAIN 09). 6)	115-213	-							<u> </u>
INTOTES FIGAL FOURTH BLAT EPHEN BARE VIEW SHAIN BIS IN 101	4 5 CE	PROB DRA REPLEATION PROJECT USE.	COLPERATE VIRIS (STRAIN B91 a)	8							<u> </u>	<u> </u>
INTODICE ILCA POLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTODICE CASTOP FOLITY BOLLY INTO INTO INTO INTO INTO INTO INTO INTO	uii EDV	HYPOTHETICAL PROTEIN BALINA	STATES OF THE COLOR AND THE STATES OF THE ST	101	_							
HANDE CAND PROTEIN PROMISE READILANCE CITY COPROTEIN FOR THE STACK BOLD STACK BOLD STACK CONTROL OF THE STACK CONTROL OF THE STACK BOLD STACK CONTROL OF THE STACK BOLD STACK BO	FB (15	INPOTIETICAL PROTEIN BOLF	CONTRACTOR CONTRACTOR OF THE C	167.676	_	<u> </u>						
PROPABLE MEGALANG CLYCOROICM EPTEM BALL VALUE SIGAM PET 1 CLYCOPOLITIN CATE PRECAKOA EPTEM BALL VALUE SIGAM PET 1 TO TOPE OF THE CATE PRECAKOA EPTEM BALL VALUE SIGAM PET 1	VCV EI	KAJOR CAPSID PROTEIN	EFSTER/GAMM VIRUS TO THAT BY THE	101.101								
CAYCOPOTEN CRISPACCURSON (ESTEN-BANK YRUS ISTAAN BY 1)	VCL 2 EBV	PROBABLE MEMBRANE GLYCOPROTEDY	EPSTECH BARK VINUS (STILLAR BYS) B		27.114							
PA VECENIER CALIFOLDINGON (EPSTER) DAMA WAUS (STRAND BYS.1)	VCI B FRV	CLYCOPROTEIN GP110 PRECURSOR	EPSTEDUBALL VIRUS (STRAIN B91-1)			ļ						<u> </u>
	NU PRO	RSOR	EPSTEIN-BAAR VIRUS (STRAIN BPS-II)				1					
BEODARI F LEMINALING ANTICEN CPET. EPSTEIN BARA VIRUS (STRACH BOS 4)		GEN GP85	EPSTEIN BARA WINUS (STRAIN BOS.4)	104 144								

TOTAL PARTY	F12121		ī	ARCAI	ANCAS	A A Z	AMEA S	ARTAG	N V V V	N N	ARIA 6
72.0	CAPSID PROTEIN PAR	VELIS (STRAIN BOS D)	!	ī	7		_			:	<u>;</u>
PVTER ERV	ROTED	(STRAIN 69): ()	21:30						İ		
		CHART IN THE BALLS	100						İ		
l	THE STREET STREET		l				-			1	:
1	MINOR IN THE PART OF THE PART					Ī				Ī	:
	HAYOUR IKAL BLID I MOILEM									-	-
	HTTO ILE INCAL BELLI PROTEDI	(SIRAIN BY)-D)	į								-
WED EBY	BZLF I TRAMS ACTIVATOR PROTEIN		R								1
Povel Esv	MAJOR DHA-BBEDRIG PROTESY	STRAIN BYS. ES	8	1901							į
PEAL EBV	EASLY ANTICEN PROTED/R	ş	3:0								
VED 164.	LATENT MEMBRANE PROTEIN !	EPSTEIN BALLA VIDUS (STRAIN 695.1)	151.53						İ		İ
STATE OF THE PARTY	CENE TE ENDINE PROTEIN	EPSTEIN BALL VIEUS ASTRADA DOS. 13	100						-		
1011	I A VENING LANGES AND DE APERILA	CONTRACTOR LANGING AND AND PARTY.									
		STATE OF STATE STA									
Trees can		EZ SIEGRA ZAGUS (SIEGRAFIA)									
PUCAS MSVD	MAJOR ENVELOPE GLYCOPEGITER 100	EQUIPM HEIDESVIAUS TYPE I	345.175								
PVCLC MSVED	CLYCOPROTEIN C PARCLASOA	1 TAAL SOYAS SOYAS TO THE SOYAS SOYAS TO THE SOYAS SOYAS TO THE SOYAS SO	134-151							Ī	
BVCL B MVE	ICL VCOMBITERS RECTARION	FOUNDER HEADER WILLY TYPE I ANGULATE HYSTEAN	441.410	19.96					Ī		
VENT B DAG		PE I CT DA PA A MAIL	9						Ī		
	26.00								-		į
TAILS POST	S C C C C C C C C C C C C C C C C C C C	ITE I DIEM ADVI		Ĩ					į	İ	•
VATOV MSVED	İ	EQUARE REPUBLISHING 1 VPE I (STRAIN ABA?)	331 310								
PHELL HSVED		EQUIDGE IEEESVINUS TYPE I (STRAIN ABAP)	=======================================	: :::							Ì
PRORI HISVED	ARGE CIV	EQUING HEADES VINE I (STRAIN ABA)	35.103						ĺ		
PTECU HISVER	I ARGE TECHNORY PROTEIN	THE LIGHT AND	230.344	10, 191	1304.1313						
PAR AL LICKER		OF LICENSING ABOUT	440 649				Ī				
	l	-11]						İ	į
MEN HOVE	N.	ΞI	147.386	Ī	ĺ						!
PA 21 HSVE	•	Ē	=							İ	ŀ
PLESS HIS WEB	ľ	EADES VINUS 177	35.24	913-1014							
NAME OF STREET	CANA BEDI ICATION PROTEIN IS (5	PREVAIN TY	110	47.0						ĺ	İ
										Ì	
WOU HISVE		EQUAG IERGES VICOS 177 I 131 KAIN ABAT)	2					İ		ļ	į
VOLD HISVED	•	ERPESVOUS TYP	977	74.76							
PVCECO HISVED		CERESVIAINS TYP	111.416								į
VD-0 115 VEB	PROB INTEGRAL MEASIRANE PROTEIN	CAPESVIDIS IVE	11.11					:	:	i	:
PVF26 HSVED		ERPESVINIS IVPE I (SI					ĺ			:	:
PYCOD MSVEK		REPENDENT TYPE	. 21.57					-	i 	:	į
PVCI B HSVEL	CA. V. COPROTED DA DI PRECTUSSON	ERPESVILLE IVPE LIST	100	0.00			Ī		i	!	!
POET IL MENER	5	TENEST CONTRACT OF STREET							İ	-	1
10000	12	CORDIN STATE A					Ī			İ	
										į	
12.6	GLICUTADIEM PRECUESOR			2							İ
PVCEO PISVE	CLYCUPOLEM OPPLETUNOR	EQUINE IRRESVINOS I VEE 4			İ				į		
PDC1 IISVEA	DECKTO STRIPASSIN MOCHEDROLASE	15 1 TFE 4 (5 (RAIN 1942)	2			i					
PVEJ PAPVE	PROBABLE ET PROTEON	EUROPE AM ELK PAPILI OMAVIRUS	20.50								
	ENV POLYPROTED	TAUS (ISOLATE PETALUNIA)	630 410	13.149					İ	ļ	
PPOL FIVE	POL POLYPROTEIN		42.43							İ	
	ENV POLYPROTEIN		13 15	12.8						Ī	
١	EXV POLYPROTEEN		15	21.744				Ī	!	İ	
PENY PLYCS	ENV POLYPROTEIN										; i
l	MYC TLANSFORMOND PROTEDY		27.70				Ī			1	;
7	LAYC TO ANGLOS LONG PROTECTION	FEI ING A FIRE BATA VARIA				ĺ		-			i
1				İ					j		į
١	ENV PUL TEROIEIR	PELINE LEGIENIA VIRUS (SIRAIN ACA ASCOW.)	5								
PENV FLVIA	ENV POLYTROTEIN	FEINELEUREAIA VIAUS (STICAIM LAMBDA-DI)	30 31								İ
	DAY POLYPROTEIN	FELDIE LEUKEMIA VIRUS (STRAIN SARMA)	407.516						İ		i
	DAY POLYTHOTEIN	FALES CO LA LIN ENGLY VIRUS (150LATE 51)	551.55								i ;
L	DAY FOL 19 LOTE IN	FACEND MATION I EIN LADA VIRUS ASOL ATE FROM						-	: !:		!
NA LA TA	DAY FOR YPEGIT DA	PREDICTION LEGIC END VIRIES LISON ATE PARTIES		; ;				1	: .		
PENN CALV	ENV POLVPROTER	ELFLECTOR VIEW				-		j 		:	
	Contractions of the Contraction		Ē	2					-	-	1
200	CAC POLTFROTEIN			411.434						!	
7	POL POLITICISM		115-162	416.701	į						
1040	DHA POLYMERASE	GROUND SQUIRAFL HIPATHIS VIRUS	131.135					İ			:

-75	1	į		. :	:		į	_ ::	i		!	:	:	i	_	_	:			•	_	:	-		<u> </u>			_	:	!	į	ļ	i	:	-	 i :	_	-		j	_					į	-	1	:	•	i	1		i	:	•	-	1		1	7
1 48532	 			<u> </u> -		1	<u> </u>	-	<u> </u> 	<u> </u> 	<u> </u>	:	!	!	1		! -	<u>:</u> :	:	<u>i</u> ::	<u>-</u>		-		!	<u>!</u> 	<u>.</u>	1	:	:	1	1	:	:	•				<u>_</u> 		<u> </u>	İ				_ <u> </u>	<u> </u>	<u>-</u>	-	i	-	<u> </u>			•		<u> </u>	 	+		4
1 ABEA1	<u> </u>	-		<u> </u>	<u> </u>	<u> </u>	1	<u> </u>	 	<u> </u> -	<u> </u>	: i	<u>;</u> !	<u>:</u> -		<u> </u>	ì	:	<u>!</u>	<u> </u>	_	<u>i</u> :		<u>. </u>	:	!	<u>.</u>	:	; ;	<u> </u>	1	1	<u> </u>	<u>:</u> i					<u> </u> 	<u> </u>	<u> </u>	<u>i</u> 	<u>L</u>	<u> </u>		_ <u> </u>		<u> </u> 	<u> </u>		<u>:</u> 	<u> </u>		<u>-</u> 	i	:	i	 	<u> </u>	<u> </u>	_
14142		<u> </u>		<u> </u>	<u> </u>	1	1		1	_	 	! -	<u> </u>	-		 -	1	1	!	! 1	· ·	i		_	! -	1	: i	:	<u>;</u>	-	 	1	1	1			<u> </u>		! 		<u> </u>	<u> </u> 	<u> </u>	<u> </u> 			į		_	-	<u> </u>	<u> </u>		<u>. !</u> 		!	_	<u> </u>	+	<u> </u> 	_
17717						1	1						ļ	_		<u> </u>		<u> </u>		i	;	-	ļ	_		<u> </u>	1	-	!	<u> </u>	<u> </u>						<u> </u>	_	<u> </u>	_		<u> </u>		 -	L				_	3	1	_					<u> </u>	1	$\frac{1}{1}$	-	_
7																					 - -		_							-										<u> </u>	_				<u> </u>					8									4		_
ABGAL	2	1454-1411	141.141									İ														-	!																							200						11.5					
4364	17:1149	1117-1100			Ì	İ		10)	10)-114			1	į		Ī						Ì			Ī		Ī		İ																						10.05	Ì					=					
ABIA! A	100	1031-1601	100	1	1		=:	Ξ	101.10	<u> </u>	İ	<u>.</u>	-	2003	945.1073	ALIE SING				-	1011			=			i	;	-	2	2	2	1		İ	į		900			7111		Ī							116.763	(0e 0g		36.38				29.166	2	33.33		
			_		1	╗	-	_	_				_	=	7	ī	E	21	!	2 :	_	=	_	i			-	<u>-</u>	2	=	2	2	11:33		<u> </u>	240.275	,	13	•	=		•	. 500	9	2	=	<u> </u>			201.00	=	=	133	Ξ.	1			, 1	_ i	134-303	
ABEA1	2	 	1			=	2	101.101	100	12.22			202	103.13	707.73			8	ż	=	2	2	2		1	<u> </u>	ġ į	<u> </u>	8	<u> </u>	2	<u> </u>	i <u>i</u>	! <u>:</u>	<u> </u>	2	100	1				<u> </u>						 -	<u>!=</u> 	2	3	<u> </u>		<u>:=</u> 	<u>:§</u>	<u>:=</u> 	<u>:</u> 		Ĕ	2	
All Virones (no backerlaphs (ct)	VICEUS 1 140 110 2010 404 105 105 1	HEPATITIS A VICTOR OF THE COLUMN TO THE COLU	HEPATITIS A VINUS IS INCHAIN 24A)	INSPATITION A VIRUS (STRAIM 4)C)	LIEPATITIS A VINUS (SILAIN CRIDS)	DISPATIBLE A VIRUS (STRAIN GA74)		15	THE CALLED A CORP. A CORP.		IS D VIRUS	IS & VIRUS	SITE OF			PEPATITIS C VISUS (150C A IE 11)	Ĭ	S CVE	Š	Š	THE ATTENDED ON A PLANTAN	į	İ	Ì	IGPAINIS DELTA VIRUS (ISOLATE AND PRAM)	=	2 061 7	100	- HEPATING DELTA VIRUS (1504 ATE ANGRICAN)	5	THE THIRD I WASHE SCHOOL SCHOOL STORY	THE STATE OF CHANGE AND LIVE AND LAND AND IN		THE STATE OF	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	STATE OF THE PARTY	TOTAL STATE OF THE	TO THE STATE OF TH	5 II	THE ROLL STREET WHICH IS NOT THE TANK THE THE TANK THE TA	MADE A	51	IGANES SOOTLES VINOS (11TE 1/2) INAMA 1/3			Company of the state of the sta		THE PART OF THE PA	THE PART (TABLET VIEW	Ž	12	THE SECTION OF VINUS LIVE 67 STRAIN GSI		INDICES SUPPLIES VALUE OF STRAIN CS.		THE PROPERTY OF THE PARTY OF TH	THE PERSON NAMED IN VALUE	CATE 675	HEAVES SEIGHT VINUS (TYPE 6/STRADI LICANDA-1101)	SURIN X STACK STACK	
1107417894	IPROTITIE	GENOME POLYPROTEEN	CENCLE POLYPROTEIN	CONTRACT DAIL VOROTEDA	MELLOS POR COMON PRINCIPAL	CONTRACTOR OF THE PROPERTY OF	CENCINE FOR THROTEIN	GENCIAL POLITICISM	CENDRE POLYFILDTEIN	GENOME POLYPROTERY	DNA POLYNERASE	PAR WERES	-	CENORE POLYHOUTH	GENORGE POL YPROTERM	GENOLE POLYTROTEIN	CENTAL POLYPROTERY	CENTRAL FOI VALOITON	Charles Let Gardiere	THE PERSON NAMED IN COLUMN 1	- Concrete Control Control	7	- 1		DEL IA ANTIGEN	1	DELTA ANTIGEN	77.00	-	-	MONESTRUCTURAL PURE TITLE	ī	M-STRUCTURAL FOLYKOTEW	HON-STRUCTURAL POLITIKOTEIN	DNA POLYNEJIASE	MAJOR SURFACE ANTIGEN PRECURSOR	THAMSCRIP HOMAL REGULATOR HEAS	DOGDIATE EALLY PROTEIN ESS	LAIGE TECHNENT PROTEIN	VIDION PROTEIN ULA	VILLON PROTEIN UL.) 4	PROTEINULT	DMA-BD/DD/G PROTEIN UL-12	VINION PROTEIN ULA?	CLYCOPROTEIN CPAECURSOR	ALPHA TRANS-DAD FACTOR 18 KLD PRO	VINOR PROTECT U. 47	ALPHA TRANS. DED FACTOR 17 KUPAU	GLYCOPROTEDY C PRECURSOR	CLYCOROIEM E PRECUCO	ī	GLYCOPROJEIN H FAELORS		IIYYOTIE IKAL PROTEIN ILI	- 1	1	MAJOR ANTICOPAC STRUCT	- 1	Ī	T	
PCCEME	THEMANE	PPOLO HOAVE	PROLIDITANE	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		POLO INA	PPOLO UPAVO	POLO IPAVII	PPOLO IBANL	PPOLO IBANA	Phene impay	17941		PROLO JICVI	POLG HCVBK	PPOLO HCVI	10.01	10-01			PPOLO INCVIA	POLO HCYTA	PANT HOVAL	PAART 18VD)	PAANT IIDVS!	PAANT IBVES	Carre Land		WANT IDON	PAN PONE	FOLN MEVEU	POLN MENGE	FOLK IS VAC	POLY MAY	POPOL NOTING	PVACSA IORNICE	PEAS HEVIL	PER MSVII	FTICE RISKII	PUL 66 MSVIII	PUL 14 HSVII	PLEST INSVIE	HEAT HIVE	PUL ST 18VII	PVCLC HSVII	PATE MIVIE	MA 43 HISVIE	PATES HISVIE	PVGLC MSVIK	VCL HSV	300	1246	PYNJI IISVAG	PTRES BISVAG	PYRU HS VICE	PYTU 4 115 V&G	AND HEAD	FIG.13 HSV6U	74.73 ISVE	NA IBA	

PCT/US95/16733

11						- 1				7	7	٦	7	Ī
1	Profits	NAUS.				338	45190	ABEL	3	38	PER	A LATE	ARELIB	6BC.) 2
		HEAVE SYMUS SADA	TRI (STEAL			_								
POUT MSVIA	DROLASE	HEAVED WALLS SAID!		410		110-01								
•		GENERALITY SALVERY		= = = = = = = = = = = = = = = = = = = =		-						<u> </u>	<u>-</u>	į
THE DEVEL	AMERICA PAR	PARTICIPATE STREET	1217/10/	117		13.5	18.00					-	1	!
	١	AN A DESTRUCTION OF THE PARTY O	711										İ	:
ALM HOUSE	1			2								İ	i	:
VKITH HSVSA	THYNUDOK KINASE	PRINCESVINOS BAIN											İ	į
TEST HEND		PERFESTINDS SADA				14-331		•						
PTECU MSVSA	ENT PROTED	MERPESVIAUS SAIMIN	IN CHAIL	=======================================		12.603		333.014	346-698	149.886	#30:1013	1467.1491	10: 1111	!
PTYSY MSVSA	INVAIDYLATE SYNTHASE	HERDESVINUS SAIM	ITALI (STRAIM			10.14							İ	
PIE DE MENEA	VIBRAL CENT AS PROTEIN	INCRETE SVIEITE (AISHE)				1	101.14	141.403				İ	İ	i
1000	Color of the Color						1	18				İ	Ì	
	COLETA	SERVED SAIR					100				İ		İ	
AL SEAS		HEAPESWARDS SADA	12 ST TA	=======================================	-	101.235								
FE 37 HSV\$A		HENES WAUS SABAIN		=======================================		19	12:33					İ	<u> </u>	
A 11 11 CAN	AC AL PROTEIN	THE PROPERTY OF STREET				2						İ	Ì	ĺ
	١													
ME 73 HSVSA	HITTOME INCAL GENE 33 PROTEIN	HENVESVATUS SALMIN					-						İ	i
PLE IN HIS VSA	HYPOTHETICAL CEME 14 PROTEIN	HERPESYINUS SAM	UR) (SIRA	=		Ş								
PULTI HSVSA	HYPOTHETICAL GENE 31 PROTEIN	HEAPESVIAUS SAINGIA		===		17.122							-	!
PADAC MEVEA	IMACO DAMA CO VODEM ACE	IN THE PARTY CANA		2		111.111						i	-	:
					İ					Ī	Ī	-		;
WCA HSVSA		IL KILLINIKUS SAIM				11.11								
PVCS HSVSA		PERPESVINUS SAIN	IRI (S18A)	=		36.165								
PVC48 HSVIA		IEMPESWAUS SAIN	IN SIES	=======================================		100.001							Ī i	
SUCCESSION OF THE PARTY OF THE	HYDOTHETH'AL CENE OF BROTEIN	INTERESTANTING CALL	1			27.50	ļ						1	
											İ	Ī		
PVGLI) HSVSA		HE KVESVINUS SADA		(1) N		2								
VDO HSVSA		HEAPESVIAUS SAIM	ILI (SIAA	22		10.00								
PURE DEVICE		IN THE PARTY OF THE BANK	1			-	 						Ì	-
						L	-				Ī	Ī	Ī	i
Perio III PAR		THE PLANT OF THE PARTY OF THE P							j				Ī	
PVP40 HSVSA		ILEANE SVIRUS SAD	IIII (SIRA)	=======================================		20:50	344.372							
PVP 15 HSVSA	PROBABLE MEMBRANE ANTIGEN 15	HERVESWINDS SAIN	IN CHANGE	137		101.100	939-019							
POND! MINE	MAINE DIMA. BRINDING PROTEIN	HE SO STANDER SAIL	THE SERVE			10.16	\$11.510				Ī		İ	İ
											i	1	İ	İ
12 H3 12	CTCLIPTIONOLUG	HERICOANOS SAN		TO COSTANT AT								-	_	:
PYDHU HSVS7	HYPOTH 34 I KD IN DIGH STECTON	DERFESVINUS SAIM	THE COLUMN	N 484-77]										
PYDEL HISVIC	LITTED THE TALE IN DIGHT STREETON .	ICEPESVIRUS SAIMIN	111 (SUBC	COM C / STRAIN 400)		2.5					!		- : !	
PYDII HSVSC	HYPOTH # 9 KD IN IND R INEGION	HE LIPES VIRUS SAIN	IN (SUBC	SUBGROUP C / STRAIN 460)		1						:	i I	
2 1 CAN	DO NOT VALUE OF	HINADR VINEROFIFICKENTA VIRUS	FICKERNA	VILK		10.040						İ	<u>-</u>	1
TOTAL PORCE		THE MAIN CYTONES	THE PARTY OF	CIRAM ADIAN		1		-				Ì	İ	Ī
171	20 810	THE PARTY OF THE P	T AUTOM	CIEVE AND ADDRESS.									İ	
	THOUGHT INCIDENT TO CO.			Total State of the		1						j	Ī	ļ
AND MONA			COMMON	SIRAIN ADION)		1					Ì	j	1	Ì
PER HONA	2	HEREAM CTTCHECALOVINUS (STRAIN ADIOV)	COMMIS	STRAIN ADIOS)		3	ĺ					j		
PINEL HEMYA		HEALT CYTOMEG	COVINIE	SILAIN ADIGO	1	7								
	1030	3	SOMPON	STAIN ADIGO		633.649								
PTEGU HOMYA	T PROTEIN	3	TOVINUS	IN CYTOMEDALOVIRUS (STRAIN ADIAS)		136-156	100						Ī	
1		3	TOVIEUS	STRAIN ADION		1						Ì	İ	Ī
ı	1	IN BALLAN PYTONA GA	T AVELIA	STRAM ANIAN		103.134					Ī	Ì		
		STATE OF THE PARTY	1000	S I A A SA A SA A SA A SA A SA A SA A S							-	İ	İ	
- 1												İ	İ	ĺ
- 1				(SIEVIN ADIES)									ا	
	INTOTICETICAL PROPERTY ULTI	RUMAN CYTONEGA	LOVINUS	(STRAIN ADIES)	-		151.211							
PULIS IKMYA	INPOTIETICAL PROTEIN ULSS	INDIAN CYTOMEGALOVIAUS (S	LOVINUS	_		133 362								İ
PUL () IKMYA	PROTEIN ULA	INDIAN CYTORIEDAL OVINUS	TOVINO	(STRAIM ADISE)		=======================================	11710	2.38	107.153				İ	
ALIE SO INCLUDA	PROTEIN LE SO	INDEAN CTIONE GALOVOLUS	LOVBUS	E		159.124				-			Ì	l
ME (9 INC. VA	MONOTHER PROTEIN U.S.	HABAN CYTONEG	LOVBUS	STRADI AD1491		10.5							Ì	İ
1	SECTION AND AND THE PARTY OF TH	BAND SYLVERGAL OVER	TI STATE	CONTRACTOR AND ADDRESS.								l	Ì	1
	TACO CAN ALL TACOLOGY OF THE PARTY OF THE PA						İ					-	-	-
THE SECOND	III.7) GLYCOPROTEIN PRECURSOR	TANK CLICKE		DIRAIN ADION)								<u> </u>	i	i
MEN INChA	HYPOTHETICAL PROTEIN UL 74	HAMAN CYTONG GALOVIN	AL OVERUS			=								
PLE 11 INCHANA	PROTEDIUM.	HABLAN CYTONEGALOVINUS	TOMBOS	•		26-51	14.31							
PLE-95 HICHIVA	HYPOTHETICAL PROTEIN UL95	SAIDAM CYTOMEGALOVIRUS	TOVERS	(\$1 RADI ADIAS)		11.31						Ī		
PULAS HOMYA	VIDION PROTEIN ULION	PRINTYN CALONBOS	COVEUS	2		17.	117-111						Ī	
PIA DF HCMVA	INTOTAL PROTEIN UL 119	HUMAN CYTOREDALOWAUS	KLOWAUS	(STRAIN AD169)		1	اً				Ī	İ		
				·										

	1.00 at 1 2 a.d.	All Ware	All Western (no beclierhophsgri)	11				Т	1 7487	48643	AREA	ANEAS	AREA	ARIAI	ABIAL.	<u>ج</u>
1	Photon	YOUR						-		Г	Г		Г			
100	AND THE ALPHOTESICALISM	MALANIC	TOPECALC	VINUS (S)	KAIN ADI	٤									İ	
-1	TAXABLE TOTAL BACKETS INCHES	NAME OF THE PERSON	TOPECALC		(SIEAIN ADIAS)	(6)		7			Ī				!	i
ı	MINISTER THE PROPERTY OF THE PA	NYTH	THE LAND CYTONE GAL OVINUS	VIAUSTE	NEW ADI	69		17.10		Ī					-	j
- 1	HAPOTHE I PALE PROJECT WALL		PARTY CANADAS DABLES	VIETTE	RAIN ADIAS	5		19:51							!	1
MINISTRATA				11007	A MAR	-		25.61	107-424	140.467	131-131					i
VCLB SICHVA								101.16	130.76							
AVAIN HENVA		HARM	MONECALL							1						-
VCS I MENOVA	Į.	HIBAN	HERALN CYTOLEGALOVING	2	2	5									 -	i i
	M310		MOLEGAL	S) STIMAC	BAR ADIES	£			!						İ	!
AND MANA	ı	TANK THE	PYTOKE GAL OVIRUS	Symbol (S	SILVER	(4)		13.464						İ		:
VOICE HOW	MADOR DAY-BACON PROJECT		HELLEY CYTONICON DVIETE	.=	I LAIM EISEMIARD!	MIARDI		14:31								<u> </u>
PVDEK HCMVE	NO MAJOR CARLY PROTEIR			-12	AND INVEST	1975			191-430	13.463	153.130					
PVC1 I MCMVI	CL YCOPADITIN B PRECUASOR	PANA	STATE CALCADE CALONING													
POLITICAL DI POSSO	PAT CHASE CHESA IN PREPATE LOS	3	ETTOLEGAL OWINUS	SHEUSING	STRAIN TOWNE	76										
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TAX PARTY	A STANDE	CHNCYV	TAI SOF	(SAVAL)	(SOLATE)	364-392	210:01				1			1
DAY MAIN	DIV FOL YFUJER		100	V VALUE OF	HALL TVA	KANESONE PIECE VINIS IVE I JANVAS I SOLATE	150CATE	817:18							j	
POAG HIVIAS	GAG POLYMOTER			2	12	11 A 10 1 10 10 10 10 10 10 10 10 10 10 10 1	ICM ATEN	2	120 61						į	
PICE HVIAI	POL POLYPROTEIN	N. P.				1	1980	=								
DVALL HVIAS	VPU PROTES	HEAR	S GALDHOOE	CIENCY		INDIADACOETICIEMOY VINUS ITTE I JARVESTA INCLAIR	DALAIE		1							_
	Val. 650 11 B4	MANAGE	DORMODE	CHECKY	INUS 177	I (BRIGAND	RAILM DORDWOOK! ICIENCY VIRUS 17PE! (BRIED AND HIXDLATES)									İ
200	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COL	MALAN	HALA PRODEFICIENCY	V V VIII V	TACS TYPE	1 (81116) 1500	(A16)	145.384								
PENV HVIBI	ENV POLYFOLDIN		PASSACRIC IENCY VISUE	VANA	THUS TYPE	VIELLS TYPE 1 (MILLO ISOLATE)	LAIE	330 237	613-633							1
PPOL HVIBI	POL POLYPROTED		1	1	1111 1111	THE PROPERTY WALLY WALLE TYPE INDICATED	1	136 351	11.01							
POL HVIBS	POL POLYPROTEIN					3	1365	1	414.475							_
PENV HVIDS	ENV POLYPROTERN	7	REMANDE FOR THOSE SCIENCY VIRUS	CENCY												_
Parket alvanda	Section 1997	30.00	RIPAN INDIANODE I ICIENCY VIRUS	CENCY	TACS TA		ATE									
	100000000000000000000000000000000000000	MALABO	PART PROPE	KIENCY		TO CONTRACT SE	OLATE)									
VENY HVIBN	ENV POLITICAL PROPERTY AND	7	MAGNORIA	CHACT	TALES 177	I (BILADA 15C	OLATE	=								
MAIN OAN	VPUTRUITE		SELLIN BEARING PRINTY VILLE	AJMAN	14 115 170	CALUISOL.	ATE	250.58	£16-688	2						1
PENV HVIBB	ENV POLYPROTEIN		1000	20000	Charles Several	The same of the last	1915	200.55	413.633			_				
POL HVIBA	POL POLYPROTEIN			LIEM	1	The state of the s										
BVP(HVIAL	VAC PROTEIN	HACAN	RALAN BARDNODEFICIENCY VIRUS	CIENT	Si	TO LEGIS	A16)		200	100	10.00					
	ENV IN VOLUTION	HELLEN	HATTINGOE!	KIENCY !	5	TO I COCASI ISOCATE	SOLATE									<u> </u>
STATE OF THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDRESS OF THE PERSON ADDR	THE STATE OF THE S	HUMAN	INDIANA BERINGSEPECIENCY VIRUS TYPE !	KIEKY	TKUS TYP	{cpc+}	SOLATE	2								_
NAME OF STREET	CHAPTER STATE OF THE PARTY OF T	MALAN	TOOM BEE	KIEKY	5	[] (ELL 150LATE)	416)	255-296								ļ
TI MAN	ENV POLITICAL DE LA COMPANION	NA PARA	BANDACHE ICLENCY VIRUS	CHENCY	TRUSTY	11 RLI 150LA	(11)	=								1
THE HAIRT	MEGATIVE FACTOR		1	PIETO ACTUAL	14	A PARTIES	1917	117.764	934.660							_
PPOL HVIEL	POL POLYPROTEIN		100		Œ	THE PART HERE AT 18 IN THE PART HERE		13								_
PVPU HVIEL	VPU PROTECT	THE LAND		A LIE PAR. V	3 I				100	10.107				_		_
CHIAN AND	ENV POLYPROTED ^A	HERITAN	SEATHOOF!	ICIENCY VI	-		XAIE				1				<u> </u>	<u> </u>
100 Marie	POL POL VPROTEIN	INTERN	SALMODE	KLENCY VIRUS	ARUS IVE	-1	NATE!		2				1			<u> </u>
	CALL DESCRIPTION	335	DOM: NO.	KIENCY	TRUE IVE	=	KAIE)	7				 -				1
PVPO HVING	VPU FROIEW		MAGINOOF	ICIEMCY \	CIENCY VIRUS 1YPE	E I DUST ISOLAT	LAIE	345.594	63:15	3						<u> </u>
	ENV POLYFROILIN		BAN MODE		HEV VIEW 1998	-	ATE	15.32	26.60	945-299	103-139					<u> </u>
PENV HVIII	ENY POLYTRUIETH				200		THE PERSON NAMED IN COLUMN									_
PCAC HVIII	GAG POLYPROTED	3						2						_		
EVPU HVIII	VPUPROTEIN	NAMA	P. B. M. POOR		KIEMY VINOS 1778				113.635	111.011	<u> </u>	<u> </u>	_		<u> </u>	L
PERV HVIB	ENV POLYPROTE IN	YME.	THE WINDOW	A LEAR		- ; :		1	77	_						_
POL HVIR	POL POLYPROTEIN	MAMM	D. B. A. C. S. C.	R. IENCY VIALUS		31	1									Ļ
WINTER LINKIN	VPU PROTEIN	HERAH	INDICATION OF THE INC. VIEWS 1 YES	NO.	AL SOUN		ULA 1E)		7	ī	1				<u> </u>	!
PENV HVIMA	ENV POLYTROIEIN	ILLALAM	BERTHODE			E MAL SOLATE	KATE)				1	1			<u> </u>	!
PPOLINIA A	POL POLYPROTEIN	MACAN	SECREPODE PICIENCY VIRUS T				n. A.T.E.)			1	1	1		!	-	:
THE PARTY	VALIDADIEM	348	DOMEST	ICCENCY	VIRUS TYPE	E PIAL 150	(A)E)	2	:	7				1		ļ
	THE PART OF THE PA	3	DOG MODE FICIENCY VIRUS	KIENCY	VIEUS 1V	IVPE I (LOTA ISOLATE)	(LATE)	543-592	•	1	Ť			1		1
VENV DVIDO	THE CALL WAS DEED	DEMAN	A DESCRIPCIENCY VIRUS	CENCY	WALES TO	E DENISOLATE)	(A1E)	50.05		633.684	191-119					1
PENV HVINO	DAY TO THE OTHER		I ILAA INDOMINIENCY VIRUS	TICLE NO.	-	THE DENISOR	.ATE)	= 1	_					-		<u> </u>
PCA0 HVIE	GAG POLITIKO IEM		WAR MODERNIE WITH	A LE LE V		S MAL	ATE	22.160	_	1	<u> </u>	<u> </u>			-	<u> </u>
2	POL POL VPROJECIA	1	PAGENCIAL PROPERTY VINCE	VANDO	VINTE IV	PE I MEDIK ISOLATE!	CATE	20.50	516.583	1					-	_
2 2 2	ENV FOL YEAGIEST	NAME OF THE PERSON NAME OF THE P	KARANDER ICHENCY	NO.		VPE O'DK 1SO	KAIE	1	<u> </u>		1	<u> </u>				i
ANEL IN	NEGATIVE PACTOR		200000	N.	12	100	M A 161	22.25	434 660	<u> </u> -		_				_
TO EVINO	POL POLYTROITEM		NO.		1	5	MATE		:	 	<u> </u>					
PVPC HVIND	VPU PROTEIN		THE PROPERTY OF THE PARTY OF TH			I DEW YO	THE PROPERTY OF THE PARTY OF TH	136.160					<u> </u>	_		
PER HYINS	DAY POLYPROTEDI		To a distance of			1	THE LITTLE ATES	318.344	,		<u> </u>			<u> </u>	_	
PPOL HVINS	POL POLYPROTEDI			-		20100	1		919	220.030				<u> </u>	<u> </u>	_
PENV HVIOY	ENV POL YPROTEIN	3	STATE OF A	FR	5	201121			٦.	1	-					

PCGENE		All Vignore (so bectering heart)	1.401		1 7487		2 7497	, , , , ,		1 1 1 1	
CILLERARE		HARMAN BEACHACHES ICHENCY VIRUS TYPE FROY I SOLATES	7	7	Т	1	Т	т	$\overline{}$	T	75035
SELA LIVIDO	ENVIOLENTED	HAMAN BAGANOSTICIENCY VIELS TYPE I IPVIS 150LATES	ī	107-119	31.0			İ	İ	İ	
HOL TOWN	POL POLYPROTER	HELIALAN MERAINODES KIENCY VALUS TYPE I (PV12 ISOCATE)		111-111							
PARC HALPY	VPU PROTEDI	HIGHEN BEAROOGICENCY VALIS 1776 I (PV11 ISOLATE)	7								
PENY HVIRH	ENV POLYMOTEIN	INDAM BOARNOEFICENCY VIXUS TYPE I (MAIAF ISOLATE)	ī		3	ş	2	Ì		Ì	=
POL HVIEN	POL POLYPROTEDA	HERAN DEPARTMENT FLERCY VIRUS 1978 (RIGHA) BOLATE				Ī	Ī	İ	Ī	ĺ	
VO HVIEN	REAVEST VECTORS	INTERANT MACHINE INTERACT VIRGIS 17PE 1 (SC 150LATE)	7	\$45.593	1				Ī	Ī	!
PEN UNITE	EST BOL VEGOTERS	HOBEAN BESCHEINE HEISNEY VIRIUS TYPE I 155 ISOLATES	131.181	36.365	117.00	508				Ī	
PVEUTINIS	VPU PROTEIN	INDAM BANNODE KIENCY VINUS TYPE I (SPIGE ISOLATE)	┰						Ī	Ī	
PENV HVIS	DAY POLYPROTEDI	BOURODE!	_	10.15	=======================================						
PENV HVIKE	ENV POLYPROTEIN	MARKHODE!	201.301	33.58	21.63	136.824					
POL NYICE	POL FOLYPROTEIN	F-R-RINODE		313.540	95.6						
PENV HVIWI	ENV POLYPROTEIN	BARRHOOE!	311-365	100		311-116					Ì
PENV HVIWS	ENV FOL YPROTECH	PACUMODES		316-314	100	103-00					
PENY HVIZE	ENV POLYPROTEIN	INDEAN INCOMERCINE OF VIRUS TYPE I (2-14 ISOLATE)		2.60	2000	797-678					
PENV HVIZE	ENV POLYPROTEIN	INSAM INSTRUCTOR FICTORIES TO STATE I (22CDC-234 ISOLATE)	,	303.501	99 83	200	İ		į	į	
POL HVIZZ	POL POLYPROTEIN	INMAN BERNODE I KIEMCY VIRUS 1798 I (23CDC-234 ISOLATR)	_ :	3					İ	Ì	1
PENY HVIZS	ENV POLYMOTERN	INDIAN BERMODEFICIENCY VIRUS TYPE I (ZAINE) ISOLATE)			1	1				j	1
-	DAY FOL YPROTEIN	HIGHAM BACAGOEFICIENCY VIEWS TYPE I (ZAIRE 6 ISOLATE)		2							İ
PNEJ HVIZE	NEGATIVE FACTOR	HENCAN MORNOCOLO (CENCY VINUS 1778 1 (ZAINE 6 ISSUENTE)	-								1
1	ENV FOL TRUITE	SAMURUDI M. IEM. T. VIRUS]		ļ
1	ENA POL TPROTEIN	MONITOR OF THE PARTY OF THE PAR	1						İ		i
	GAC FOLTFRUIEIN					Ì	Ī		į		!
Prof. HVIDE	FOL FOL VAROTEIN	A CHANGE		9,41					İ		i
1	CAN THE STATE OF T	THE PARTY AND IN									
	Con the Contract	LAMBORE INTEREST		95.15	100.55	117.77			İ		
۱	20 10 10 10 10 10 10 10 10 10 10 10 10 10	ARRESTOR I FIRM VIAIL					-	-	-	İ	:
NA NATIONAL	POR POR VPROTEDN	A DE L'ANDOETIC IENCY VIRUS	100.00	-			i		:	į	:
L	POL POL YPROTER	DOM DO DE FICE	101.560					İ	!	!	:
	ENV POLYPROTEIN	D.D.R.DACOEJICIENCY VIRUS	60.63	2	18.35	9.0	100.13				
l.	FOL FOL VPROTEIN	BOALMODEFICIENCY VIRUS	476.962								
PENV HVDAZ	ENV POLYPROTEIN	P.D.R.MODE FICIENCY VIAUS TYPE	-	=	=	3	3			İ	
PCAO HYZNE	OAG POLYFROTI IN	HERBEAN BORNACORFICERCY VIRUS LYPE I (1904 A 12 MIL Z)							İ		İ
FOL MYDEZ	CAN BOX VORDITION	A GRANDELLE MAN VINITA TAPE		1	10.00					1	
POL NYMO	POL POLYPROTEIN	SOUTHODES ICHENCY	- 19.10								
PEN HYSS	DIV POLYPROTEIN	P.D. RUNODE FICTENCY	31.21								
PPOL HY256	POL FOL YPROTEIN	PORTOODE INCIENCY							i		
PENV HV25	ENV FOL FPROTEIN	HABIAN BERRADESTCENCY VIRUS TYPE P. 1150LATE ST.	3	=	316.316	3			İ	į	İ
PCAG HV25	GAG POLYPROTEIN	HALLAN BORROODE K. G.M.Y VIRUS 197E 3 (1904 A.E. S.)			Ī				İ	-	i
Prof. HV251	FLAV ENG UPPOTE IN	HANDAN BERANDON TO BEACH VIRGO FOR S (1904 A 12 ST)		191	110 104						
PUT UPVIL	K	SERAN PAPE LOSA VIEWS 1 YPE 11	10								
PVEIA IOVII	2	HABLAN PAPEL CALAVIRUS TYPE IS	3								İ
PVI IPVII		HEDRAN PAPE COMAVINUS TYPE IS	21.164	191.51							İ
PVES HOVIE		HERAM PAPEL CALAVIRUS TYPE IS	10.10	11.10							
PIAGI PANE	EAPROJEIN	INDIAN PAPE COLLAVIPUS TYPE IS	3								
PVEL 10VI	E1 PROTEDY	HUBIAN PAPELOMAVIRUS TYPE IS	60.03	٠							
	ES PROTEIN	IRDAM PAPEL CALLVIRUS TYPE 13	111.140								
	PROBABLE E4 PROTEIN	PRACAN PAPE LOS LAVIRUS TYPE 19	20.5								
	EAPROTEIN .	HARAN FARE CALAVIETS TYPE II	2	İ			İ	İ	i		;
	PROBABLE LI FRUILIN	STATES A PART CRIAVISIS TYPE IS			Ī					į	;
M S HOVIA	PROBABLE 12 PROTEIN .	ARLOWANIAUS I	101.00				Ī	Ī	Ī	T	
	TRUBALLE LATROLEM								Ī		ļ
100	CI TRUITING										

				┝	П	П	7		1	1 1 1 1 1 1	ABEAT	ABCAS
PCGINE	00717014 V	VIEW		3	4	3		Г	1		1	
		CALLANDAPO I CALAVIAUS TYPE 1A		_	İ	İ	Ī	İ		<u> </u>	<u> </u> 	
		TALL STREET COLLAND IN THE		20		j	Ì	Ī		<u> </u> 	<u>-</u> 	<u> </u>
Γ	A PROTEIN			20.00				İ		<u>!</u>	<u> </u>	į
Ī		REPART OF COMMITTEE		10.00						<u> </u>	<u>:</u> 	
Ī		THIN PAPILIONIANIANIANIANIANIANIANIANIANIANIANIANIAN		2		Ī				-	<u>!</u>	. !
		HELIAN PAPEL ON AVIAUS I'VE			Ì					_		
		THE STATE OF THE PASSAGE AND PROPERTY.		-					<u>-</u>	<u> </u>	<u> </u>	-
	PROTECH	THE PERSON NAMED IN COLUMN NAM			2				İ	!		:
Ī		CHAMPANEL COM		3:5					i	<u> </u>	<u>.</u>	i
Ī	SESSIAN E ES PROPER	REAL PARTON OF		01:00					j		<u> </u>	ļ
Ī		REPART PAPITIONIA VIBUS IVI			2					_		
		HARAN PAPIN COMAVINUS 177E 19	50 24				Ī			<u> </u>		İ
		VI MINISTER STATE OF THE PARTY	-	2		Ī	•		İ	İ	<u>:</u> 	
	7010161	THEY PAPEL USEA VINOS IN		2							<u>:</u>	į
Ī		THEAD PAPELONAVIRUS IN				İ						-
	1	THE PART OF LAND IN THE PARTY I			-	١				<u>-</u>	_ 	
				* · · ·			İ		:			
		STATE OF A PARTY OF A							į			
Ī	PROTEIN	HEMAN PAPELLONIAVINUS 177										
		THE SAME SAME COME VINCE TY			İ					İ	Ī	
V.1 100		VE STREET, SALES OF STREET, ST		23.58							İ	į
		MUNICOLO SECTIONAL SECTION		35.101							1	Ì
		INDIAN PATELONIA WAS IN							_			
1		IN BLAN PAPILLONIA VIBUS IV	rre 4)			100						
	Water 1	VI MICHARIA CALACIANTE							-	İ	ļ	
PVE I DVE				13.51	_				į	<u> </u>	İ	į
THE LAST		THE WAY PAPEL COLLA VINUS IN										j
		THE MAN PAPEL ONTAVIBUS TO	YPE 5		1							
PVE4 IOVOS		T SUBIATION DESCRIPTION OF THE PARTY OF THE	YPE 51		1	!		1			-	i
PVE1 10V51				£				į	-	1		
		I STILL TO THE LOS IN THE PARTY IN THE	Tre 31		İ							
		THE LAND TO THE TOWN VIRGIS IN	VPE 51	1	ا	İ				į		
111 1073	PROBABLE LI PROTEIN	The Part of the Pa		7						i	İ	
	EI PROTECT	SUPPLY FALL COLL STATES		2						į	! ! !	1
	To be not a second	INTERNATION TO THE PARTY IN THE	176.37		1						1	1
		INDUCATION PAPEL OF LAVINGS TYPE SE	YPE 34		į	İ						
		PANAL PANAL MANALANTA	25		į			ļ	İ	!		
VL1 10136			V-56 CD	==					j	į	:	!
		IN MAN PARIL LUNG VIEWS		2						!		
ŀ		SUPPLY PAPE LONIA VINUS	1146.30		!							į
1		IN BLAN PAPEL COMAVERIS I	VPE-38		-							!
		I SUBVAVA PAPET PARAVAUS I	9344	9						Ī		
PVEJA HOVE		THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAM	75 25	3						ĺ		
ı	PRICE A BLUE ETA PROTEIN	IN MAN PAPEL CALAVIERS	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	114.303								
1		INDIANA PAPEL CASAVIRUS I	YES									
١		HEMAN PAPEL CONAVIAUS 1	YPE MEID					ļ				
PVEL LIPVACE		A PARTITION AND A PROPERTY AND A 1	VIRUS (STRAIN C35)	-	2						Ī	
PECT PIE		THE PARTY OF THE P	CHAIR ACTOR AND PROPERTY.	333.404	117 117						Ī	İ
PLICAP PINC		HINDER CANADA CA		1	34.360	173.416						
	T SUBSTRAIN	INTERVALABLE INTERVAL	VINUS (STRAIN C.19)		775. 416							
100	SEL	HALAN PARADELUENZA I	VIRUS (STRAIN COM)	1								
PVCL TIME	THE PERSON NAMED IN	INDIAN PARAING I PRIZA I	VINITS (STRAIM CI-1483)	1	!			<u> </u>				
PACE TITE		TANKE THE PARTY OF	VIETE AT BATH CI-14-03	=======================================								
TAXE THE		A STATE OF THE PARTY OF THE PAR	Cities At the Party City City City City City City City Ci	=	192-112	37.7						
County Daniel	Count	HELLAN PAICHTURE	COLUMN TO THE CASE OF THE PROPERTY OF THE PA	1011	25.33					į	!	
	MOASE.	THE MANAGEMENT AND THE PARTY IN	VIRUS (STRAIN WASHING) CONTO	!								
TOTAL PINE		LINKAN PANABOLIENZA I	VIEUS (STRAIN WASHINGTONIEST)	1							! !	
PHCAP PILITY	ľ	A VINE LA BANA ARACTICA LICENSE	A 3 VIBUS	167.194	22 226							
PARTY PLIN	1		200018	2		# ====================================	=======================================					
DATE PATH	FUSION GLYCOPROTEDN PRECURSOR	IN BACK PAILAING LUENCA	VIROS	100	1	311.766	113-500					
	STATES OF VANDOUTED MECHASOR	LABORAN PACADRICENZA I	MRUS (STRAIN GREEK)									
ACC MINO	FUNCTION OF THE STREET	THE LAN PARABOLIENZA	VIRITS (STILATIN TOSHITIA)	122.140			_					
PARK MUST	ANA POLYMERASE BETA SUBURI	- 125 THE PARTY OF	CORNE (CERADI TOMBA)		22.22						i	
1100	ANA POLYMERASE ALPHA SUBURIT	THE PROPERTY OF THE PROPERTY O	S LABOR OF THE POSITION	100	2	236.206	# · · ·				i	!
THE PERSON	THE TON OF Y COPROTE DY PILE CLINSOR	STANKIN PARAINULIANEA		1			-					ļ
	TO THE PROPERTY	ILIBEAN PARABOLUENZA ?	VIRUS (STRAIN TOSHIBA)				<u> </u>	1				
NAM.	MAINTA PROJECT	ALADOLGENZA	VIRUS (STRATM AUSHIZASIAM)	2								
PHEMA PILIM	SENANGE UTTOWN WE UNANUMENS	ACMARITMENTA	VIBER (STRADA ICD) MARS	3								
PHEAD PLINA	HUCLEOCAPSID PROTEIN	HUBON PARAMY LIEFE	1 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	141	_	L						
77110	HELLAGGE UTBOWNEURANDASE	HEREN PARADOLUZNZA	VIRUS (3 I MAIN PROTEST)		7	404 404	1001	101-101	1 3115.3110			
	ALLA GAS WASSEA SEE BETA SUBLINET	HEIMAN PARABITUENZA S	VIRUS (STRAIN MBI 47003)			7	Ť					
	THE STATE OF STREET AT PICK SURLINGS	HIMAN PARAMACIEMZA 1	S VIRUS (STRAIN MIN 47883)		٦							
PRINT PINA	MAY THE THE WAY											

PCCENE		All Virues (as becierophogra)	H	П				1			
THE PARTY	CAUSION CLACOSON SERVINE CITE CON	HORAN PARAMOLLENZA I VIRUS ASTRAIN MAN 475651		1.0	Ţ	ī	I	1	τ	7	7 0 0
ALL PAYA		SECRETAR PARADOLLENZA I VIRUS (STRADA NO) 478231	ī	İ	İ	İ	Ì		İ		İ
PVNSC PURA	HONSTRUCTURAL PROTEDY C	HIGH PARADG (UEMZA) VINUS (STRAIN MOI 1768)	1	Ì	İ	İ	İ		į		<u> </u>
PIGMA MISTY	۱	INMAN PARANGI CENZA J VIBUS (SIRAIN TEXISORM)	1 2 2	Ī	İ		Ī		İ	İ	=
PIELL PINT	MDASE	INDIAN PARAINTI UENZA I VIRUS (STRAIN TEKSHINO)	2								<u> </u>
PIEALA PINITO	١	INDIAN PARADA LUENZA J VIRUS (STRADY TEXPOSOT)	ا ۱ ۱	1	Ì				<u> </u>		j
MENA MICE	1	HENGEN PARAINT LIENZA I PARUS (STRAIN WASIUTSHITT)			-		Ì		Ī		4
PIGNA FINA	-	HEDNAM PARAINT LIERZA I VIRUS (STRAIN WASHING)		-	1	İ	Ì			-	j
A LINE	LINA POL THE LASE ALPITA SUBURIL	THE TATA TATA TO THE TATA TO THE TOTAL TO THE TATA TO THE TATAL TO THE TATAL TATAL TO THE TATAL		!		-	1	i	!	-	: :
7101	100	INTERNATIONAL DEPOS AND VINCENTIAL DESIGNAL		1	Ī	Ī			İ	Ī	i
	ı	MALAN DECEMBATION OF STATE AND ASSESSMENT OF STATE AND ASSESSMENT OF STATE AND ASSESSMENT OF STATE ASSESSM			İ	İ	İ	Ī	İ	İ	
THE PERSON	1	MARAN RESPIRATOR STANTAINE VINOS (STANIN AL)	7		T		100				
WILL MASA	KNA POLYNGRASE BETA SUBURI	THE AND RESTRAINED STRUCKING VINUS (STRAIN AL)	١,	ī	X .		Š.		93.1410	2	7.70
PRUP ICISVA	THA POLYNGRASE ALPHA SUBURIT	WCTIAL VIEUS	Ī	1	7		Ì				
PVGL BUSVA	PUSION GLYCOPIOTEIN PRECURSOR	STICKTIAL VIRU		2			Ì				İ
WAX HESVA		MCVIAL VIRC	=======================================				-				i
WALT IBSVA	١	HERACH RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	200	i	-	İ	-				
VCLO MISV	O NO	Z ZZ	3			İ					-
VCLO HESVS	۱	KYTIAL VAUS	=	1	-	ī					
PVCLF HOLSVIE	100 E	(KENAM RESPIRATORY STACYTIAL VIRUS (STRAIN ASS.))		20.50	2	7	=				j
PRELITY HOUSE	ANA POLYNERASE AL PIUS SUBURIT	HUMAN RESPIRATORY STACKTIAL VINUS (SUBGROUP A / STILATAL LONG)		ĩ							
VCL MSW.		HIDRAN RESPIRATORY STACYTIAL VIRUS (SUBGROUP A / STRAIN LONG)	2	٦,	2	3	3				
PHCAP HOLSVI	1	HUMAN RESPONTORY SYNCYTIAL VIRUS (SUBGROUP BY STRAIN 18117)	=	2	Ξ	İ					
PREPP HOLSVI	SECONT.	HERACH RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP BY STRAIN 18117)	=								
PVCLF HOLSVI	108 EON	HILMAN RESPIRATORY STACYTIAL VIRUS (SUBGROUP B. STRAIN 11111)	=	16.30	17.	16.515					į
PVCLG HASVI	EING	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP BY STRAW 18337)									
PYCLO HOLSVS	- 1	INDIAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN DAD)									
PEN MIC		INDIAN T-CELL LEUX ENDA VIRUS TYPE I (CAMBBEAN ISOLATE)									
PPOL MILIC		INDIAN I CELL LEUKEAIA YINUS TYPE I (CALIBBEAN ISOLATE)									
EN HEIM		' INMAN I CELL LEUKENGA VIRUS BYPE ((ISOLATE MT. 1)		-							
NEW MELIA		HENDAN T. CELL LEIMENA VIRUS TYPE (STILAN ATK)					-				
POL FILE	POL POL YPROTEIN	INDICAN I CELL LEUKERRA VIEUS TYPE I (STRAIN ATK)	2	-			İ				
PENY HELV3		INDACANT CELL LEURENDA VIRUS LYPE II	2							İ	j
7070 X3VII		ICTALULUS ISSUINTS I	3	20	1				j		
PKR76 MSVI										-	
-		R. I.ALUAD INARES VIALES I		:							
	STRUCTURE IN ALL DENE 17 FROILING					İ				İ	
1	-			-	100						
	HIVEOLIGITICAL CENT 14 PROTECT		1						Ī	Ī	Ī
	HYPOTHE INCAL CENE 19 PLOTEIN	ICT AL UNIO ICT DE SVIR US I	le	. 607.50	İ						
L	5	ICTALUMD IGENESVINUS I		1	1						1
L		ICTAL URID HER PESVIANS I	5				Ī				
PVC39 115VI	1	ICTALIBID IERPESMANS I	621.63	511.800							
ı	200	ICTAL UNID IE WESVIRUS I	10:16		***	100)				Ī	İ
PWGSI HSWI	TE PROTEIN!	ICTALIMID IERPESVIRUS I		2					Ī	i İ	İ
PVCS6 IISVII	INTOTAL CENE MPROTED	ICTALUM SIEAPE SYIRUS I	809 (85	İ							
ı	HYPOTHETICAL GENE 63 PROTEIN	ICTALUND HERFESVIRUS I	530-310								
	HYPOTHETICAL GENE IN PROTEIN	ICTALUND HERDESVIRUS I	473.504	Ī	Ī	Ī	Ī				Ī
l		ICTAL UNID IRAPES VIRUS I	10.03	_							
l		ICTALIBED IRAPESVINIS I	. 907-791					İ			i
PVG47 115VB	2	ICTALIMID IE BPESVINIS I	1343-1344								
	DIVPOTIBLICAL GENE 46 PROTEIN	ICTAL UND IERPESVIKIS I	161.181	İ		Ī					ĺ
	2	ICTALUMD IERPESVINUS I	7			<u> </u>				Ī	
Į	INTOTIETICAL GENE 35 PROTEIN	ICTAL UNED ICENTES VIRUS I	70.73								
PYON HSYLI	HYPOTHETICAL GENE 14 PROTEIN	KCTAL LINED HEAPESYINUS I	306-231								
PVTER HSVII	PROBABLE DNA PACKAGING PROTEIN	ICTALIMO IB PESVIRIS I	116.13								

PCCCME	107117814	All Viruses (no botterloghoger)	_	L	L	L			İ	-	
CILLERANG	PROTEIN	Thurs	AKKA	A ORKA	T AREA I	2 AREA 4	SHEAS	ANTO	OREA!	AMEAI	APEAS
PHENCA CADRITY	HEMAGGLU1 PAIN PRECURSOR	A VIRUS (ST	11-55							_	
PIEDLA JADRIZ	HEMAGGLUTINH PRECURSOR	A VIAUS (ST	157-116	15						İ	
Pyrair Laber	NUCLEOPROTEIN	INTELENZA A VITUS (STRAIN ADUCKAKOW ZEALANDATING)		2	<u> </u>	 -				İ	İ
PHENA IADUI	HENCYCT LITTING PRECUASOR	A VIDIS			<u> </u>					ŀ	
PIESKA IADUS	HEMAGGLUTININ PRECURSOR	A A VIRUS (STRAIN		135	<u> </u>					1	
١.	MUCLEOPROTEEN	A WAUS		1	<u> </u>	 -				İ	į
PWALE LADAS	MUCL EOPROTE DI	BOLLENZA A VIDUS (STOATH AENGLANDVIPSS)	12.61	100	<u> </u> 	<u> </u>			İ	İ	
li	HEMAGGLUTDAN PRECURSOR	A VIRUS (STRADA	3	10.03	<u> </u> -			Ī	Ī	Ì	1
PIEMA INEM	HEMAGGL UTPAIN PRECURSOR	A A VIPUS (SIRAIN	25	<u> </u>	<u> </u> -	 -				1	
	HEMAGGLUTOWN PRECURSOR	A A VIRUS (SIRA)	116-55	÷	 -					İ	1
	HEMAGGUIDAN PRECUISOR	A A VIRUS (STEAT			Ī	 -				Ī	İ
	HEMACCLUTING PRECURSOR	A A VIRUS (STRAI		Ī	ī					İ	Ī
MEMA IMICI	HELLAGGI UTIMIN PAECUNSON	A A VIBUS ISTRAI	Ī		Ī	 -			Ì	Ì	İ
	INE LIRAMONIDA SE	A A VIRIS IS IBA		1	,	 -					İ
PIEMA INDE	INDIANGEL UTTOWN PRECIDENT	A A VIRUS STRAIL		1		 -				İ	
PREMA IANGO	NOWACCE IN DAIN PARCIE COS	THE LIE NOT A VIBIL OF SALES ARCHITECTURE AND A SALES		Ī.	Ì					į	;
PURE INTE	Sarves Carr				1	1					
	Marked Rolling		1/8:40)	1	_						
THE PARTY	MEURAMONIDASE	INGLIGHZA A VITUS (STRAIN ACQUINE/KENTUCKY///21)	-	9.	164 400				İ		·
FILEMA IAITE	HEMACCALUTININ PRECUASOR	7	386-	_	_	 -				:	!!!
PIEMA IAIRA	PEMAGGLUTINGN PRECURSOR	INTLUENZA A VIRUS (STRAIM AEQUINERENTUCKY/1/86)	11.0	_	ŀ.	_				Ī	İ
PIEMA INDE	HEMAGGLUTHAN PRECURSOR	A A VIPU	i i		111-657					Ì	
PIEMA IMEO	HEMAGGLUTININ PRECURSOR	INGLUENZA A VIRUS (STRAIN AEQUINELONDONILLIATI)	2	196.22	ļ	-					İ
PIUV INIEO	RNA-DIRECTED RNA POL SUB P2	A A VIRUS IS		Ī.	ï	<u> </u>			İ		i
PWAC LAIRO	MUCLEOPROTEIN	A A VIAUS (STATE)		-	!	<u> </u>		İ	İ	-	-
PREMA INDA	PREMAGGLUTION PRECURSOR	A VIEW AND AND A			:	1			1	!	
PVNUC IAIBAD	NEICH FORDTEIN	A VIETIGE		-	!	 			j		į
PARTY ALABA	MENACCI ITEMA SPECI POS			1	ī					Ì	
	MCMACAL INTO TALLINGON	A VIII SIRAIN	3	7	28.45						
TOTAL POLICE	NEWACCE UT IN PRECUESOR		26-43	2						<u>-</u>	
MONTH THOU	REMANCE UTOWN PRECURSOR	A VINIS (STRAIN	29.56	100.22	100.453				<u>-</u>	Ī	!
- 1	INA-DOLECTED RIVA POL SUB P)	INTLUENZA A VINUS (STRAIN AEQUINE/PRAGUE/1/16)	=	05 017					İ		į
VMCE IANVE	MULEUMOIEIN	A VIKITS (STRAIN	=	50					:	:	!
- 1	JEMAGGLUTDEN PRECURSOR :	A A VIBUS (STRAIN	316.4	2					į		i
PIEMA MISA	IEMAGGLUTOWN PRECURSOR	A A VIDOS (STRAIN	1	~						<u>:</u>	
- 1	BEMAGGLUTBON PRECURSOR	A A VIRUS (STRAIN	39-36	194 33		_			İ	İ	
PIEM WHI	HEMAGG UTDAD PRECURSOR	A VINUS	110-4						Ī	<u>:</u>	
- 1	KMA-OKECTED IMA POL SUB P3	A A VIDES (SIBARA	-	-						İ	İ
WAR LAINE	MUCLEOFRUIEIN	A A VINUS (SIRAIN	-	403						İ	
THE MAN WATER	IEMAKCE UTINON PRECURSOR	A A VIDUS (STRAIN	50-93							Ī	i
THE PARTY	HEMANALUING PACLUAGA	A VICTOR (STRAIN	2	16-43							İ
The state of the s	MANAGEMENT CONTROL PROTECTION OF	INCLUENCE A VINUS (STRAIN APORT)									
ł	MONEY BECTION IN DECITED INC.			9					1		
1	NEICH FORMOTEDA	TACKY MAN TO SOME A VI			<u> </u>						
	NEACL EGPROTEIN		TOTAL TOTAL		 	1			1		İ
PHEMA LATA	IEMAGGLUTINEN PRECURSOR	A VIRUS		-		<u> </u>			i	Ì	İ
1	ANA-DOLECTED RNA POL SUB P3	A A VIDIOS (SIEADA			<u> </u>	1				İ	j
•	NUCLEOPROTEIN	A A VIRUS	100		1	$\frac{1}{1}$				Ì	Ī
PHOLAL INSPIN	HEURANDASE	A VIRUS	PGE	9	1			Ī	İ	İ	Ī
PITEMA INCAE	HEMAGGLUTINAN PRECURSOR	A VIBUS		Ϋ.	1	<u> </u>		Ī	İ	İ	Ī
1	AUCLEOPROTED	A VIRUS (STRAIN	200	-	<u> </u>				İ	İ	
	HEMADOLUTOWN PRECURSOR	A A VIRUS (STRAIN	1	 -	<u> </u>	<u> </u>			İ	Ī	-
1	MUCLEOFROTEIN	A A VIRUS (STRAD	11 40	 - s	<u> </u>	 -	İ		İ	Ī	<u> </u>
H	MICI EOPROTEIN	A VIRIS (SIRAN	100	-	<u> </u>	<u> </u>			1	İ	Ī
PYPAUC IAGUS	MUCLEOFROIEIN	A VIRUS (SIRAIN	171.40	 -	<u> </u> -	<u> </u>		Ì	İ	Ť	Ī
PYRUC IACUI	NUCL EOPROTEIN	A VIRUS (STRAIN	1111	:5	<u> </u>				Ť		
PHEMA MGU	HEMACOL UTDAN PRECUISOR	DATE UDIZA A VINUS (STRATIN AVGULLIALARIYI ANEDITOATI))	100						Ī	Ė	Ī
I KALE IAUDO	MAN-DOCCIED MA FOL 308 F2	INTELLEREA A VIREIS (STRAIN ACCULTACARVIANDITOCATI)		9					Ï		

1	PRECURSOR PRECURSOR PRECURSOR AN POL SIN PI AN POL SIN	MATCHERY A VINUS SERVE MATCHE	VALUE SERVINE	STAN ACUL LALANDRATION STAN ACUL LALAS CAUSE TYDING STAN ACUL LANGE SOTANITOR STAN ACUL LANGE SOTAN	(603)	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$								
2		40116227 A V 40116227 A V 40116227 A V 4011622 A AV 4011622 A AV 401162 A AV		IN ACCULARISACIONE IN ACCURATIVA IN ACCURATIVA IN ACCURATIVA IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCURATIVA IN ACCURATIVA IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE IN ACCULARISACIONE	(607)	11111	1111							
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1 CEPP A A CEPP A A CEPP A A CEPP A A A A A A A A A		IN ACIAL LABORE SOLVANIE TO ACIAL LABORE SOLVANIE SOLVANIE ACIAL LABORE SOLVANIE SOLVANIE ACIAL LABORE SOLVANIE SOLVAN										1 +
		# (1002) 7 V V V V V V V V V V V V V V V V V V		IN ACIA (ADDRESSO) ANALYSIS IN ANALAS INTERNASIONAL IN ANALAS INTERNASIONAL IN ANALAS INTERNASIONAL				T	ĪĪ		T			141
		4		IN AVALEBRICATION IN AVAILABRICATION IN AVAIL							Ť			+
		4		IN AMERICONO IN AMERICONO IN AMERICONO IN AMERICONO IN AMENTO IN AMERICONO IN AM									İ	- -
		4011622AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		IN AN IONG TORGOLDS IN AN ION					-				İ	14
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		41		IN AND AND AND AND AND AND AND AND AND AN			-	İ						ļ
1 1 1 1 1 1 1 1 1 1		41414141414141414141414141414141414141		A A A A A A A A A A A A A A A A A A A								-		-
				IN AND ANDON'S) IN AND ANDON'S) IN AND EVIEWS IN								;	•	
1 1 1		14141414141414141414		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		.		1		Ì	İ			!
1 1 1 1 1 1 1 1 1		141414141414141414		HI AN EVINOR AND		1000		-			İ		-	!
- 1		1414141414141414		IN AMI WITH A		6 9						-		
		MILENZA A MILENZ		(19) AV (18) (19) (19) (19) (19) (19) (19) (19) (19		19								
1		10111111111111111111111111111111111111		AND			:					1		
1 1 1 1 1 1		74 LENZAA 106 LENZAA 106 LENZAA 106 LENZAA 106 LENZAA 106 LENZAA 106 LENZAA		N. A. T. DIE AATBAN AN AT GENERALD FOR IN AN AT ENKRAND FOR IN AN AT ENKRAND FOR I AN AT ENKRAND FOR I AN AT INVESTED FOR I AN AT AN ATBAND FOR I AN ATAIN AND ATBAND FOR IN			-	Ī		ĺ		į		i
111111		POLICENZA A POLICENZA A POLICENZA A POLICENZA A POLICENZA A		I IN A SINCE AD TO 11 III III III III III III III III III				-	į		-		: : : :	:
		NA LUENZA A MANANA MANA		AIN AT ENINGRADO 1971) AIN AT ENINGRADO 1971) AIN AT ENINGRADO 1971		::	_					:		
		MILENZAN		AN ATENIKGRADI (191) AN ATENIKGRADI (191) AN ATENIKGRADI (191) AN ATENIKGRADI (191) AN ATALI REPORTED (191) AN ATALI REPORTED (191)		: ±						-	į	
		NA CHENT		AND ALESKERALIS SELLEN AND ALESKERALIS SELLEN AND SELLEN AND SELLEN AND SELLEN AND SELLEN AND SELLEN AND ALESKERALIS SELLEN AND ALESKERAL			!	!						
		INTERESTA INTERESTA		AIN AI CNEGRAIN 1971 AIN AT ENIXGRAD 1971 AIN AT ENIXGRAD 1971 AIN A AIN TAPPAL BERTA 197				:	:	:	:			
		MI LENIA A		AIN AT LYKKAAD 1641 AIN AT LYKKAADTUT AIN ANAT APPAL BENTA BE			_ !:	i			;			
$\overline{111}$				AIN AT ENINGRADIUM AIN ANIAM ANDAL BERTA BU			1		i			:	1	:
77		MI LENZA A	CIRIS ISIN	AIN ANIAI LABINAL DEBIA IN		600	-	-	j		i	:	:	;
7		AAMANIA			_	=		1	į	į	1		i	
ĺ		: +<		AND A SILLI ABOVA CTRACKIAN	<u> </u>	100	:							
		A A MAN THE		AIN A MAIL AND AS INAMINA			-				!)
PUMAY TAMAA MECLEOPROTEON		DOLLENZA A	A VINITE ISTR	AIN ASIALL ABUNAS HARITAR									l i	!
ī			VIBUS (SIR	AIN ASIAL ABDIASTRAKITIAN 19141			-		ĺ	İ		İ		İ
Ī		DAIL LENZA A		AIN ASIAI LARINNE W YORKA		=							1	
╗	OTEN	1	1	AND AN AND A PORCE		111.403						İ		
	100000000000000000000000000000000000000			# 100× 11 February 11 11 11 11 11 11 11 11 11 11 11 11 11		10.01								
Г		DOLUMAN		ALS APPALL ARTHUR WITHOUT			100				İ			i
STREET STREET	GELLACOL INTEGN PRICURSOR	DILLENZA A		AIN ASEADIII SIAN							ļ		i	İ
T	MAKE	PALLENZAA	VA US (ST	AIN ASSESSESSESSESSESSESSESSESSESSESSESSESSE										:
The state of the s	TOTAL PROPERTY OF THE PARTY OF	Del LIENZA A	VIEWS 1815	AIN AGE MPIGNION 2)	ĕ						İ	1	!!!	;
Ī	The second secon	MAIL LENZA A	VIEW IST	KAIN AMERIPHENTAL	Ā	26.51	11:41				!	i	;	:
1		A A STATE OF	THE PERSON	A A THI A A SINK /SWEDEN/161		=	:					!	:	
Ī	EMARGE UTDAIN FAR LURSUR			12		300 000							•	
		THE CALL A				500				!				. !
Ī		A LUENZA A		In the second second		::						:	į	
Γ	ALLACCE UTION PRECURSOR	DOLUENZA A	VID CS	KAIN AM (40%)			i	Ī						
ī	LNA. DOLECTED BUYA POL SUB P3	SECTION A	NICS (SI				İ					1		į
Ī	MILE	PALLENZA A	VIRUS (ST	RAIN AMINONS			Ī		-		1			i
ı	7,318	DOLLENZA A	VIRISISI	RARI AVOIDOVADI)		9		1	-			ļ	į	;
TANK INCHES TO SELECT THE SECOND SECO		PRICENTAL	VINUS (SIL	AAIN AFARROIAR SIERTI		3	-					!	:	:
- 1		PALLENZA A	VIRUS (S)	TAIN APARAGIAL SILBAD		101						į	1	i
٦		DATE IN TAX	1000	LAIN APILOT WITH EMINEDING		\$05.314						j		į
PHEMA IAPIL PEMAGGAI	MEMACOLUTININ PRECUESOR	A A VIEW A	VARUS AST	BARN APPINTALLYAL BERT ALLINION	181	2				İ		İ		-
ī		PAGILENZA A	VINUS (ST	BARN APINI ALUAL BERT AUSINO	197	131.161					-			
	MUNICIPAL PROPERTY	A A CAN DIT I SAN	VINITE AL	BAIN APINIALLAL BERT AUSBOR	1	101:11						İ		-
٦	CION INCIDENT	1177	12			26.20	115.478					İ		
Ī	EMACCAUTING FIRE CORSON			BAIN APPERIONICONO		1						į	1	:
	MEURAHONDASE			AAN APIRE IN BILLY BALL		19:00							j	:
	CTLD RNA FOL SUB FE					170 003	<u> </u>							į
	ROTEU	מומהאלא	2 ::	TOTAL STREET										
Γ	ENAGGLUTTION PRECURSOR	MILEDIA	Zi	EAST ACTUMENT	PEN PER CENTANNI									
1	LUTINIH PALCUMSON	DELUENZA		IAIN AXIDOT IUMPSIONER	The state of the s									Į
Г	AMA-DERECTED BMA POL SUB PI	DELUENZA A		LAIN ANLIBOT TURNSTONEME WITH SELVENING	THE PERSON AND THE PE								İ	
Т	AOTEM	DOLLEDAZA	200	KARY AN LOOF TURKS I ONEAR	TE WILL TO UN WEST									İ
T	DODASE	DATUENZA.	VINUS (SI	RAIN ARLIDOY TURNSTONEN	٦									
STORES AND SALES FOR STATE OF	#OTION	IN LUENZA	VIXUS	RAIN ASEALMASSACITUSETTS IVO	٦	2			1					
Т	LETTONIN PRECLESSOR	VZNGD 1940	NAMES OF	RAIN ASEALAIASSACINSETTS/13941)			_							i
Т	AND A COLUMN PRECINSOR	DALLENZA	A VINUS	RAIN ASIE ARWATERAUSTR		*	3	3			-			į
Ī	TO SECURITION OF THE PERSON OF	DOLLERZA /	NO STATE	STRAIN ASSERANWATERAUSTRALIAM)		331-405								i
PWACE LASTED	MACLE COLUMN	ATH I THE	VINE S	RAIN ASINGAPOREWS		=								

	107:178:4	All Virgan (na batteruphages)	\Box	П	П	17	П	17	17	17			
П	PROTEIN		3	3	ABGAL	ANTAL	1739	4104	CHEST.	MICH.	181		
7VE 128	NUCLEOPROTEIN	A A VILLE IS IN A	-	į					-	i	:		
PHEMA INSTA	HEALAGGLUTOWN PRECURSOR	A VINSCEINAN	•	3					-	-			
PWACE INTO	NUCLEOPROTEIN	A A VIRING (SIRA	200					İ					
PWEC INTO	MUCLEOPROTEIN	A VIRUS (STRA	9										
PYMIC LAZCA	NUCL EOPROTEIN	DOLUENZA A VIRUS (STRAIN ASWINE/CALGRIDGE/1/13)	2 to								: :-		
PHELIA IAZO	HEMAGOL UTDON PRECURSOR	A VINUS (SIDA	40 ° 63	167.11					<u> </u>	İ			
PVNAK JAZDA	MACLEGARDIED	A VINUS (S	370.405						-	İ	:		
Pydic IASGE	MACLEOPROFEDA	A VIRUS IS	336.405					İ		!	i		
PHEALK IAZHU	ISTMACKEL LITTINGS PRECUESOR	A A VIRUS	10110		Ī						İ		
147111	THE DISCUSSION AND COMPANY	1		į				İ	-		:		
	TO THE PART OF THE			1					İ		-		
1	MALEUTAULIA									İ			
WALK IAZHO	MUCLEOPROTEIN	A A VIRUS ISIRAIN	336	ļ									
PWC INTRI	MUCLEOPROTEIN	A A VIAUS (SI	\$ 6								į		
PHEMA IAZHU	HEMAGGLUTININ PRECURSOR	N S I S I S I							Ì		İ		
PLUS IAZHS	AMA-DIRECTED RNA POL SUB P.1	INTLUENZA A VIBUS ISTRAIN ASWINFAIONG KONGALIJES	110.106				Ī			į			
BUSAA LAYIN	WENT ACCOUNT NAME OF COME OF	A V CIBIL CENTA		100 00				!	į	!	:		
	ACMADOLOGININ PRECOMBON			9					i	į	!		
	2	A A VIRUS (SIRAIN									-		
	MUCLEOPROTEIN	A VIRUS (SIRAIN	9										
PWOKE IAZIS	MUCLEOFAGIEN	INSTUENZA A VIRUS (STRAIN ASWINEADWAID) WILL	100										
	MUCL EOPROTE IN	DELIGNA A VIRUS (SIEAIN ASWINEADWATE)							İ		į		
	MICLEOPROTEIN	DOLIGHYA A VINIS STRAIN ASWINEDIAL VIOLES	171 401				İ		:]	i		
10.11				:	;	į	-	: !	!	: :			
1	MALIEUROIEIN	INTELLEPTEN A VIRING (STRAIN ASSWINGTON)			1					-			
PWCC IAZII	MICHEOPHOIEIN	A A VIRUS ISTRAIN	6			;							
	PUCLEOPROTEIN	A VIRUS (SIRAIN ASWI	2	İ			İ			:	:		
1	MUCI EOPROTEIN .	DELIENZA A VIRUS ISTRAIN AS WINEJIANE SOURCAST	100	! -			İ		i	:	:		
SWEET INTHA	Marci Echanistra	A CHAIR AND	702100000000000000000000000000000000000							İ			
7	MACLEUMADIEIN	A VIEUS (SIEVER AND	ê					į					
MEMA INTO	HENACCE UTDAN PRECURSOR	A VOUUS (STRAIN ASW	-	38:50									
PARC MOR	NUCLEOPROTEIN	DOLLENZA A VIRUS (STRAIN ASWINE/ONIO 1171)	378.405						 		 !		
PVAUC IAZON	MUCLEOPROTEIN	A VIAUS (STRAIN	110 435						<u> </u>	!	:		
PRUS LATE	RNA-DURECTED BNA POL SITE PT	A VIALIS (SIRAIN	::	1					<u>.</u>				
PWOC LAZE	MUCLEOFIGIEIN	DITLUENZA A VIRUS (SIRAIN A/SWINE/TEPOGESSE E/JA/1)	178.405	i	İ			İ	1		:		
PAULY WATER	RIVA-DOLECTED RIVA POL SUB P3	A VEICE CHICKIN									İ		
PIEMA METER	HEDRADGLUTDAN PRECURSOR	ON LIENCA A VIRUS (STRADY ASWINEARKEUIA)							İ	Ī			
PVPAUC LAZWI	MACLEOPROTED	A VIBUS	100-02							İ			
PVNDC IAZWI	MICLEOPROTEDI	15							Ì	Ì	Ī		
PAGENTA IAPAI	HEMACCA LITTOWN PRECIDENDS	A VIETTO					Ī			Ī	İ		
TALL IN LES	MAIN ROSSOTT DA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1							1	Ì			
A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Mena Con Province Bus Com Com	A VIETE ATTENDED								İ	1		
1 1 1 1 1 1 1 1	THE ALTERNATION OF THE PARTY OF	2								Ì	İ		
STATE OF THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN CO	- Land Education	12 THE PERSON A		İ					1	Ī			
A SWELL SAME	NAME OF THE PROPERTY AND	A VIBILE							İ	Ì			
**************************************	ALI PLEASON TO LA	21217							İ	Ì			
1	Water & Constitution										ł		
1000	MOCKED ROLLING		5						-	Ī			
	PARTITION OF THE PARTY.								1		į		
PVNSI IATRC	MONSTRUCTURAL PROTEIN INS		-										
PIEMA IATE	HEMACCLUTHIN PRECURSOR	DOLUBEZA A VIRUS (STRAIN ATURKE YAREL AND) 13/31)	5										
- 1	MUCLEOPROTEIN	NA VEICE	110-403										
PHEMA INTRM	HEMAGGLUTTHIN PRECURSOR	INTI CENZA A VIRUS (STRAIN ATTIRKE YATINMESOT AND 1-10)	1						İ				
	ANA DIRECTED INVA POL. SUR P3	A A VIBUS ISTRAIN	12 12 12					į	i 	İ	:		
ı	HEMACCLUTOWN PRECURSOR	DELUTIVEA A VIBILS (STRAIN AT LAKE YONT ARIONI 1948)		::	!		•	; {		:	:		
L	HEMAGGLUTOGN PRECURSOR	DELUENZA A VIRUS ISTRAIN ANTIRKE YOMT ARION INGS	107.134	į					İ	İ	i		
1	MAICH FOFROTE IN	A A VINUS (STRA	19						İ	Ì	Ì		
PHEMA LATER	HEMAGGLUTDYDN PRECURSOR	ZA A VIRUS (SIRAM		16.31	1								
PVMS3 LATER	HOWSTRUCTURAL PROTEIN MS!	A A VIRUS	11:11						Ī	1	Ī		
PIEMA IATEW	I BEMAGGLUTONIN PRECUBSOR	INSTUENZA A VIRUS (STRAIM AATURICE YAWASCONSINAMA)		419.00					İ				
PHEMA JAIDO	INMAGEN INTININ PAPETIMSON	A A VIRUS	40.6						Ì	İ			
									1	1]		

Crat	167813884	All Vieners (no bacteriophoger	bacterioph	14184	AREAI	ARCAS	ARIAA	ARIAL	ABEAE	ARGAL	46754	ALL
PANK	PROTEIN	ZINIZ		181:101								
2010	MANATELICHTAAL PROTEIN MS!		MEUSIS									
S			A VIAUS (S	SIRAIN AADORNAINS)	1						Ī	
ALC IAUDO	i harringon		A VINUS (S			1					ľ	i
TOW YOU			VIRUSIS							İ		-
TAM MOSS	ME UNAVINOVASE		\$0 \$11E12 V					Ī			İ	!
PYPES IAUSS	MONSTRUCTURAL PROTEIN NO.			139.403								
VALUE IAUSS	MUCLEOPROTEIN			10:10	111-111							<u>ا۔</u> ا
EMA IANIT	HEMACCLUTOWN PRECUMSOR	7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2			12				ļ			ļ
100		DELLENZA A	VINISC		1	ļ						
	Section of the least the l	DALITIMS A A	₹			İ				İ		
WIGHT WAS		A CHAILE	1									
HALL IAWHER												
AGE LAWRE	MACLEOVADIED	DOLLERCA A VINO		197 161	<u> </u>							
SWIT INDE		DELLENZA	VINUS	WHALEFACIFIC OCCAPITION								
	200 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C 1 C	A LIGHT	VIEUS	WIT SOM SMITHTING								
HEDEA LAWIL				WIN COM CARTINITY							İ	
PHALL LAWEL	MEURALONIDASE	INOTITE A VINUS IS INCHINA		100.100								
PERSONAL PARTY		BULLENIA										
Mar. 1		DECLERAZA A	2555	WILL SOM SAUTHURS								į L
		DOLLENZA A	425524	ANTISCONSTRATIONAL)								İ
MAC IAMIS		ACHIE LESSON	THE U.S.	AZKIAMEMCAME								
				THE PARTY OF THE P				_				
		MICHAEL		THE PROPERTY OF A SPANISHING	\$25.50							
	ANA DISECTED BNA POL SUB P)	BOLDENZA										
1	BULL PARKETER BULL POL LIES PI	DALUENZA			1		-					
	THE PARTY STATE AND THE BIT	BATTENZA	N VIRUS	1	2							
- 1	MAN DELIED FINA FOL SUS 7			1700	=		-			j		
KENA DODE	HENACCE UTDAYS PRECURSOR	No. Lee Page		16.66								
HALLA MORRO	THE MARCOL LITIDADY PRECUESOR	BALLENZA!	555									
	THE PARTY OF THE P	DOLLENZA		STRAIN DENGLANDALMI)								
EM POLY	The contract of the contract o	TENS	1011115	17.50	Ş						j	
MENA DAMA	HENADOL UTBON PRECURSOR	FOLUERA		017'001	7	 -						
ı	HEMAGGLUTENTO PRECURSOR	BALUENZA	SOUN OF	- 11								
	MAST IN ALCOMODASE	MELLENZA				1						
	LAST CONTRACT PROTEIN MS.	DALLENZA	3 <u>40 m × 9</u>	82:15	į							
TANK INTER	A COLUMN TO THE PROPERTY OF TH	AND LENDA		STRAIN BALARYL AND/SS)	3							
	The state of the s	ASSESSED		187-761	₹ ?							1
ı	PENAGGLUTING FRECUESOR		1	36.43	=							<u> </u>
MENT PROPE	HENCOCH LITTON PILE CURSON	TA P. CA.		101.10								
PVNS1 DOPA	NOVISTRUCTURAL PROTEDY MS!	BOLDENA	-	100 000								
MALLA DANCE	HEMACKLIFTOWN PRECURSOR	DELLEHEA	_			<u> </u>						
1000	ALLA PARSCIED BNA POL SUB P.)	DALUENZA I	_	•			<u> </u>					
	SCHOOL STREET	NACE REAL	_	101411								
PENA MOUS	HEALTH CONTRACTOR OF THE POPE	ACTION A	H	16783	7	_				İ		
PIESAG POTA	PENAGGLUTING PRECUESOR		14	77.00	100							j
	IEMAGGLUTININ PRECURSOR			11.12 St. 12.12 St. 12.12 St. 12.12	!	: -						
VNS1 DBYA	MONSTRUCTURAL PROTEDY MS2	V CENT	<u> </u>		!	-						İ
PREST CHANGE	MANA-DOLECTED RIVA POL SUB P1	DATLEMENT				<u> </u>						
MENT DAGE	HE MACKEL LYDOWN PRECURSOR	DOLLENZA		STRAIN CCALIFORNIANI)	<u> </u>			1				
1	MAIN POPEDIEDI	DELCENZA	2550			1	1		<u> </u>			
	THE LANGE THE WAY PRECIDENCE	POLICE NZA	•	(SIEATH CENCLANDAPAR)								1
	TOTAL STATE OF STATE	DOLLENZA		51167/34)	_	-		<u> </u>			ļ	
TOWN OF THE	CENTAGE OF THE PROPERTY OF THE PARTY OF THE	ACHIEN		(STRADI CALYOGOVA))	_							
HENA DIGIT	PENCHOLING PRESENCE	A CALL IN LAND A	PER PE	15 19 A DA CA11/501	_	i						
PLUT DACE	RNA DOLECTED IMA FOL. SUB F.			SET AND CALLED STATE OF THE PARTY OF THE PAR	<u> </u>	<u> </u>	 -	<u> </u>				
PVMAT BYCL	MATRIX (A) PROTEIN	INC. OF THE			<u> </u>	<u> </u>	<u> </u>					
VASS PRO	NOWSTRUCTURAL PROTEIN NS!	DOLLERY	CAMO			 	 -					
PHENA DICTI	INDIAN COLUMBIA PRECURSOR	DOLLENZAC		JAMIANNES BURGINGS	Į,	<u> </u>	 			ļ		
PIESZA NAKY	INTERACOGL UTDON PRECUESOR	STOP S	٤	(STRAIN CK YOTONIAZ)		 					l	<u> </u>
PERMIT PATE	HIGHTACKS UT BADA PRECUESOR	220150	CVIBIS	(STRAIN CMISSISSIPPING)	1	<u> </u>	-	1	!	:		:
ALL PARTY	THE MACCOLLINE OF PRECIESOR	77 CEX 27	CVE									<u> </u>
	SPECIAL OF THE PARE CLIPSON	DAILUENZA	CVINE		-	<u> </u> -	 					
1	- Control of the second	DATI IRMA		7		<u> </u>						
1000	- Constitution of the cons	A SALIENT	CVIRUS	-								
PIEMA DOT!			3147	ì		<u> </u>		<u> </u>				
HEMA MOTA			1					 -				
PIEMA DICYA												

Process	1007017014	AN Viscos (see Assessment)				Ī					1
THE PAPE	PROTEDI	T						т	П	7	
1	ENV POLYPROTEIN	KINSTEN HARING LEUK EAUA VIRUS	7	7000	Т	_	т	4	4	P	9650
ē	GLYCOPROTEIN B PRECURSOR	Ī	9.130	10.13		Ī	Ì		İ	İ	
1	ENV POLYPROTEIN	ī					Ī		j	j	i
		A16 C. W.				Ī			İ	i	İ
			15				Ì	Ī	İ	1	
PONDI MONYS	_	MURINE CYTOME GAL OVIEWS STRAIN SAME						Ī	İ	İ	-
PICIS MONYS		MURINE CYTOMEGAL OWNER CERAIN CAUSIN					1	Ì	İ	Ì	
PVGLB MCLVS		PRURINE CYTOMEGAI OVIRUS (STRAIN SAUTIO		100		Ī	Ī	Ī	j	İ	ij
VIET MCMVS	L		1			Ī	I	Ì	j	İ	j
PVE2 PCPVI		PYGMY CHING ANZEE PAPIL CHIAVIBUS TYPE I	167.784	191.151				Ī	İ	İ	!
PVES PCPVI	PROBABLE ES PROTEIN	PYGMY CHING ANZEE PAPIL COMAVIRUS TYPE I						Ì	İ	İ	
PENV ME VILD			1					Ì	i	j	
PPOL MAYON				110,00			Ì		İ	İ	
PENV MEVIK									İ	i	1
PPOL ME VIEK				3					İ		j
PONBI SCHVC	OTEN	SIMIAN CYTORIS CALOVIDUS ISTRAIN COLINIAN		İ		i		İ	-	İ	:
PPOLG IDAVS		SOUAN IEPATITIS A VIBITS (CIBAIN ACKLUT)				i	į	i	İ		!
PPOLG IPAVT					• •		İ			İ	
PENY SIVA!				100 191	100	10.00	1	1	-	İ	
PPOL SIVAI	POL POLYPROTEIN	SOULAN INDIAMODE FICIENCY VINUS (ACALLES ISOLATE)	=					Ī	İ	-	
PPOL SIVA3	POL POLYPROTEIN	SIMILAN INDICHOCE IICIEMOV VIRUS (ACAIS66 ISOLATE)	1.0					İ	i	-	
PENV SIVAD	ENV POLYPROTEIN	SIMILAN INDICIPINCY VIRUS (AGAI) 150LATI)	770.101	166.691	- 779 (8)	100	1915	į	i	İ	-
PPOL SIVAG	POL POL YPROTEIN		40.40						i	Ī	-
POL SIVAL	POL POL YPROTEIN	FICHENCY VIRUS (ACADIT) (SOLATE)					İ		İ	İ	
PEN SIVE		KIENCY VIRUS	7		277	1				j	
PCAC SIVSA		ICIENCY VI						Ì	i	1	j
POL SIVE		ICHENCY VIRUS OF INVENDIGATION ATE				Ī	-		 	i	!
PENY SIVAS		IENCY VIPUS LISOLANE AGNI/ CLONE GIL II	25.301	114.111	197	101	Ì		<u>-</u>	i	i
PGAG SIVAL		TEMEY VIAUS (1504 A 1E AGA! / CI ONE GAL.)	101 101				Ì		į	!	:
PINES SIVAL	`	I	-	1			Ì		:	!	į
POL SIVA	POL POLYPBOIETH	IF NCY VIRIS (1908, A 16 AGAI, CI ONE CRI. 1)	-115.11	:	1	ļ !	İ	1	:	:	_
-	1 ACTOR	E MC / 1.	=	ļ					i	1	
PDV SIVE		E MC A CE	=	18.18	9.00	100	Ī		-	-	-
1			11:11	16.430		-			!	i i	:
1	LAV FOL YPROTI IN	SIMUAN INDRANCOETICIENCY VIRIUS (Kow 150), ATE)	9			į		İ		İ	i
		NCY VIRIS IN W ISOLATE	=					<u> </u>		-	Ī
No.		NCY VIRILS IN NW ISOLATE)	3	<u> </u>	!		Ī		i	:	
1	CAN POR VEROITE		_						<u> </u>	<u>-</u>	<u> </u>
1		IN (ABAILED IN 1800, ATE)	-	20 60	21.15				<u>. </u>	<u> </u>	į
		A POST OF THE PARTY	٠,	į							i
PENY SIVE			,	2						_	İ
PGAG SIVSP		SPOAN PORNOCE KEENCY VIEWS PRINCE INC.			2			j	-	<u> </u>	
PPOL SIVE	POL POLYPROTEIN	15 (PBI/OCT) ISOLATE	9	ĺ		1	Ì	İ			-
PGAG SIMMS		US (STANISOLATE)		1	1		Ī	Ī		i	;
PEN SIVAT	-		į	161.300	15		İ	Ī	İ	i	Ī
PPOL SIVAT	TEIN		Is	Ī			Ī	İ	İ	İ	1
PREV SIVAT			1	Ī		Ì	Ì	İ	i		1
PDV MON			017.00	Ī		Ī	İ	Ì	Ì	Ì	Ī
PPOL MONTE		ET VINUS	=	10005	Ī	Ī	Ť	Ţ	i	İ	Ī
PGAO MONO		A VIRUS (PUNV)	-	Ī		İ	Ť	İ	<u>-</u> i		i
2 2	ASE	TRUS (STRAIN DURIAS)	:::::::::::::::::::::::::::::::::::::::	İ		İ	Ì	İ	<u> </u>	1	i
PAGE 1 VZ VB		VARICES LA 2051ER VIRUS (SERAIN DUNIAS)	!	101.10		Ī	İ	T	<u> </u>	<u> </u>	-
THE VEVO	LARGE CHA	IRUS (SIRAIN DURIAS)			Ī	Ì	İ	İ	İ	İ	_
2000	LANCE IECOMENI PROTEIN	IRUS (STRAIN DUMAS)	2	15 79 . 1600		İ	i	İ	<u>-</u>	1	Ī
200	GENE 11 PROTEIN		101-9					<u>-</u>	<u> </u>	<u> </u>	Ī
	Dere de la Caracteria	A COSTER CIRCIS (SI	100 00							<u>-</u>	-
										l	Ì

					-				-		Ī
Incore at	1.02012004	AB \ truese (no but terteghalfit)		7 6 7 4 9 7	4 4 4 4	V V V	14.5	ILA 6 AI	173	46	1.02
	100000	WRUS			1				<u> </u>	<u> </u>	
1		VARIOTI A 20STER VIBUS (SIRAM PURIAS)		Ī	-			<u> </u>	1	1	
74.74	VINOW GENT IN PROJECT	111111111111111111111111111111111111111	107.134	13:51		8		-		-	-
0 A A A	CENT 31 PROTEIN	TEALS INCHASE					-	<u> </u> 		_	
	The standard wastow seconds				İ	İ	İ	<u> </u>	1	<u> </u> 	
20.20	MOI MOI WANTED	TA POSTER CARTE CONTACT DEPLACE	<u> </u>			j	-		1		
MESS VAVO	COG 15 NEXOLUNE PROTEIN		-				_	-	_		:
CAN IS THE	PROMINA REP CENE 4 PROTEIN	VANCELLA 205 FER VIRIUS (SIEAR) DUPLAS			İ	İ	<u> </u>		<u>_</u>	<u> </u>	
	The state of the s	A. ZOSSER VINUS	10.00		j	İ	i	Ì	<u> </u>	1	ŀ
PVCAC VZVD	CLYCOMOIES CO.	THE PERSON NAMED IN	7.70	₹ 2:E	_	!			-	<u>'</u>	1
DAZA STAN	CAPSID PLOTE DY P40					_				-	-
2000	THE PARTY PACKAGING PROTEIN	LA ZOSTER VIRUS (STRAIN			Ì				_		-
200	CACALLO WENT CACAL	VARICELLA POSTER VIAUS (STRAIN SCOTT)		1		-			<u> </u>	1	
PVGC VIVS	CC TCUTCHEIN OF		22.52							-	
POPOL WITH	DHA PYC YYGLASE	WUCK HALK THE PARTY OF THE PART	1								
Shared Laborate	PARA BOY VASS A LE	WOODCHACK HEPATHIS VIRUS 19			İ	Ì	l	İ	<u> </u> 	<u> </u>	
	THE PARTY OF THE P		<u> </u>	200					_		
POPOL WAY	DNA POLYNGRASE			30.00					-		
Photo:	DAIA POLYNERASE	WOODCHACK IEPATITIS VIRUS I	ļ			Ī	İ				
	ALL BY WAS BACE	WOODCINCK IE PATITIS VIRUS &			1	1					
	The state of the s										

TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS

		Praharrade Sequences	Т	CASA CASEA	-1	1		AREA 6 AREA 1	П	AREA! AB	ARCAL
Т			10110		1	638-672 746	346-838 116	1202	+	+	T
TAKARI	TANKE OF THE ACT OF THE PROTEIN	TISH	Τ		\mid			7			0361 000
Т	THEOR		-	460.487 607-634	Г	754.781 829	951-621	904-931 11220	1220-1254 154	2	
Т	R (CELL SURFACE)	NCKETTSIA NICKETTSII	72	12	-	-			-	1	
Т				120.147	-	-			1	1	
9	Q AND BE ON THE PARTY OF THE PA	OBILIS	1	T	-		Н		1	+	T
	PECT/MSOR.	3			\mid	H		-		+	T
	LANG PROTEIN				-		-	-	1	†	
100	LANE PROTEIN		٦	444.524	-			1	1	1	T
	SKI PROTEIN	43	Γ	218.246	-			1	1	1	T
	A AB A BLOCKHOOL HOONATE DEHYDROGENASE	2	Ţ		-	\mid		-	+	1	
3	THOSE THOSE TO THE DELIVERAGE NASE				-	\mid	-		-		
MAGD ECOL	PROSPRIOR LOCAL SECTION OF THE PERSON OF THE	7	103-501	-	+	+		-	-		
PARO SALT	PROSPINATION OF THE ANGERASE		7		+	+	-	-			
PAACA STAAU	S.AMONOGLYCOSIDE PARCELLINGS			717.621	+	\dagger	+	-			
PAAT BACSP	ANSFEANSE	COLI	151-378	-	\dagger	+	1	-			
PAAT ECOLI	ANN EMASE		٦	7	1		-	ļ-	-		
PABC ECOLI		CTIS		10.204 209.27	=	+	+			T	
PABIC LACIA	SISTANCE PROTEIN ABIL	AND A CHESTING TIMEFACIENS	127.154		1	1	1	+	+		
PACCE AGRIU	PRESSOR ACON	ACCOUNT ON 1	198-432		-	1	+	1		T	
PACEA ECOL		SCHOOL COL	48.75					+	\dagger	İ	
NOVE NOVE	351		Γ	613-640				+	+	1	
	CONTRATE INDIATASE		Ţ	-				-	+	1	
NOW.	CONTRACTOR OF A REGISTRO	ALCALIGENES EUTROPHUS			-					1	
NOW ALCEU	CELOIT CALMENTER	ESCHERICHIA COLI			+	-					
PACP ECOLI	ACYL CAULEA PROJECT TO THE OTHER A BRECHMSOR	ESCHENICHIA COLI	713-747		+	1	t	ŀ			
PACE ECOL	ACTUAL AVIN RESISTANCE PROTEIN A PRECEDENCE	PECHERICHIA COLI	┪		†	t	t	+	1		
PACES ECOLI	ACKETAVE RESISTANCE PROTEIN B	ECHEBICHIA COL	\$12-550	726-753	+		1	-	T	Ī	
PACE ECOL	ACRUELAVIN NESISTANCE PROTEIN ?	STATESTON VERY CORT ICOLOR	137-184			1	1	1	1		
PACTS STREE	NUTATIVE KETOACYL REDUCTASE	STREET WONDCYTOGENES	237-264	\$16-603	1		1	+	T	T	
PACTA LISMO	ACTINASSEMBLY INDUCING PROTEIN PRECUASOR	SACKADIA I ACTANOMIANS	1139.3163		+		1	1	1	T	
A COS NOCIA	ACV SYNTHETASE	TO CALLIA CI MATILIA	136-170		7			1	1		
PADAA BACSU	VETPHOSTILESTER-DNA ALKYLTRANSFERASE	DACES CONTRACTOR	527-101	454-481 532		1005-1032	1	1	1	1	
USAN AGA	ATP-DEPENDENT NUCLEASE SUBUNIT A	DACETOR STREET	Г	170-903 943	941.977						
PADOR BACK	ATP-DEPENDENT NUCLEASE SUBUNIT B	SACRES SOCIETY IN THE SACRES OF THE SACRES O	115-52	-		-		1			
AND CLOAN	_	CLOSI REGIONA ACETORICA VICINI	398-125			j		1	İ	1	
SAN CLOAB	\neg	CLOSIALION ACETORICI VICTORIA	298-325		-				j		
ADM CLOA	ADH-DEPENDENT BUTANOL DEHYDROGENASE B	CLOSI MINIONINI ACETORITY LICLY	653-680	779.BIN				1			
ACT PATA	LCOHOL DEATH	LICS I MOION ACCTOR	271.298					1			
THE POST	TOHOL DEM	ESCHEMICHIA	25.22	-					1		
THE PARTY	ATATIVE REGU	ESCHEDUNA COC		697.724 92	923-950	2101-066	1109-1190	1387-1414			
	A KD ADIESD	MYCOPLASMA GENTLALICAT	314	-							
	THE CON P. P. P.	MYCOPLASMA PREUMONIAL	276-307					_			
	Nº ATP CARRES	RICKETTSIA PROWAZERII	324.305								
	SHOW YEAR PRES	AEROMONAS HTURUPHILA	410.481	107.61							
1	I PHACALACTO	STREPTOCOCCUS MUTANS	17.4								
	PETA-AGARASE PRECURSOR	PSEUDOMONAS ATLANTICA	1 36.150	165.192							
	ACTERIORY CEN	STAPHYLOCOCLUS AUREUS	47.01								
A STAN		YEASDA'A ENTEROCOLITICA	9	266.491 50	501.530						
1	SVIN AVAILABLE	ESCHEDUCHOA COLL		Т		Ī					
AKIH EOOT	_	ESCHEDICHIA COLI			T						
	NAME OF THE PARTY.	GBACTILUS SUBTILIS	8		Ī						
PAC MON	AVAKIAI E REM			1	T	T					
TAKE BE	AVAILATION DE DICH	ESCHENICHIA COLI	2 007								
7	THUC TOSCHES		200			Ţ					
PALOS PIEAE	_		2	1							
PALCE MEAL	ALCINATE PROP			†	1						
PALCO PIEAR		PSEUDOMONAS OLEOVORANS		110 166	T						
WITH LAND	STREET STREET STREET SECURITIES	PSEUDOMONAS OLEOVORANS									
THE LAND		ESCHERICHIA COL!	200								
NIN ECOL	ALANINE PAR										

PCGFNE	107537654	Sequences	1	-				71.10		ANTA	ABEAS
		ORGANISM	1:	4		_	_				
PALA BACSY	ALANINE IACEMASE					Ť	T	İ			
	ALS OPERON RECULATORY PROTEIN										
PALYS BACSP	AUTOLY SIN PRECURSOR	34 15					İ	İ			
PALYS BACSU	AUTOLYSIN PRECURSOR	A1 19 C1 16	246.27								
PALYS STAND	AUTOLYSIN		L	307.118	446.473						
PAGA STILL	AMIA PROTEIN PRECURSOR		1								
	ON ICOREPTINE TRANSPORT PROTEIN ANIE	STREPTOCOCCUS PARUMONIAE	187-214						į	i :	:
PANDA ROOLI	ANGWORE PTIDASE AN		П	199.236		j	!				
PALE URLA	HETA LACTAMASE PRECURSOR		331.356					1			
ALM BAY	YTOSOL AMENOPEPTIDASE	8		2.8				1			
1,000	LIMINOPEPTIDACE N		189-559				j				
100	CARD AMMORPTIDASE		110-133								
OVER DAY	A LONDON PITTO A CE T	sns	80(-192				i				İ
	LI PAIA ANY ASE I										
	LI PHA ANYLASE 2		131:13	\$07.534				١			
TANK STATE	POTANIA SUMP AI BAIA, ANNO ASE		20.00								!
	I BUALANYI ACCI	145	210-307								
1200	BETA. ALVI ACE PRECIBEOR		61.88								
OUT TANK	RETALAKYI ACE		48-09		143.1184			١			
THE COUNTY	PALYAR CHOTHINETA ANYLASE THERMOPHILIC PRECURSOR	DSULFUROGENES			459.486						
	CLINDANY ASPRECIMENT		103-148	410-510							
TANK TAKE	MAI TOCEDUC ALPHA-AMYLASE PRECUASOR	BACILLUS STEAROTHERMOPHILUS	(\$0-920	П							
DAM BACK	RAW. STARCH-DIGESTING AMPLASE		210-237	435-465	615-642						
VALUE AND A	AL PHA-AMYLASE PRECURSOR		415-453								
PALLY ALTHA	AT PHA. ALM ASE PRECUESOR	ALTEROMONAS HALOPLANKTIS	(61-991								
DATA BACAL	AL PHA. AMYL ASE PRECURSOR	UEFACIENS									
PALM WACH	ALPHA-AMPLASE PRECURSOR		212-239	437.476							
PAMY BACK	ALPHA-ANTLASE PRECURSOR	นบพ	П	441-483							
PAMP BACSU	LPHA-AXMLASE PRI		Т	Т	1,2,1						
PANA BUTFI	LPHA-AMMLASE PR		Т	66.00	20.676			Ī			
PANY CLOAD	PUTATIVE ALPHA-AMMLASE										
PANY CLOTU	LIPHA-AMMIASE PRI	LFUXOGENES	200	780-710							
PANY STRUM	ALPIW-AMMLASE PR	STREPTOMYCES LIMOSUS	313.400								
PAUTA AZOVI	MITROGEN FLYATION PROTEIN AND		1								
PANTO AZOYI	THOCENASE INON-		369.396								L
WALL ACOVE	WE SOUTH		93-130	169.203							
PARCE ESERVE	PHYCOSII ISOME 120 KD LDOKER POLYPEPTIDE	NO	31.78								
PAPE STATE	HYCOBILISOMA LDO		17.64	383-613							
PAPCE STONE	PHYCOBILISONG 120 KD LDKER POLYPEPTIDE	SYNECHOCYSTIS SP	\$2.79								
PATHE SALTY	ALKYL HYDROPEROXIDE REDUCTASE C11 PROTEIN	SALMONELLA TYPHIMUNIUM	62-89								
PAM ACIGLY	PROTEASE I PRECUISOR		478-505								
PAPE ECOLI	PRÓBABLE CYTOCHO		2								
PAPRO PSEAK	ALKALDÆ PROTEASI	PSEUDOMONAS AEAUGINOSA	2	7							
PAPRE PSEAE	ALKALDIE PROTEASI	PSEUDOMONAS AERUGINOSA	133.193	20:33	247.277						
PAPT ECOLI	ADENDÆ PHOSPHOR	Ī	21:121			7101 000	,,,,,				1
PAPU THEET	ALPHA-AMTLASE-PULLULANASE PRECURSOR	R ETHANOLICUS	276-303	Т	936-982	987-1014	210-1234	1381-1408			
PARCA MYCAR	ARGINDYE DEDWINASE	MYCOPLASMA ARGININI	99	2							
PARCE ECOLI	AEROBIC RESPONATION CONTROL PROTEIN ARCB	ESCHENICHA COLI	02.150	207.700	199-426						
PARCE PSEAE	PROBABLE ARGINDIE/ORNITHINE ANTIPORTER	PSEUDOMONAS AERUGINOSA	274-301	02790							
PARGA ECOLI	ANDNO-ACID ACETY	-	5								
PARGT ECOLI	LYS.ARG-ORN-BINDE	ESCREDICARA COLI									
PAROA STAAU			20.00								
TOO SOUN	HORISMATE SYNT	SALMONELLA TYPHI	24.33								L
PAKOL SALTI	HORDAGA IE STATA	BACH LUS SUBTRUS	49.76								L
PARUD BALSO	STANCHOLINA										

		1 34 94 mm		7	AMEA	ARIAL					
	071704			Т	Г			1	1		
	CAULTIN CE I	ESCHERICHUA COLL	T	137.157	266-324						
PAROK ECOLI	SHIKDATE KIPASE I	YOGENES	T	Т							
ı	N PACCOR		797-562	1							
ı	ALL PROTEIN	SCHENCHIA COLI	201-238								
_		FCCHERICHIA COLI	_								
_	ARSENICAL PURO MEMO	TAPHYL OCOCCUS AUREUS	1	107-111							
PARSE STAND	ARSENICAL PUND MEMBILANE PROTEIN	KTAPHYLOCOCCUS XI/LOSUS	٦	22.5							
ALES STANY	ALSENICAL PUND MENDELLARE PROTEIN	CTABLIST OF OCCUS AUREUS	\$6-93								
PARSA STAAU		SCUEBICHIA COLI									
ARTA ECOLI	ALTA PROTEIN	PACIFICALIA COL		213-240							
ART ECOL	TRANSPORT SYSTEM PR	EXTREMENTA COLL	176-206								
1001	TRANSPORT SYSTEM PR	ESCHENCAIA COLI	Г	478-505	199.118	820-836			İ		
	ACCRECATION SUBSTA	ENTEROCOCCUS PAECALIS	Т								
	A COARTATE - AND CONTA	ESCHENICINA COLI		:							_
7	AVARIALE	FECHIERICITY COM									
	ASPARACING STRUMBLASIS	EXTERICITY COL.	=								
PASHC ECULI	KEGULA KINY PROTEIN	BACH LUS SUBTILIS	7.34							L	L
PASPA BACSU	ASPARTATE ANDIONIA	ECCUTENCHIA COL	204.236								L
ASPA ECOL	ASPARTATE AMORIONIA	SCHOOL STANDERS	204-231								L
ACOA CURALA	ASPARTATE ANDMONIA-LYASE	SEUCH IN MANCESCENS	252-288		L			:			
PAS PAG	ASPARAGINASE	BACILLUS LICHENIC COMMISSION	100.210	•							1
TOWN BY CO.	I ACPARAGINASE PRECURSOR	ERWINIA LITATORINI.	9								1
200	CLITTAKINASE.ASPANAGINASE	ACINETOBACTER OLUTANITASSITICATO	154.101			L					1
	A PRINCIPLINA TE SYNTHASE	ESCHENICHIA COLI			1						1
PASSY ECOL	ALGINIO SOCCOLA TE	KETHANOSAKCINA BARKERI		976					L		
PASSY METERA	AKCINENCONCECON	STAPHYLOCOCCUS AUREUS	0					-			
PATEP STAAU	POTENTIAL ATP-BINDING FROM THE ATPASE A	ENTEROCOCCUS FAECALIS	9	1		1	-				Ц
PATKA ENTIA	OTASSUMACOPIES.	ENTEROCOCCUS PAECALIS	280-310								
PATKS ENTRA	NO FASSIUMICOPPLE.	SALMONELLA TYPHINDINUNI	20.50 00.50				ļ				
PATHO SALTY	MG(2+) TRANSPORT	CYNECHOCOCCUS SP	333-260								
PATTE STATE	ATP SYNTHASE A CHADA	VIRRIO AL GINOL YTICUS	11:38			1					
PATTY VIBAL	ATP SYNTHASE A CHUIN	ANABASNA SP	9.36	2	_						<u>!</u>
PATTA ANASP	ATP SYNTHASE ALPHA CHAIN	PACIFIE MEGATERIUM	4-36	\$ \$ \$							L
PATPA BACM	ATP SYNTHASE ALPHA CHAIM	ECCATEBICHIA COLI	486-513			1		1			L
PATPA ECOLI	ATP SYNTHASE ALPHA CHAIN	ENTER COCCUS FAECALIS	4-16	484.518				1	1		1
PATPA ENTRA	ATP SYNTHASE ALPHA CHAIN	CONTRACTOR OF THE PROPERTY OF THE PARTY OF T	362-409				4		+	1	ļ
PATTA MYCGA	A ATP SYNTHASE ALPHA CHAIN	MYCOTASPIA CALLIST	9						1	\downarrow	1
A TO A PROME	S ATP SYNTHASE ALPHA CHAIN	PROTICE COMPANIES OF THE PROPERTY.	165-200	459-416	L				 	1	1
HEAVE AND A	ATP SYNTHASE ALPHA CHAIN	RHODOSPINIT.UM RUBRUM	10.16	\$62.589	L	_	_	Ц			4
	ATPACE ALPHA CHAIN	SULFOLOBUS ACIDOCALDANUS				-				_	4
1	ATT CONTINUE ALPHA CHAIN	SWECHOCOCCUS SP		163.180				L			4
WINT STATE	ATT CONTILAGE ALPHA CHAIN	SYNECHOCOCCUS SP		5	-		-				4
PATPA STRUM	ALT STATISTICS AT BUILDING	SYNECHOCYSTIS SP			1	-		L			
PATPA STATE	JAIP STRINGS ALTER CUADA	THE DAY OF THE BACTENIAN PS.3	97.4		1	+	-	1	-	L	L
PATPA TIED'S	ATP STRINGS ALTER CHAIN	VIBIUO ALCIMOL YTICUS	3		1	1	-	-			L
PATPA VIBAL	ATP STRIPAGE ALTER CITY OF	ANABAENA SP	200	200	1	-	\downarrow	ļ	-		L
PATPE ANASP	P ATP STREMASE BEIN COMM	MACELLUS FIRMUS	<u>3</u>			1	1	1			L
PATPE BACK	ATP SYNTHASE BEIN CHAIN	LAYCOPI ASMA GALLISEPTICUM	375-402		4	-	1	1	-	-	ļ
PATPE MYCL	PATPS MYCOA ATP SYNTHASE BEIN CHALL	RHODOSPORT LUM RUBRUM	359-386		4		1	1	1	-	-
PATPB RHOR	U ATP SYNTHASE BETA CHUM	SUB SOLOBUS ACIDOCALDARUS	161-191					1		-	ļ
PATPS SULAC	C ATPASE BETA CHAIN	ENARCHOCOCCIIS SP	381-408				<u> </u>	4	1	1	\downarrow
PATPS SYNPI		SAMECHOCOCCIS SP	116.162	301-408			-	1		$\frac{1}{1}$	1
PATE STIPS		PANETION VETTE CO	191-406	L	_				-	1	\downarrow
PATEB SYNY	ATP STATTICASE BET	ANABARNA CP	109-139	143-170		Ц		4	4	+	1
PATTO ANASP	ATP SYNTHASE DEL	STORY ST.	8	133.160					-	1	+
PATPD BAC	ATP SYNTHASE DEL	SACULOS TOMOS	112.159						-	-	+
PATPO BACME	WE ATP SYNTHASE DELTA CHAIN	SACILLOS PLOS INCOMES DE LA IS	73	_					1	4	1
PATPO ENTRA	A ATP SYNTHASE DELTA CHADA	ENTEROCOCOS PACACIO	3.16	116.149					4	1	+
PATPO PROMO	AO ATP SYNTHASE DELTA CHADA	FROMODORICE INCAMANA E BI ACTICA	133-152	Г	_				4	4	+
	MANUAL TAX STREET	MOUNTARULEMENT FOR					-	ļ-	_		-
			***			-	_	_	_	_	Ì

	1	Prohasyoth Sequences	П			Т			_	
FILE HAME			J	AREA? ARE	AREA AM	1 V V V	TOTAL PART	4	1000	4
A 19/18 OTTA	ATP SYNTHASE DEL TA CHAIN	1.5.	121-00	+	1	+		+		
PATPD SYNY3 A	IACHAIN				1	1		-		
PATPO VIBAL A	TA CHAIN	VIBRIO ALGINOLYTICUS	10-13	1	+	+	1	+		
PATPE BACFI AT	ONCHAIN		23.50	$\frac{1}{1}$	+	$\frac{1}{1}$	1			Ī
PATPE MYCGA AT	ON CHAIN	=	97.176		+	1				Ī
PATPE PROMO AT	KAN	DESTUN	200		+	+		-		
PATPE SYNPI AT	ONCHAIN	CUS,SP1	25.10		77.55	$\frac{1}{1}$	+			Ī
PATPE ANASP AT			T.	1	<u> </u>	$\frac{1}{1}$	-			Ī
PATPE BACFI AT			1		+				Ì	
PATPE BACME AT				122-170	1	+		+		
PATPF MYCGA A		ISEPTICUM		130-197	1		-	1		Ī
A THE SYMP!	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	П	111.159	1	1				
A THE SYNTA		SYNECHOCOCCUS SP	13.39	128-155			1			
1	80	THERMOPHILIC BACTERUM PS.1	\$0-77							
			176-310		-					
C C C C C C C C C C C C C C C C C C C			253.283		_	-		ļ		
PAIRO ECULI	ALL STRINGS GAMEN CHAIN	LISEPTICIAN	T	92.140	-					
AIN MYCIA			270-297			-			_	
PATPG RHOXU A			280.303				_			
PATPG SYNPI IA			Ť	200.103	-					
PATPO SYNN'S A			T.		1	<u> </u>				
PATPI MYCOA A		UALLISEFIICUM		$\frac{1}{1}$		+				
PATPX ANASP A			Т		+	1		1		
PATPX BACF! A			2	28-36	+			+		
PATPX RHORU A		กอสบาง	٦		+	1				
A LANK SYNDIA	ATP SYNTHASE B' CHAIN		٦	131-155	1			4		
A SYNCE A	TP SYNTHASE B' CHAIN		20-100		1	-				
A LYNY STATE	ATP SYNTHASE B' CHAIN		104-135	-				1		
PATPZ BACME A	ATP SYNTHASE PROTEIN!	ושו	14-62		1	1	1			
PATPZ SYMPI	TP SYNTHASE PROTEIN I		╗	1	1	-	-			
Т	AVIRULENCE B PROTEIN	TUNGAE	=	233-260	+	-	-			
PBA71 EUBSP 7	7.ALPHA-HYDROXYSTEROLD DEHYDROGENASE		6.53		+	+		+		
PBA72 EUBSP 12	7. ALPHA-HYDROXYSTEROID DEHYDROCENASE		26.53		\dagger	+	1	+		
PBACH HALHM HALORHODOPSIN	1	AL OBIUM!	163-170		\dagger	1	+	+	1	
PBACH HALSG H		15	12.00			$\frac{1}{1}$	$\frac{1}{1}$	1		
PBAES ECOLL S	SENSOR PROTEDN BAES		_	T	7	301.17	200 (20)	1014-101		
PBAG STRAG H	IGA FC RECEPTOR PRECURSOR	AUALALIIAE	7	97-97	907-107	Т	Ţ	┱		
PBANO VITSP B	BACTERIAL HEMOGLOBIN		21.4.1	1	+	+	1			
	BILE ACID-DIDUCIBLE OPERON PROTEIN C		✝	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	\dagger	+	-			
PBAIN ECOLL IS	SENSOR PROTEIN BARA			100		+		<u> </u>		
-	SENSOR PROTECH BASS			+	1	+		+		
-	PUTATIVE BACTERIO-OPSIN ACTIVATOR	IALUBIUM!	7	-	\dagger	1		+		Ī
=			5		\dagger	1	1			
PBCC ECOL	BIOTIN CARBOXYL CARRIER PROTEIN	ESCHEMICHIA COLI	100	+	\dagger	$\frac{1}{1}$	1	+	ļ	
PBCHH MHOCA	METHYL HANSFERASE		340.376		t					
AND AND A	TROUGHTON TOTAL		Ť	\$15.646	-	-		-		
PBCN3 CLOPE	BACIEMOCIN BUNG	PROCENT CONTACTOR	T		T	 				
		ACETOBACTER YOUNGE	١	1055.1012	T					
PBCSC ACEAY	CELLULUSE STRIPAGE OFFICE CONTROL	ACETOBACTED XVI MIN.	T		l	Ì		-	-	
		ACMETORACTER CALCOACETICUS	20.21	l	t	+				
7	BEACON IS INCOME OF THE NAMED IT PROTEIN	FSCHEBICHIA COLI	243-270		T	\mid				
_	MCH AFINITI CHOLING INCOME TROUBLE	HAEMOPHII IIS INTILIENZAE	9	l	\dagger			-		
Т	BEXA PROJECT	HAEMOPHILUS INTLUENZAE	Ŀ	236.253	\dagger	+	-	 -		
	SEAL TROITER	HAEMOPHILUS DIFLUENZAE	Т		 				_	
THE VITA	PACTERIORERATION	MITROBACTER WINDGRADSKY!	=							
1-	EVOLVED BETA-GALACTOSIDASE ALPHA-SUBUNIT	ESCHEDICHIA COLI	955-985	-		<u> </u>				
٦.	RETA-DALACTOS DASE	BACELUS STEAROTHERMOPHILUS	199-633		r					

l		Prokaryon Schoolson				-					ļ
PCCENE			I	3	1000						١
٦	O STATE OF THE PARTY OF THE PAR	1		T	Ť						
PROAL CLOAB		CENTS	5	Ì	Ť	-	-	Ī	-	i	
			245-272		İ	İ	Ī	Ì			
POGAL KLEPH	DETA-CALACTOSIDASE	CKII	105-332			1					
PBGAL LACDE	BETA-GALACTOSIDASE	us	<u>_</u>			Ì		T			
BOAL STRIR	SETA-GALACTOSIDASE		39-86	179.206		Ť					
PEGAL SULSO	BETA-GALACTOSIDASE		139.156		1	Ì		T			
BOAM LEULA	BETA-GALACTOSIDASE SMALL SUBURIL	NCUS	36-160		İ	1		:	į		
BOAM SULSO	SETA-GALACTOSIDASE			ī			-				
PBGLA CLOTIM	DETA-GLUCOSIDASE A		259.286	315.409	554-501	- F					
ACL D CLOTM	THERMOSTABLE BETA-CLUCOSIDASE D		460-494	\$36.363							
1,001	RETA CALUCURONIDASE		i								
200			Т	414.463	692.719	118.165					
ACC.		2	Т	Т	T						
	A COLUMN		3	-							
7	LASE DIN		163-197								
_	SOLVASE	PEANING OCCURS AUREUS	061-(91								
5		BACH CHIAFEITHS	33.60								
Г		SACILITY SELECTION	145-172								
1		BACILLOS STINCESCO	130-157								
PRICE ECOLI			141.131								
PRICE BACKH	IASE	BACILLUS SPRAEJULUS	11110	335.305							
DACK	RETALLACTAMASE PRECURSOR, TYPE I	BACILLUS CENEUS	130	204.33							
712 17 17 18	BETALLACTAMASE ROB-1 PRECURSOR	HAEMOPHILUS INFLUENZAE	Т	301.338							
TOTAL STREET	BETA J ACTAMASE PR	BACILLUS CEREUS	Ī						L		
ומייים היייים	BETT ACTANAGE PR	BACILLUS SP	T	95.					_		
Party BALS	PETAL ACTALANT	BACULUS CEREUS	Ţ							L	
NBLAN BACK	DELACTOR AND SECTION OF THE SECTION	PSEUDOMONÁS AERUGINOSA	R							L	L
PBLA4 PSEAD	7	BACILLUS CEREUS	\$ 2	27.7						L	
PRIAB BACKE	BEIA-LAU AMASE FRE	BACTENOIDES FIXGILIS	\$								L
PBLAB BACK	BEIN-LACIONAL PROPERTY	BACALUS CEAEUS	93-170							L	L
PBLAC BACLE	BEIN-MANAGE BECTIESOR	BACILLUS LICHENIFORMIS	67.76							L	L
PELAC BALL	SETA LACTACACE M	PROTEUS MIRABILIS	181-221							L	L
Tark right	SELA-MEINER	PROTEUS VULCARUS	5							L	L
PBLAC FROVO	METALI ACTAMASE PRECURSOR	STREPTOMYCES ALBUS G	2								L
מושר פווער	BETA I ACTAMASE PR	KLEBSIELLA PWEUMONIAE					-			L	L
	BEINGE I MAKE REPR	STAPHYLOCOCCUS AUREUS	2.6	8							L
PBLM STAND	PERIL LEGITATION OF PRINCIPLE PR	ESCHENICIDIA COLI	3	200		1					L
PBLA0 ECOL	_	ESCHENICHIA COLI	<u>₹</u>				\downarrow			-	L
PRIA ECOLI	_	BACILLUS LICHENIFORMIS	20.52	200			95		1	1	L
THE DATE	TOWN A TOWN THE	STAPHYLOCOCCUS AUREUS		22.72							L
PILAR STANC		TREPONEMA PALLIDUM	2				1		1		L
PBM TREPA	т	BACLLUS SUBTILIS	23. 24.			1	\downarrow	1	1	1	L
PENC BACSU	MULTIPACO RESIST	PSEUDOMONAS PUTIDA	3		1		\downarrow	1	1	L	L
BNZA PSET	BENZENE LA PROVINCE NETA SUBLINIT	PSEUDOMONAS PUTIDA	119-153							-	ļ
PBNZB PSEPU	BENZENE I, J. DIOA I GENALE CENTRAL	PSEUDOMONAS PUTIDA	139-213						1	1	ļ
PRINZO PSE-TO		DESULFUROLOBUS AMBIVALENS	2.2	263-280		130			+	1	-
PBPS2 DESAM	C BF22 FROILIN	PSEUDOMONAS AERUGINOSA	<u> </u>	200				\downarrow	1	-	1
TBIMB ISEA	-	PSEUDOMONAS AERUGINOSA	7.75 7.75 7.75	1	1	\downarrow	1	1	1	-	L
PBIAE TSA	ILANSTON I PROIE	PSEUDOMONAS AERUGINOSA	7-74					-	+	-	ļ
PBIAO PEAE	7	ESCHENICHEA COLI	27.486		1	1	1	1	1	1	-
PBTUB ECOL	THE AND BUT THE ANG	┪	ŝ	1		1	1	1	1	-	1
Partie Conc.	THANKE IPTION REC		\$. 32	\downarrow	\downarrow	\downarrow	\downarrow	1	\downarrow	-	Ļ
PBVGA BURG	I BOARSCHOT LINE	BONDETELLA BRONCIUSEPTICA		\downarrow	\downarrow	\downarrow	1	-	+	-	-
	THE PROTEIN BYGB PRECURSOR	BONDETELLA PERTUSSIS	2		1	\downarrow	1	1	-		L
PBVCB TOTAL	CASON PROTEIN BY	BONDETELLA PERTUSSIS	20,00	┱		1	1	+		-	-
DOG COM	THE SEASON PROTECTION PRECURSOR	BOXDETELLA BRONCHISEPTICA	2	7	7	•		900.000	1159-1207	 	
PBVGS BOXBA	A VIKULENCE BYOS PROTECTIVE A PRECURSOR	CLOS TRENUM BOTULINUM	3	686-739	737-762		Т	13		+	╀

					Ī				-		ſ
PCGENE	107117014		AREAL	AREA 1	AREAJ	AREAS	AREAS	AREA S JAREA ?	П	ARGA! A	ARIA!
PRXCI CLOBO	BOTUL INUM NEUR				П		-7			†	T
PBXD CL080	BOTULINUM NEUR		╗	٦	727.770	T	Т	100-901	1000-101	1	T
PBXE CLOBO	BOTULINUM NEUR	CLOSTRIDIUM BOTULINUM	٦	П	704.753	Ť	Т	A 101 7 A	4	\dagger	Ī
PBXE CLOBU			Т	30-36	200.73		100-017			1	
PBXF CLOBO	BOTULINUM NEUROTOXIN TYPE F PRECURSOR		01/40	271.5	414.741	201-1101			1	t	
PCSSO MICAE	CYTOCHRONGE CS50	MURUCYSTIS AERUGINOSA	Ţ	100.111	165.192	376.306	333.567				Ī
CADA BAGI	PROBABLE CALMUNA-TRANSPORTING ATTACK	CTABLIC AND STORY	8	\$36.570		Г					
THE PERSON NAMED IN COLUMN TO PERSON NAMED I	PROBABLE CAUMINOS INVARION CANCES	ESCAFAICHIA COLI	Т	413.443							
PONT NEWS	EL CAPRER ANCHORNO PROTEIN PRECURSOR	YERSINIA PESTIS	ē	416-457	\$30.557	99-619					
1		BACKLUS ANTHRACIS	106-136								
NAME OF TAXABLE PARTY.		BACILLIS ANTHRACIS	Š								
PCAPP ANANI	_	ANACYSTIS NIDULANS	348-393								
PLABO ANASP	PHOSPHOFNOL PYT		20.135 1.23	157.184	687.728						
PCAP CORGE	PHOSPHOENOLPYR	CORYNEBACTERIUM GLUTANICUM	15-42								
PCAPP ECOL	PHOSPHOENOL PYRUVATE CARBOXYLASE	ESCHERICHIA COLI	15-62								
PCARA BACSU	CARBAMOYL-PHOSPHATE SYNTHASE	BACILLUS SUBTILIS	114.319					•			
PCARE BACSU	CARBAMOYL PHOS	BACILLUS SUBTILIS	790-831								
PCAUS ECOLI	CALBAMOYL-PHOSPHATE SYNTHASE LARGE CHAI		=							1	
PCAT2_STAAU	CHEORANDHERICOL ACETYL TRANSFERASE	STAPHYLOCOCCUS AUREUS	1	2.114						1	Ī
PCATO STANU	CHLORANTHENICOL ACETYL TRANSFERASE	STAPHYLOCOCCUS AUREUS	T							1	
PCATA ACICA	CATECHOL 1,2-DIOXYGENASE	ACINETOBACTER CALCOACETICUS	9							1	
PCATA BACST		BACELUS STEAROTHERNIOPHILUS	2								
PCATA ECOLI		ESCHENICHIA COLI	378.606						1	T	Ī
PCATA MOCLU	CATALASE	AUCHOCOCCUS LUTEUS		10,000						\dagger	Ī
MATA SALTY	CATALASE IOI	SALMONELA L'ITANINOMIONI		380.001						\dagger	
PCATE ECOL	CATALASE HOU	Control of Control							Ì	İ	
3	CHOOLANDIEMICOL ACETTLINAMS ENASE	CONTRACTOR					T			T	
XX1 0.000	CHECKLORAL OFFICE AND CHECKLORY	ECONEDICAL COLL	9							İ	
2004	CHI DE AMPHENICOL ACETYL TRANSFERASE	PROTEUS MINABILIS	93.110								
PCAT STAB	CHE DRANDHENICOL ACETYL TRANSFERASE	STAPHYLOCOCCUS INTERNEMUS	=	1							
PCAT STICAGO	CHLOLALOPEDACOL ACETYL TRANSFERASE	STREPTOCOCCUS AGALACTIAE	ī	17.114							
PCBME COXOLU	CENE PROTEDY	COXIELLA BURNETII	204-336								
MENT THEN	CALBOXYPETIDA	THE LUNDACTINOMYCES VULGARUS	46.75								
D003 V224	TRIVA MUCLEOTIDI	ESCHENCHIA COLI	10-40								
PCO-CK SYND)	COS CONC MECH P	SYNECHOCOCCUS SP	2						1		
SOOT SUPER	CO3 CONC MOCCH P	STREETHOLOGOS ST	200							T	Ī
MOAS THERE	CTCLOMAL TODEA I MANASE	-+-	110.444	616.641						T	Ī
TO TO TO	כאכן טאיין נטפני		10.23	436.466	6 5.642					T	
	CYCL CALAL TONE XT CLINCANOTRANS PRECURSOR		217.244	442.472	594 651						
DVI DVO	CYCL CHALL TODE XT GLUCANOTRANS PRECURSOR		217.244	447-172	594-647						
PODGT BACO	YCLOMAL TODE		10-01		·						
NODOT INCS	CYCLOMALTODEXT GLUCANOTIVANS PRECURSOR		210.217	292-512	615.642						
PCDOT BACKS	CYCLOMALTODEXT GLUCANOTRANS PRECURSOR		409.471								
PODGE BACS			210-237	435-462	19-919						
PODOT BACSP	CYCLOMAL TOOL		20.27	435 465	3						
PODOT BACSS	CYCLOMALTODE		217-744	27.673	394-65					1	Ī
PCDOT BACST	CYCLOMAL TODE	-	316-646							1	T
PCDOT KLEPN	CYCLOMAL TODES	-	212-239						1	1	Ĭ
PCEAL ECOLI	COLICTN EI PROTE	ESCHEMICHIA COLI	-	285.326						1	
PCEAL SHOSO	COLICIN EI' PROTEIN	SPUCELLA SUNNE!	114.14	67.5					1	T	
NO.	COLICINES	FOCHSTICHA COLL	114.164							T	
	_	ESCHERICHIA COLI	334.368							T	T
PLEASE FOR	_	ESCHENICHIA COLI	283.341							T	Ī
75%	7										

FILE RAME FCEAD ECOL FCEAD ECOL FCEAN ECOL	PROTEIN		11:31					_			
				1		1	i	İ		<u> </u>	
	COLKIND	Total Control Control	176-227			1		Ť			
	COLICINA		Т	133:300			1	Ì		i	i
	COLICINA		236-258				İ	Ì			1
т		CITROBACTICA THE COLUMN TO WITH	130-167					1			
L	ISOPENICILIN W EPINEBASE		Г	185-282		415-452		1	-		
т	COL MOR IA PROTEIN		Γ	Г	176-412	415-452					
	COLICON IN PROTEIN		Γ	ĺ							
٦.	I'M I INIDAL YL TRANSFERASE	INOM	9								
			1								
	CFAN FINGRUAL SUBUNIT A PRECURSOR	ESCHENICHA COLI	2	311-436	\$61-195			1			1
	CEAN FINERIAL SUBURIT C PRECURSOR		Т	Т							
2	PEAN ENABLY STRANGT D		Т	344.371							
	STATE OF THE PARTY IS	-	Ţ								
_	CAN PROPERTY SUSCESSION	ISUNI SYNIBIOTIC BACTENU	\$7.93							L	
7	10 KD CHAPERORUM	_	ŝ	1				-			
┪	10 KD CHAPEKURIN	IOMATIS	2								
_	10 KD CHAPERUNIN		2.5							L	L
	10 KD CHAPERONIN		64-93	1						L	L
1	10 KD CHAPERONIN		57:14								
PONIO LEGAG	10 KD CHAPERONIN	NSMI	65.92								ļ
Г	16 KD CKAVEROKIN	5.	16-99								-
L	10 KD CHAPERONIN	TIC BACTERIU	341-382								ļ
		ACTA INCOME TO THE PARTIE ACTOR ACTO	117.163	119.370	425-466						1
POSSES ACRED		ACKORACIEMON IONES ACTERISM	299-333							1	1
SOUTH STORY	LO KD CHAPERONIN	AMOLEA TROITES STREET	201.332	117.364						1	1
NAME OF THE PARTY OF	AND CHAPERONDA	BACELUS SUBTILIS	179-163	296.368							1
11490	AN IN CHAPERONDS	BORRELLA BURGOOK EN	7.144	139.366		L					1
	NAME ON A PERONIN	BRUCELLA ABORTUS									\downarrow
	AN KED CHAPERONIN	CHEAMYDIA PNEUMONIAE									1
THE STATE OF		CILLANYDIA TRACHOMATIS	100-127								1
CHO CARV	60 KD CHAPERONIN	COCOMATION VINOSOM	211-332	337.364	455-482					1	1
SALAN COLORER	60 KD CHAPERONIN	CLOS I MUNICH ACET CENT	337.364	417-444	L	ļ_				1	+
SO O ONCO	60 KD CHAPERONIN	CLOS I CONTOUR PER PARTIE	300.33	26.36						4	+
DEN COMP	IN KD CHAPERONDA	COMMENT BOOMERS	339.366	417.444	L	L				1	1
DATA HAPPU	AND CHAPERONIN	KAEMURIEUS DOCUETT	290.333			L				-	4
PCN6 LEGA		LEGICALLA MACUACIO	298.332	452-479						1	4
		LEGIONELLA PREUMUTILLA	135-161	136.263	337.364	L					4
A LUAN SHITE	SO KD CHAPERONDA	MYCOBACTERIUM LEPIWE		33.55						4	4
		MYCOBACTEMUM TUBERCUCOSIS & BOTTS	110.166				L			4	1
	1	PSEUDOMONAS ALKUGIMUSA		133.170	432.486		L				4
A MAIN STREET	Т	RIGIZOBIUM LEGUNGMONARUM	5	301.116	166.39	L		L		_	4
	6 ID CHAPETONEN	ACKETTSIA TSUTSUGAMUSHI	104.115	33.380							4
POST SYNDS	60 KD CHAPERONTM	SYNECHOCOCOUS	336.363	455.489				Ц			+
CANTO SYNCE	IN KE CHAPERONIN	STREETING STATES IN CO.	3.5			L			_	-	+
CAST ONCY	46 KD CHAPERONTN	TREMOUTURE BALLICAUMITS	10-148	3.5						-	+
POK2 STRAL	60 KD CHAPEROND!	SINE TOM TEST ALBORS	7	172.79		L				1	+
POR VIBRA	N. DIACETYLCHU	VIBRIO MAKVETI	33.400	19:065					1	4	+
PORT BACK	CHEMOTAXES PROT	BACILLOS SUBTILIS	32.35	L							+
DOM VEGO	CHEMOTAXOS PROT	ENCHANGE COL	162.197		-					1	4
KIND THE LA	CHEMOTAXAS PROT	SALMONELLA I FEMINISCHE	134.15	_						4	4
POET BACSU	CHESMOTANDS PROT	BACALUS SUBTINIS	51.5	L			Ц			4	$\frac{1}{2}$
POLEW ECOL	=	ESCHEDITUM COLI	=	L					\downarrow	$\frac{1}{1}$	+
ACIDEM SALT	PURINE-BINDING CI	SALMONELLA I TETTINOMONI	240	L						<u> </u>	+
POLEY ECOL!	_	ESCREDICTION COLI	240							1	+
PCIEY SALTY		SAL COLOCIA ANS	115.105	\$66.593					1	+	+
PCHI MACCI	CIGIDNASE AI PRECURSOR	AT TE DOMONAS SP	345.372					4	1	+	+
CORA ALTSO	CHITDIASE A PRECURSOR	SA STANTA MARCHAN	346.373	_			4	$\frac{1}{4}$	4	4	

		Post arrests Seminantes		1				 -			
PCCENE	10717014		AREAL	A CANA	70117	7	AMEAL	AREA ABEAT	_	T TOMO	AWA.
NO BACC	CHITINASE D PRECURSOR		7	3.2		1		1	+	\dagger	Ī
NOUT SACEA	HITMASE	YTIIRAEA	91.5		1		1	T	\dagger	1	
STEP TOOL	CHITINASE 63 PRECURSOR	CATUS	230-254				1		İ	Ì	
PCHOATU BACSU	HORISMATE MUTA		2		Ì	Ì	+	Ì	i	<u>:</u> 	-
PCHOD BREST	HOLESTEROL OXID	STEROLICUM	DZ-192	1	1		1		T	T	
PCHTA VIDOR	CHOLERA ENTEROTOXIN, A CHAIN PRECURSOR					T	T		T		Ī
PCHYA AGRTU IS	BETA-(1-23)GLUCAN EXPORT PROTEIN	AGROBACTERUMI, TUNIEF ACIENS	1	5		1		T	T	T	
PCHIVE AGRIU	RECEITOR PROTEIN CHYE PRECURSOR		i i		1	1	İ	T	T	T	Ī
PCIN CITTA	CITROLYSIN PROTEIN I		201		1	Ì			İ	T	
PCIENT ECOL	COLICIN I RECEPTOR PRECUASOR		9				1		Ì	Ì	
PCISA BACSU	PUTATIVE DNA RECOMBINASE		178-405				1	1	1	Ì	
ACISY ACIAN	CITRATE SYNTHASE	LATURE	2.E				1				
	CITE ATE SYNTHASE		24.51					1	1	1	
	CITE A TE BEOTOM CYLOROT	JRIUN	184-181						j		!
	CITALITY COLUMN COLUMNS		184-321								
N. P. P.	CIENTE SOCIETA		104.721								
NAME OF THE PERSON	CITALESOUNDES	191	104.221					•			
SAL SAL	CITACIESCUCIONST		9:50								
MICA PSEPU	CHLOROCATECHOL		10.00	İ			İ			- 	
אכוסו בכסרו	CHAIN LENGTH DET		Т	11.00							
CD ECOL	CHAIN LENGTH DETERMINANT PROTEIN	0 0 1 0 1 0 1 0 1	Т	18.32		Ī					Γ
NG D SALTY	CHAIN LENGTH DETERMINANT PROTEIN		T	1					İ		
PCLOS CLOHII	ALPHA-CLOSTIUPAIN PRECURSOR	OLT III ON	Ì,			Ī			T	T	
אקשע בנסת	ATP-BRIDDING SUBUNIT CLPA		560-560				Ì			T	
PCLPA RHOBL	CLPA HOMOLOG PR	RHODOPSEUDOMONAS BLASTICA	Т			1		Ī		T	
PCLPB_BACHO	CLPB HOMOLOG PROTEIN	osos	T	2	338-343	1				1	
MAN ECOL	CLPB PROTEIN		Т	303-330			1	Ī	1	Ì	
MOLEX AZOVI	•	VELANDII	٦	22.30			1		1	Ť	
NO. Y ECOL	ATP-BRYDONG SUBU	ESCHENICION COLI	27.52				1		T	T	
PONIS ECOLI	T. S. CYCLIC NUC T.	ESCHENICHIA COLI	20.77							1	T
PCODA ECOLI	CYTOSINE DEALIDAY	ESCHEDICHIA COLI	1							Ī	Ī
PCOMI_INCSU	A COMPETENCE PRO	BACILLUS SUBILLIS	1					Ì		T	
PCOMO BACSU	COMPETENCE REGULATORY PROTEIN	BACOLUS SUBILLIS						T	1	Ť	T
PCOPS STANU	COP-4 PROTEIN		57. 07.				T		T	Ī	
PCOPB PSESM	COPPER RESISTANC	PSEUDOMUNAS STRINGAE							T		Ī
CORA ECOL		CALIFORNIA TYPHING BURN	194.161							Ī	Ī
COM SALIY	MAGNESIUMCUBA		(6.6)								
PCOTE BACSU	SPOKE COAT PROJEINE	APONICUM	380-407								
200		PARACOCCUS DENITTUFICANS	383-410								
POOK PROCE	CTI CONTROL CONTRASE POLYPEPTIDE I	RHODOBACTER SPHAEROIDES	196-423								
PCONT BACE		BACILUS FIRMUS	19-91								
PCOXX BACSU		BACILLUS SUBTILIS	49-76								
POPP NEIGO	CRYPTIC PLASAGE	NEISSERIA GONORUHOEAE	12.99	602-591							
NOSB ECOL	1	ESCRENICHIA COLI	109-116								
TAS SALTY	MANNOSE-I-PHOSPHATE GUANYLYLTRANSFERASI	ESALMONELLA TYPHOMOJUNI	311-338								
PCYX ECOL	SENSOR PROTEIN C	ESCHENICHUA COLI	154-281								
PCPXG STRSO			157.184								
PCPXU SACEA	6-DEOXYERYTHOLDIN		33:360								
PCPYON BACSU			20.20						1	Ī	
PCPXN ANASP	PROBABLE CYTOC	ANABARNA SP	9E-123							T	T
PCR27_BACTI	27 KD CRYSTAL PR	BACILLUS THUMUNGIENSIS	137-187								
PCR37 BACTM	27 KD CRYSTAL PROTEIN	BACII LUS THUMINGIF.NSIS	13.11								
PCR41 BACSII	19 KD INSECTICIDAL TOXIN	BACH LUS SPIAFAICUS	176.308							1	
PCR42 BACSH	I 9 KD INSECTICIDAL TOXIN	BACH US SPHALKICUS	276 108				ļ				
PCR40 BACSH	STATE OF STA	BACH LUS THANKIENSIS	207.134	252-279	429-463						
PCK 20 BACTO	SECTION ALTERNATION AND AND AND AND AND AND AND AND AND AN	RACILLUS TAUMUNGIENSIS	2.5	135-159	27.464						
LEAN BALL											

	41,196.4	Problem all in the second seco	7.407	_	AREA 2	AKLA	1		T		
	01/11/10	ORGANISM	Т		т						
	SAME CONCLAS DECIFIES	BACILLUS THURINGIENSIS	Т	Т	\$19:615						
NORTH TACK	STATE OF STA	BACILLUS THURINGIENSIS	T	Т							
	JOKO CRISIAL PROJECT	BACILLUS THURINGIENSIS	7	Т	101 111						
KTZ BACTI	S FU CA LOS CALLES	BACILLUS THURINGIENSIS	7	Т							
K72 BACTK	IN KU CKTSIAL TAU ILIN	BACILLUS TITURINGIENSIS	7	200	T						
AV BACTI	T KU CKTSI AL TROILLIN	ESCHENICHTA COLL	20								
NOTEC ECOLI	SENSOR PROTEIN CACK	ESCHENICHIA COM	2.2								
NED ECOLI	DOJEK MEMBAAME PROJECT CALL	FSCHERICHIA COLI &	26-53	ž							
POST ECOLI	CATABOLITE GENE ACTIVATOR	CHICELL A FLEXNER!				İ			İ		
		RATINGMET & A TYPHINGURIUM	26-53	127.154							
PCIE SALTY	CATABOLITE GENE ACTIVATOR	A PROPERTY A PROPERTY									
Т		KLEBSIELLA ALAUGENES	300								
DANGE COLUMN	MAY TO ENE DEHYDROGENASE	ERWINIA HEMBICOLA									
KII LAWA	HY I UCKE DENI DAG	AHODOBACTER CAPSULATUS	389-410	T							L
CRTI MHOCA	HYTOENE DEHTURO	RHODOBACTER CAPSULATUS	3	34-361	-	1	;	<u> </u>	:	÷	_
RTJ MIOCA	CRTJ PROTEIN	DACH LINE THURINGHENSIS	311.355	175.302			!				
AYS BACTA	132 KD CRYSTAL PROT	STATE THE THE PARTY IS	130-771	165.892	1053-1080						
PCRYS BACTB	136 KD CRYSTAL PROTEIN	STATE THE PARTE NAME OF THE NAME OF THE NAME OF THE PARTE NAME OF THE PARTE NAME OF THE NAME OF THE NAME OF THE NAME OF	736-770	16.061							
PCRYS BACTE	133 KD CRYSTAL PROTEIN	BACILLO3 INCIDIOSCICIOS	210-232	701.728	175-802						
1	IN KD CRYSTAL PROTEIN	BACILLUS THUMORENSIS	111.111	165.892	1053-1080	L					
	IN KD CRYSTAL PROT	BACILLUS TITUIGNOIENSIS	216.770	16-068							
PURVE RACTS	INDICAYSTAL PROTEIN	BACILLUS IMURINGIEMSIS	110.11	201.00	1011.1080					j	
ATTACK AND	IN KO CRYSTAL PROTEIN	BACILLUS TITURINGII:NNIN		70.00			İ				
	MANA CENTAL PROTEIN	BACILLUS TIRUMURIENSIS			301.338	774.802					
מונו מערוב	TANK CANCEL PROTEIN	BACILLUS THUMINGIENSIS	217-201								
CILL BACII	SO TO CALL STATE OF THE PARTY O	BACKLUS THURINGIENSIS	737:11	Z I							L
CAYT BACIT	Date Carsina Protein	BACILL US THURINGIENSIS	136-770	2							L
CAYO BACTA	D) ID CRTS I AL PROTEIN	MACH LUS THURMGIENSIS	117-251	100.127	174-801						L
CAYU BACTI	130 KD CRYSTAL PROTEIN	BACTILLIS THUMBIGIENSIS	110.111	866.893	1034-108	_					
CRYU BACTK	PCRYU BACTK 111 KD CRYSTAL PROTEIN	PACH LIN THURWGIENSIS	111.111	163.193	1053-1080						1
CAYV BACTA	130 KD CRYSTAL PROTEIN	BACH LICTRIBUGIENSIS	110-131	145 772	819.810						1
CRYV BACTI	115 KD CRYSTAL PROTEIN	BACH LUS THURWGIENSIS	136.770	16.001				1			1
CRYV BACTK	13) KD CRYSTAL PROJEIN	BACILLIS THURDNGIENSIS	1745.779								1
CAYW BACTA	INOKO CRYSTAL PROTEIN	BACH US THURWGLENSIS	408-659	99	92.68					ļ	1
CAYW BACTA	133 KD CRYSTAL PROTEIN	BACH LUS THURDNGIENSIS	97.110	27.74	3		3	-	1	\downarrow	ļ
CRYX BACTK	139 KD CRYSTAL PROTEIN	ECHERICA COL!	\$4.50	136 :51	100: 100:	2					1
CS33 ECOLI	PCS32 ECOLI CS3 PGJ SYMMESIS 63 RD PROTEIN	ETCHERICHIA COLI	90-117	184-181	208-242						1
CS33 ECOLI	CS) PQ.1 SYNTHESIS OF KD PROTEIN	ESCHEDICHIA COL I	10.43	34.108							1
CSM ECOLI	CS) Paul SYNTHAESIS 33 KD PROTEIN	LAT ANACTEDITAL MALOBIUM	9:43	584.611							1
KSG HALHA	CELL SURFACE GLYCOPROTEIN PRELUKSOR	LAT ORACTE BILDS VOLCANII	21.13	113.331							1
PCSG HALVO	CELL SURFACE GLYCOPROTECH PRECURSOR	ANTONIA MOTOR BY TOUS	\$9.107	L							\downarrow
PCSO METTE		A CHANGTIE TARIS SOCIABILIS	20 101								1
PCSO METSC	CELL SURFACE CLYCOPROTEIN PRECURSOR	FE INCOME OF I	35.50								1
PCSOB ECOL	CEI FORBILIAL SUBU	C Octaining ACETORITY ICEN	===								1
PCTFA CLOAD	COA-TRANSFERASE SUBUNIT A	CLOSINGACH ACETORICAL ICLAL	176.208								4
rette again	COA-TRANSFERASE SUBUNIT B	ACTOR INDICATE TOTAL TOTAL	183-191								4
PCTILB NEDGE	DAVER AGAGRANE PROTEDY CITES	SECTIONIONAL AFRICANOSA	79:13	134.151	160	117.251				-	4
PCTX PSEAL	CYTOTOXIN PRECURSOR	E CATE WHITE COL.	3.5	163-219							4
LYVA ECOL		E COME DICHAR COLI	131-178	L						1	1
PCVAS ECOL	OLICON V SECRET	PACE LISTENIS	197-224	117	1010-1044	1				1	1
PCWPM BACBR	COOPE CELL WA	BACH LUS BREVIS	178-216	360-587	M).088		_				1
PCWTO BACE	MILE CELL WALL	BOLDETELLA PEATUSSIS	44.73	633-659	8		-		1	1	\downarrow
KYAA BORPE	ADDIVITATE CTCLASE PRECONOR	YEASING INTERMEDIA	341-383	193.620		$\frac{1}{4}$			1	\downarrow	ļ
MAY YEAR	DEMINIECTO	BOADETELLA PERTUSSIS	341-568		-	1		1	1	1	1
PCYAB BOLVE	CTAB TRUILIN	BORDETELLA PERTUSSIS	176.212			4	4		\downarrow	-	1
CVAD BOD	CTAUTHOREM	BONDETELLA PERTUSSIS	3.5	4	4		-	-	1	1	ļ
A TARE BOATE		AHODOBACTER CAPSULATUS	9		-	-	1	+	-	\downarrow	-
1200	TO A MY POOR T PROTEIN	ESCHENCHIA COLI	S.	183.409			4	+		1	╀
					· -	_	_	_	_	_	_

	Γ	107217814	Sequences	1 1 1 1 1 1	ABELL AREAS	7857	AREA!	AREA 6 AR	AREA? A	ABLAS	AREA?
VARIABILATION COUNTS SUBURIT ESPERACION COLI 11-10		and the second	CTER (P	T	Т	T			1	П	
TANK PROFESS		CLOHEXAMONE MONCOX TUENASE		10-200						Ì	
TOTOTONGE OURIGNESS TREATED 19.141		3		03-60					1		
17.1071_FROM_COL_FR		DIMINION OXIDASE SUBUNIT !		1-58				1	1	1	
17.15 17.1		PTIDYL-PROLYL CISTRANS ISONE RASE		03.141					\dagger	1	
STATE STAT	т	LI ATE PENMEASE A PROTEIN	•	5-3		+		1	†	T	
STOREGIST FLANSIELASE SLUBONELLA PTRIBINALIANI 18-19 19-19 1	т	S REGULON TRANSCRIPTIONAL ACTIVATOR		. 30		+		1	1	Ť	
ELIGE ACETIVI TANNSTEALSE SECRETICALIAN COLI 144-191		S REGULÓN TRANSCIUPTIONAL ACTIVATOR	HINEURIUM	9.		+				ĺ	
SCHEENING 19.10 19.11		AINE ACETYL TRANSFERASE		164-191				$\frac{1}{1}$	†		
BIOGEST SYNTHASE SACREMENT COLUMNICATION 00-433 BIOGEST STANDARY TO THE DELANDORYLASE BETA CHAIN SACREMENT COLUMNICATION 00-433 BIOGEST STANDARY TO THE DELANDORYLASE BETA CHAIN SACREMENT COLUMNICATION 00-433 BIOGEST STANDARY TO THE DELANDORYLASE BETA CHAIN SACREMENT COLUMNICATION 00-433 BIOGEST STANDARY TO THE DELANDORYLASE BETA CHAIN SACREMENT COLUMNICATION 00-433 BIOGEST STANDARY TO THE DELANDORYLASE BETA CHAIN SACREMENT COLUMNICATION 00-433 BIOGEST STANDARY TO THE DELANDORYLAS		ANG ACETYL TRANSFERASE		5				+	t	T	
INTERPREDENTALE TRUMPSTEAKE STOURT SCHEME COLUMBRICATION 10-131 10-	-	PORTE SYNTHASE		105-432				1	İ	Ì	Ì
U. A. THE PERCASSE WENDERN STOREGUES OF COLUMN STATE COLUMN	TAN CALLY	DOMEN SYNCHASE		105-432					1		
SCHERICHIA COLI 1911 191		SATE ADENYLATE TRANSFERASE SUBUNIT I		16-14					7		
ULTATE PENGENEE VIOLENCE VI	1 200	REALE PERVIENCE WINDOWS		121.10					1		
ALTONE EFFLUX \$15 FEAT PROTEIN CLOB ALCALGENEE EUTROPHIUS 19-199 19-1	1000	SATE PERIOR ACT OF PROTEIN							1		
STATION BITLON STITEAT ROOTEIN CECO ALCALICEMES EUTROPHUS 119-109		THOM EFFE ITY CYCLESC PROTEIN CZCB							1		
FAICTLE N-BRODING PROTEIN 1** PRÉCUASOR BACELLUS SUBTILIS		TION EFFLUX SYSTEM PROTEIN CZCD		139.169					1		
ACCEPTATE DELABORATES ESCREBICHA COL 177191				10-107					1		
ALTEROBIO D.ALANDRE GLYCINE PERRIEASE ALTEROBIONAS HALOPIANIS 113-13 ALTEROBIO D.ALANDRE GLYCINE PERRIEASE ALTEROBIONAS HALOPICED 113-13 ALTEROBIO D.ALANDRE GLYCINE ESCHERICHIA COLI 113-13 ALTEROBIO D.ALENDRE D.ALANDRE D.ALENDRE D		AND ACT DENYDROGENASE		137.154							
	N VILL VOYOR	MAN PAKED DAI ANDRE GLYCINE PENAIEASE		2					1		١
STATE DELANDORTATE SYNTHASE	STATE STATE	LLCY PROTEIN			9.180						
13-95	C CONTRACTOR	2		П	7.184						
13.19 13.19 13.19 13.19 13.19 13.19 13.19 13.19 13.19 13.19 13.19 13.19 13.10 13.1	STATE STATE	A PROTEIN CYSTEME METHYLTRANSFERASE		13-47					1		
13.13	TOUR ECOL	MA. RINCHONG PROTEIN HU. AL. PHA		13-39							
ECCEDONYLASE FOÈRENGE 194-119	PDBM CLOPA	NA. BINDONG PROTEIN HU		13-53							
13.14 13.1	POCAN PORT D	ECARBOXYLASE PROENZYME		146-173							
International control of the contr		AMMOPDAFI.ATE DECARBOXYLASE		134-161							
STATE DECARBOXYLASE BETA ESCHENCIAL COLI 111-118	POCTA PERAT	ANTHORDAEL ATE DECARBOXYLASE		57.64							
111-119 111-	C I IUU I SUU	INTAMATE DECARBOXYLASE BETA		6.31							
	POOK BATAE H	STIDINE DECAMBOXYLASE	res	111-111							
	POOK KLEN. H	STIDDE DECAUDOXYLASE		11:13				•	1		
MACRICAS STREET 19-332 19-3222 19-32222 19-3222	POCHS MORNOIN	ISTIDINE DECAUDOXYLASE	ANII	=					1		
VATORE DECAMBORYLASE ALPHA CHAIN ALVER VALANA A	DOED BACKUD	DEPTIDE TRANSPORT PROTEIN DCIAD		77.00					1	Ī	
ANY OLD CETATE DECARBOYTASE ALPIA CHAIN ALEBELLA PTRHAMADIAN 201-319 342-309	POLY HWAL L	YSINE DECAUDOXYLASE		7				1	1		
NOTALIDACET ATE DECARBOXTIANSE ALPIA CHAIN SALAMONELLA TYPRIMAUUUNI 201-131 147-209	PDCOA KLEPN 0	XALOACETATE DECARBOXYLASE ALPHA CHAIN		Т	3.369		1		Ì	T	
TALANSPORT SENSOR PROTEIN DCTB MAZGBIGM MELLOTI 171-11 171	PDCOA SALTY O	XALOACETATE DECARBOXYLASE ALPHA CHAIN		Т	7.369	1			1		
HANDORIA SENSOR PROTEIN DEB HANDORIAN LELONI 11:31	PDCOD EALTY O	XALOACETATE DECARBOXYLASE BETA CHAIN		200-320		1		1	T		
INTERPORT SENSOR PROTEIN DCTB INTERPORT SENSOR PROTEIN DCTB INTERPORT SENSOR PROTEIN DCTB INTERPORT SENSOR PROTEIN DCTB INTERPORT DC	POCTS NAME T					+			1		
ASPERTMENT NA MELICASE DEAD SUCEDICIOAN SUPERAL	POCTS INDIG			Т	- 133	1			1		
EXCEPTION EXCEPTION 19-113 11-10 11-	PDEAD ECOLL A	TP-DEPENDENT RNA HELICASE DEAD	No. of the last of	Т	200		\downarrow		1		
SENSOR MODIEU DEGS	PDEAD KLEPY	TP-DEPENDENT ANA HELICASE DEAD	ESCURBICHA COLI	Т		-			T		
MONACELASE ATE DENALOGENASE H-3 MONACELASE	LDEDA ECOL		PACE LINE CIRCLE	Т	Τ	-	L		Ī		
MADONE TATE SEAL LIDERATE ESCRENCIAL COLI 134-161	PDEGS BACSU	ENSON PROTEIN DEUS	MORAXELLA SP	Т	Τ						
ALD PHYTOE DEHYDROGENIAE	-		ESCHERICHAA COLI	134-161	-						
ASTANTATE SEAGAL DEHYDE DEHYDROGENASE BACTILUS SUBTILIS ASPATATE SEAGAL DEHYDE DEHYDROGENASE CONTREACTERUM GLUTAIICUM ASPATATE SEAGAL DEHYDE DEHYDROGENASE CONTREACTERUM GLUTAIICUM ASPATATE SEAGAL DEHYDE DEHYDROGENASE CONTREACTERUM GLUTAIICUM ALANGE DEHYDROGENASE MACTILUS STREACUS ALANGE DEHYDROGENASE COSTUDIAM BISTICLE BACTILUS STREACH CALITANATE DEHYDROGENASE COSTUDIAM BISTICLE GLUTANATE DEHYDROGENASE COSTUDIAM BISTICLE GLUTANATE DEHYDROGENASE STREACH STRAACTILAROL YICUS ALANGE SERVICIAM SERVICIAM SERVICIAM BISTICLE ALANGE SERVICIAM SERVICIAM SERVICIAM BISTICLE ALANGE SERVICIAM	_	Deliver DELVORGENASE	PSEUDOMONAS OLEOVORANS	6-33							
ASPARTATE, SEMAL DEHYDROGENASE CONTYREDACTEAUUM GLUTAHICUM ASPARTATE, SEMAL DEHYDROGENASE ESCHERICHA COLI ASPARTATE, SEMAL DEHYDE DEHYDROGENASE ESCHERICHA COLI ALADRE DEHYDROGENASE ALADRE DEHYDROGENASE ALADRE DEHYDROGENASE BACELLUS STRAKOTHERNOPHILUS ALADRE DEHYDROGENASE BACELLUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS BACELUS STRAKOTHERNOPHILUS B		COAPTATE CENTAL DEHYDE DEHYDROGENASE	BACELUS SUBTELIS	120-181	_	_					
ASPARTATE SEMALIDENTOE DENTOROGENASE ESCHEUCIGA COLI ASPARTATE SEMALIDENTOE DENTOROGENASE VIRBIO CHOCLENO ALANGRE DENTOROGENASE RACELLUS SPINARACUS ALANGRE DENTOROGENASE BACELLUS SPINARACUS ALANGRE DENTOROGENASE BACELLUS SPINARACUS ALANGRE DENTOROGENASE CLOSTIDIDIA DIFICILE DASPECTIC GLUTAMATE DENTOROGENASE PERTOSTIEDIDOCOCCUS ASACCIIAROLYTICUS (BLTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS 3.134 ALARORASECTIC GLUTAMATE DENTOROGENASE SULFOLOBUS SOLFATANCUS SULFOLOBUS SULFOLOBUS SOLFATANCUS SULFOLOBUS SOLFATANCUS SULFOLOBUS SU		SPARTATE SENDAL DEHYDE DEHYDROGENASE	COAYNEBACTEBUDH GLUTMICUM	ſ	3.139						
ALANDRE DEMTATE SEMALDENTOE DENTOROGENASE INRUIO CHOLEALE ALANDRE DENTOROGENASE RACELLUS STRAKOTERUS ALANDRE DENTOROGENASE RACELLUS STRAKOTERUS ALANDRE DENTOROGENASE CLOSTILIONIM DIFFICILE DESPECUPIC GLUTAMATE DENTOROCENASE SUFFICIONOUS STRAKOTERUMATE DENTOROCENASE SUFFICIONOUS STRAKOTERUMATE DENTOROCENASE SUFFICIONOUS SUFFICIAL STRAKOTERUMATE DENTOROCENASE SUFFICIONOUS SUFFICIAL STRAKOTERUMATE CLUTAMATE DENTOROCENASE SUFFICIAL STRAKOTERUMA GLUTAMATE DENTOROCENASE SUFFICIAL STRAKOTERUMA GLUTAMATE DENTOROCENASE SUFFICIAL STRAKOTERUMA GLUTAMATE DENTOROGENASE SUFFICIAL STRAKOTERUMA GLUTAMATE DENTOROGENASE SUFFICIAL STRAKOTERUM GLUTAMATE DENTOROGENASE SUFFICIAL STRAKOTERUM GLUTAMATE DENTOROGENASE SUFFICIAL STRAKOTERUM GLUTAMATE DENTOROGENASE SUFFICIAL STRAKOTERUM GLUTAMATE DENTOROGENASE SUFFICIAL STRAKOTERUM SUFFICIAL STRAKOTERUM SUFFICIAL STRAKOTERUM SUFFICIAL STRAKOTERUM SUFFICIAL STRAKOTERUM SUFFICIAL STRAKOTERUM SUFFICIAL STRAKOTERUM SUFFICIAL STRAKOTERUM SUFFICIAL SUFFIC		SPARTATE SEMIALDEHYDE DEHYDROGENASE	ESCHENICHIA COLI	952-622							
ALANDRE DEHYDROGENÄSE BACELLUS SPIAGRICUS ALANDRE DEHYDROGENÄSE RACELLUS STEAKOTIERAIOPHILUS NAD-SPECIPIC GLUTANANTE DEHYDROGENÄSE CLOSTADIUM BUFICILE PSPECIPIC GLUTANANTE DEHYDROGENÄSE PEPPOSTREPTOCOCCUS ASÁCCIIÁROLYTICUS STATUMANTE DEHYDROGENÄSE SULPGO,OBUS SOLFATALCUS SULPGO,OBUS SOLFATALCUS SULPGO,OBUS GLUTANANTE DEHYDROGENÄSE CORYYEBACTERUM GLUTANGUS 13.96 13		SPARTATE SEMINAL DEHYDE DEHYDROGENASE	VIBRIO CHOLERAE	309-336							
ALANDE DEHTOROGDIASE ALANDE DEHTOROGDIASE CLOSTRUDIAM DEFICIE CLUTAMATE DEHTOROGENASE CLUTAMATE DEHTOROGENASE CLUTAMATE DEHTOROGENASE CLUTAMATE DEHTOROGENASE CLUTAMATE DEHTOROGENASE CLUTAMATE DEHTOROGENASE CONTYNEBACTERUUM CLUTAMOTIC 13.19 1.19 1.10 1.1		LANINE DEHYDROGENASE	BACILLUS SPHAERICUS	149-176		Н					
NADS SPECEFIC GLUTAMATE DEHYDROGENASE CLOSTADITA DISTICULE D. SPECEFIC GLUTAMATE DEHYDROGENASE PETIOSTREFICOCCUS ASACCHAROLYTICUS 147.374) GLUTAMATE DEHYDROGENASE SULFOLOBUS SOLFATALICUS 1.34 NADS-SPECEFIC GLUTAMATE DEHYDROGENASE CORYNEBACTERUDA GLUTAMOTORI IIIE-315	_	M ANINE DEHYDROGENASE	BACELUS STEAROTHERMIOPHILUS	94-121							
ESPECIFIC GLUTAMATE DESPYOROGENASE PEPTOSTNEPIOCOCCUS SACCHAROLYTICUS 197.374 GLUTAMATE DESPYOROGENASE SULPACADOBUS SOLFA FALUCUS 1.398 HANDE SPECIFIC GLUTAMATE DESPYOROGENASE CORTYREBACTERUIM GLUTAMCUM 186-213	7_	AAD. SPECIFIC GLUTAMATE DERYDROGENASE	CLOSTADIUM DIFFICILE	П							
GEUTAMATE DEHYDROGENASE SULFOLOBUS SOLFATAUCUS 13-39 14-39-ECIFIC GLUTAMATE DEHYDROGENASE CORYNEBACTERUUM GLUTAKCUN 161-315	Т	SPECIFIC GLUTAMATE DEHYDROGENASE	PEPTOSTREPTOCOCCUS ASACCHAROLYTICUS	T	15.380	1					
INADE-SPECIFIC GLUTAMATE DEHTUROCENASE ICORTNESACTEMOM GLUTAMATORI	П	LUTAMATE DEHYDROGENASE	SULFOLOBUS SOLFATANCUS	Ť	31. 9	1	1				
THE RESERVE THE PROPERTY OF TH			CONTREBACTEMENT GLUTIMICUM			-		1	Ī		

PCCENE FILE MAME	16717714						1				
								1			
	PROTEIN	RUM				-		_		7	
3	GLUCOSE I-DEHYDROGEMASE		20.00	1	İ	-					
17029 011	GLUCOSE DENYINROCENASE	ON ACFORTBER	168-195		Ì	Ì	1	+	T		
150	KETOACM REDUCTASE I		91:319				Ì		1		
	FEILTING DELIYDROGENASE	•	117.344					1	Ì		
71.00	D. I VERPENT DEHYDROGENASE	1	183-117	190-224				1	1		
	THE SUBUNIT I PREC		101.101	190.234							
TOTAL MOST	A THE TANK THE WANTE OF SUBUNIT I PREC	Ormicon.	104.333								
100	THE THE PREVIOUS OF SUBURIT 1 PREC								٦		
POPONI PANDE	METHAMOL DENT DROOF! ACC					İ					
PERMA BACS	NADH DENTURCERASE	E CONFRICHIA COLI	110-210		1	Ì		-			
SOLA ECOL	NADH DEHYDROGENA	BACH LISE CHATH IS	13.107	406-433			ŀ				
117.1	WANTERNE DEPTY	BACILLOS SOS INTERIOR COLORIO	105-132					1			
VOHOL BALSO	CANADA PARENTE	CONTINEDACTERUM GLUINILUM	916 616					1			
S CONTRACT	MONOSCOTAL DESCRIPTION OF THE PRINCIPLE	BACILLUS SPHAENCUS			,						
POPEL BACK	HENN A ANDRE DE	SECTION TO LI	482-512			Ì	Ī				
POHSA ECOLI	SUCC DEHYDROGENA	ANT PARTY FOR THE PARTY A	(11-91	130-168							
VICE ANALY	COLUMN E HYDROGENASE 43 KD SUBUNIT	ANADALIA CI CIPONICI	133-160					1			
PURISO ALVAN	STATE STATE STATE STATE SUBUNIT	SAMECHOCOCCUS SA	,,,,								
TORES STATE	SOLUBLE PLONOLEGICENACE	METHYLOTROPHUS RIETHYLOPHILUS	200								
POHTM METAE		TECOME MONTH COLI	384-011								
DONG ECOLI		SACH LINE CITE THE SACHES	===	14:14							L
DAY BACK	DIVISION INITIATION PROTEIN	SALES STATES	93.120					1			
A		DEUDOMONAS FOLIAN	\$7.1	114.176							
	POSTATIONE NEW THEORY (E)	AZOTOBACTER VINELANDI	1								
DCDH AZOVI	LUCARIDE DELIVERACE CONP. (E.)	BACELUS STEAROTHERMOPHILUS									
DCDH BACST	_	BACELUS SUBTILIS	101.78								
POLDH BACSU	_	CCTURE ICHIA COLI	20.133								L
POLIDIA ECOLI	DUNYDROL IPO ANDE	TOTAL POLICE BY LIMBERCENS	151-921	223-275							L
THE POEM	т	rational recommendation of the second	8.69	L							ļ
	ANDROXUL WINDOW	PSEUDOMONAS PUTIDA	403.434	\$48.581		ĺ					
200	Mary Des Street	BACKLUS SUBTRLIS									
PDNA BACK	UNAN TROITE	BACILLUS SUBTILIS									
DNA2 BACSU	DRAKTAGIEIN	BACILLUS SUBTILIS	2			177.77					
PONAA BACSU	DWAATKUIEIN	BORDELLA BURGDONFEN	97.78								
DNAA BOND	DAMATRUITA	BUCINESA APRIDICOLA	3								
PONAA BUCA	DNAA PROTEIN	FSCHELICKIA COLI	966-400								L
DNAA ECOLI	_	MICEOCOCCUS LUTEUS	385-415								L
DHAA MICLU	DNAA PROTEIN	LIVERAL ASMA CAPRICOLUM	3	75.113	274.310	230.78				L	ļ
DNAA LYCC	PONAA LYCCAIDNAA PROTEIN	MICO CONTRACTOR AND INC.	365.399	_							ļ
TOTAL VANC	I DNAA PROTEIN	PROTEUS PRINCIPLIS	348-430								\downarrow
	75 - 10 - 10 - 10 - 10 - 10 - 10 - 10 - 1	PSEUDOMONAS PULIDA	1	14.110	145.180	L					4
DAY INC.	DAM TRUE.	SPIROPLASMA CITRU							L	L	
PONAA SPICI	DIAA TRUELI	CHE JAYYDIA TRACIIOMATIS	117-117							L	L
PDRAB CHO.T	A DNAB-LIKE PROTEIN	F CONFRICTION COL!	12.100								L
PONAS ECOL	DNAB PROTEIN	CALLANDER LA TYPHINGERIUM	12.109							1	1
PENAR SALTY	Y DNAB PROTEIN		146.190								1
PONT FOO	I DNAC PROTED	EXCHEMINATION	407.524	\$41.511	L	L					1
A VANA	AF DNAK PROTED	BACOLUS MEUA I ENUM	112.194	ļ							1
1000	THE PROPERTY OF	BORDELLA BURGUOIG EN		37.613	-			L			_
Diver a		BRUCELLA OVIS									_
POWAK BAUCY		CAULOBACTER CRESCENTUS	301-380		-					L	_
POWAK CAUCA		CLOS TREDICINA ACETOBUTY LICUM	499-320						L	L	L
PONAK CLOAB		CLOSTRIDIUM PEUF RUNGENS	48.33		-						L
PONAK CLOPE	E DNAK PROTEIN	METHANOSALCINA MAZEI	22.550					1			L
PONAK METMA	MADNAK PROTEIN	MYCOBACTERUM TUBERCULOSIS	\$02-529		-					-	1
PDNAK MYCTU	TU DNAK PROTEIN	REPERTURY CES COELICOLOR	45-72	533-572						-	+
PONAK STRCO	DNAK PROTEDY	ESCUEBICHA COLL	114-141							1	1
PONTE ECOL		ESCHENICIA COCI	658-712	_							1
PONT I ZYMMO	DINA LIGASE	L I MUMORIAN FILE TILLS	26.51							1	1
PUNT STRPE	THANSOUCTION PR	STREET CONTINUES TO BE A TABLETS	20.13						4	4	4
OS US ALOUG	PROBABLE SIGNAL	STEEN COUNTY STATE OF	3	417.444	1312-1416	9					4
PAPA ALGO	DNA POLYMERASE	BACILLUS SUB ILLIS	2	-	L	L	L				4
7100	DNA POLYMERASE	ESCREDICATA COLI	110.243	-				L		_	_
10.00		CHARLE VALUE VALUE OF		,		-	-				I

				-		-	-		
PCGENE	107117814 PROTEIN		AREA1 AR	ARIA1 AREA1	AREA	S P. THY	CARCE SARA	2 44541	AREA!
PDP3A SALTY		INTURIURI	77:104		-		+		
PDP1B BACSU	DNA POLYMERASE		20.11	<u> </u>		+			
POPJB BORBU	DNA POLYMERAS.	_	_						
PDP3B_BUCAP	DNA POLYNGERASE		79-16	267-100	1				
POPJB MICLU			101:218		1				
-	DNA POLYMERASE III, BETA CHAIN	MYCOPLASMA CAPICOLUM	2 9		-				
	DNA POLYMERASE III, BETA CIVAIN	PSEUDOMORAS PUTIPA	1	130.177 371.310					
PDF38 SPICE	DNA POLYAGIJASE III, BETA CHAIN		T,	Т			-	-	
	DNA POLYMERASE III SUBUNITS GAMMA AND TAU		401.741		1				
POPC3 ECOU			201.100						
בסבת בכסרו					+				
POPNO STUDY		UNIAL	1		1				
POPOI BACCA			Т	╅	T			 	
MANTS 10404		STREPTOCOCCUS PNEUMONIAE	Т	398-425 371-348	7/0-670				
PDPOI THEAD	DNA POLYMERASE	THERMUS AQUATICUS	٦	629-209					
PDPOI THEFT.	DNA POLYMERASE	THEMANS AQUATICUS	597-628					 	
PDP01 ECOLI	DNA POLYMERASE II	ESCHENCHIA COLI	269.596						
POPOL PYREU	DNA POLYMERASE	PYROCOCCUS FURIOSUS		7	╗				
POPOL SULSO		S			٦				
POPOL TIGHT		THE MACCOCCUS LITORALIS		551-580 892-926	1004-1031	3.18	-		
PDPP LACLA	DIPERTIDAL PERTURASE IV		116-753						
U DV adda			116-753				_		
POPE ECOL	BNA PROTECTION DURING STARVATION PROTEIN		Ş Ş						
Carry Carry	DEOY OF TROMING F		Г	291-316					
1000	DAINORIMICINA RESISTANCE ATP-BINDING PROTEI		286-313						
NAME AND	DINYDROFOLATE		62-89			1			
PELLIE BACC	CHAN ENDO-1 1-RETA-CLUCOSIDASE AT PREC		134-161 309	105-339 424-451					
PEAR FOOL	ATTACHING AND EFFACING PROTEIN		Т	158-185 525-552	691-123	102-136	871.905		
PERGR ECOLI	ENG OPERON REPRESSOR PROTEIN		151-178				-		
PEBR STAND	ETHEDRUM BROWEDE RESISTANCE PROTEIN	STAPHYLOCOCCUS AUREUS	86-89					1	
PECHE BROCA	ENOW COA HYDIK	INIODOBACTER CAPSULATUS	311-149				-	1	
PECPD ECOLI	CHAPERONE PROTEIN ECPD PRECURSOR	ESCHERUCHUA CÓLJ	20-47					1	
PEDO ZYNOMO	PHOSPHOGLUCONATE DEHYDRATASE	2 YMOMONAS MOBILIS							
PEDDY STAAU	EPIDERMAL CELL DIF INH PRECURSOR	STAPHYLOCOCCUS AUREUS	┪	19.146					
PEF1 DESMO	ELONGATION FACTOR 2	DESULFUROCOCCUS MOBILIS	427-461	_					
PEF HALHA	ELONGATION FACTOR 1	HALOBACTERIUM HALOBIUM	186-213	_			1	-	
PEF2 METVA		METHANOCOCCUS VANNIELII	2	-	_				
PEFT SULAC	ELONGATION FACTOR 1	SULFOLOBUS ACIDOCALDARIUS	1	٥					
PET THEAC	ELONGATION FACTOR 2	THEIMOPLASMA ACIDOPHILUM	13-20 49.76	70-747					
PEFO ANAMI	ELONGATION FACTOR G	ANACYSTIS MIDULANS	333.330	-					
PEFO ECOL	ELONGATION FACTOR G	ESCHENICHIA COLI	╗		-				
PEFO MYCLE	ELONGATION FACTOR O	MYCOBACTERUM LEPRAE	╗	130-357					
PEFO SALTY	ELONGATION FACTOR G	SALMONEL LA TYPHIMURUMI	╗	-					
PESO SPOL	ELONGATION FACTOR O	SPORULINA PLATENSIS		481-511					
PEFO SYNY	ELUNGATION FACTOR O	SYNECHOCYSTIS SP	7						
PEFT! STURA	ELONGATION FACTOR TUI	STREPTOMYCES RANOCISSIAIUS	121.251	-					
PETTS STUDY	ELONGATION FACTOR TU?	STREPTOMPCES RANDCISSINUS	221-258						
PETTI STITUTE	ELONGATION FACTOR TUI	STREPTOMYCES RAMOCISSIALUS	228-255						
PETTS ECOL!	ELONGATION FACTOR EF-18	ESCHELUCHIA COLI	<u>~</u>					-	
PETTS SPICE	_	SPROPLASMA CITIU	٦	134-161	-			1	
PEFTU BACFR	ELONGATION FACTOR TU	BACTEROIDES FRAGILIS	٦	229-256	4				
PESTU BACSU		BACOLUS SUBTILIS	Ť	230-257	_				
PETTU BURCE		BURKHOLDEXIA CEPACIA	26.53	_		1			
PETU OLTA		CHANNOLA TRACHOMATIS	216.245	1	\downarrow	1	1		
PETU DEISP	ELONGATION FACTOR TU	DEDONEMA SP	230-257	1	+	1	$\frac{1}{1}$	 	
PETU PLESS	PETU FLESI (ELONGATION FACTOR TU	HEIGHT A MARIENOSTIC	121.74	1	1	1	+	1	I
PETU KALAC	A ELONDATION FACTOR TU	INTOAK DLA MANJAMURIOI	1	-	$\frac{1}{2}$	1			

		Prehaments Sequences	П		1000	ABFA	AREA S	AREA! AREA!		AREAL	AREAS
PCCENE	071,7814]		7-	Τ	_				
LE HAME	ROILIN	CUSTUTEUS	7.57								
PEFTU MOCLU	LONGATION FACTOR TO		57.72	i	· :	:	:				
EFTU MYCHO	LONGATION FACTOR TU		20.20					•			
CETTI NVO E	LONGATION FACTOR 10	30 40 100	330-147								
	IN MANATHIN FACTOR TU		1								
O MICEO	STORY AND EACTOR THE	LNS									
_	ELUNCA INC. CALL				Ī						
┑	ELONGA I IUM PACI CAR CO	HICHOSA	-								_
	PSEUDOLYSIN PRECURSOR		6	- - i	•						_
PELTI ECOLI			73.118								
C T CAN	T. Ahil E ENTEROTOXIN A CITAIN PRECUINCIN		334.364							!	
1	TOTAL STATE OF THE PRINTING PRINCIPLES OF	CLOSTRIDIUM TERING MY					!				
PELTO CLOPE	T-LABILE ENTEROIONING CONTROLLED		154-111								L
HENTO ECOLI	ENTEROBACTIN SYNTHETASE CONDUCTION	1000	19-10								
VI IVE INVESTIGATION	CNVM PROTEIN		Ī	136.39	290-335	387-421	417-119				
	THE PROTEIN		Ť								
PEPO STAEP	II Y KD MENDING KASOKINI EST SELVENI			1		1	i	-		: 	:
PEPE STALE	EMDERANDA BIOSYNTHESIS PROTEIN EFF	A STATE CONTRACTOR		101.124		Ì		!	:		:
SERVE STAFF	CERINE PROTEASE EMP PRECURSOR	SIAMILE COLOR IN THE PROPERTY OF THE PROPERTY	١		l			•			
	MOID IN A PROPERTY IN FRIE CION	STAPHYLOCOCCUS L'PHOLENNIHIS								_	
PEMY STAEP	HYPOTHE IN AL IS A ROTE OF CASE OF	CTAMM OCOCCUS EPIDERMIDIS	8								
PEDIZ STAED	HYPOTHETICAL PROJETIN IN CONTRACTOR		Î					1			
PERA SCOL	GTP-BINDONG EAA PROTEIN	Con Charles And A	100.30								-
1000	CENCORY TRANSDUCTION PROTEIN ERYCI		77	021.130							\downarrow
	THE CONTROL OF THE ACE TYPE !	ESCHENCHIA COU		100	77.1.					_	
PLACA LAURA	CATION OF SAME MANIE & LAND 6	SACCHAROPOLYSPORA ERYTHRAEA	9.								L
PEAYS SACER	EXTROUMULIDE STRIMASE, MODELLE	CTREPTOMIYCES SCABIES	128-155								L
PESTA STUSC	ESTERASE PRECURSOR	STATE OF STANDERS	162-119								-
Secre Beech	ANY ESTERASE	PSECOCHICA S PECONICA S	6117	111.206		L					1
	PASSESSION TYPE C.I PRECURSOR	STAPHYLOCOCCUS AUREUS		206			L				
PETCI SIAMU		STAPHYLOCOCCUS AUREUS		207-66						L	_
PETCH STAND	ENTEROTORIN TITE C-1 TRECONDE	STABARY OCOCCUS AUREUS	76-13	155-:06							-
PETCI STANU	ENTEROTOXIN TYPE C-3 PRECURSOR	STATE SOCIAL STREETS	36-49	165-192							1
PETYA STAAU	ENTEROTOXIN TYPE	SIAMILLOCOCO ACTOR	200.236			L					
1000	FPS DON-TOXON, TY	CLOSING MENTANCIA	101.25	173.207		L					-
	TANK BUYON TANK	STAPHYLOCOCCUS AUREUS						L		_	
7 1 7 2	PRICE DIVINITY DE DIVINITY DE DIVINITADOR	STAPHYLOCOCCUS AUREUS	33-12	2							
200	THE POST OF THE	STAMMLOCOCCUS AUREUS	40-07							L	
PETXE STAAU	ENTEROIOMATOR	SALLACINELLA TYPHINIURIUNI	116-150							L	L
PEUTC SALTY	ETHAMOLAMINE AND	FKCHERICHIA COLI	63.89		_					-	
PEVOA ECOLI	PUTATIVE TRANSCRI	ESCHERICHE COLI	45.79	249.276	431.458	226-323	177-878				-
PEVES ECOL	PUTATIVE SENSOR PROTEIN EVUS	SOCIETION CO.	136-353							\downarrow	1
PEXAM ROOL	EXODEOXYBLBONUC	ESCHEROLINA COCI	10-107		L					1	
1	Т	ESCHENIONIA COLI	100		ļ	_	L	L			
TOWN TOWN	CHOCONOCI YCAN BE	RECOGNIM MELILOII				ļ			L		
4	PENNENNY MONITERSE	STREPTOCOCCUS PREUMONIAE	17:17			-			L	L	F
4	NAME OF THE PERSON OF THE PERS	AHIZOBIUM MELILOTI	77-077	101-176	-	-	-	-	-		L
PEXOS SOOR	EXOF PROTEIN PROPERTY PROTEIN PROPERTY	INDICATION MEL BOT!	251-279				1			ļ	-
PEXON NO.	SUCCEMBLE I CAM BROST MITTERS BROTTEN E VOR	BARZORUM MELILOTI	211-242	212-299	350-391				\downarrow	ļ	ļ
PEXOF NEGA	SUCCINOCA YCAN BY	RECOVERIONA COLU	16-63	11-204			$\frac{1}{4}$	\downarrow		1	\downarrow
PEADS ECOL		ESCURBICION COVI	220-247	L						1	+
PFADL ECOLI	FATTY ACID TRANSI	ESCHALLES CO. 1	133-157	(ST-12)	507-541	L					1
PEAED FOOL	OUTER MEMBRANE	ESCHERICARA COL	71	L		L					1
100	Т	ESCRETICATA COLI	1	10,000	104.431	710.757		L			_
	THE PARTY PARTY	ESCHENCIAN COLL	100-174						L	L	
MAN KA	TAND THE PROPERTY OF THE PARTY	ESCHEUCHOA COL!	35.51				1	-	1	-	L
PFANG ECOL	CHAPECORE PROTEIN FACE PACK	ESCHEDICIDA COLI	104-131		4		4	-	1		-
PFANG ECOL	ANG PROTEIN PRE	E COMPLICION A COL.	13-141					$\frac{1}{1}$		1	+
PLANE ECOL	I PANH PROTEIN PRECURSOR	PRES PROMONA C FRACI	27-3	245-322	L			$\frac{1}{4}$	1	1	+
PFAOS PSET	FATTY OXIDATION	WATER A CITY OF THE	64.93							1	+
US JOW CHOIN	U FDAM PROTEDA	WOLLSTON SOCIETY	413.440							4	-
HONE ECOL	Т	ESCHEMICHA COCI	10.76	166-391	L						4
BY PECE	Т	PSEUDOMORAS SP	760.11	31.16	696.130			L			
PETRO ECO.	I FORMATE DEHYDROGENASE	ESCHENCIA COLI	3		-		-				
PERCY FOR	_	ESCHEDICHAA COLI	110	-	-	L		L			4
	_	ESCHENICHEN COLI		1	-	-	-		L	Н	
	PECT PROTEIN	ESENEUCHIA COLI		4							
ALC CAN	٦.										

PCCENE	107:178:4	Negates (C.)		* * 7.00.7	1 7.007	7 7.407	AREAS	AREA 6 SAREA 2		AREA	AKI'A !
THE HAME	ROILIN	UKUMUSEL AUBISTIC	Т	1		7	_	-			
PTEMB STAND	POSSIBLE PROTEIN PEMB		15.9								
PFEM SYNT	EULEDOXIN-NAUF RELUCE I ASE	ESCICEUCHIA COLI	176.203					Ì			
200	FEAST ENTEROBACTIN TRANSPORT PROJEIN FERE	ESCHERICHIA COLI	112-234	281-308						T	
1000	FEMAL ENTEROBACTIN TRANSPORT PROTEIN FEPO	ESCHERUCHIA COLI	121-155						1		
DANA MATE	FERREDOXIN HETEROCYST		2.29					1			
PFER ANASP	FEMEDOXIN-LIKE PROTEIN IN NIF REGION		¥.6			1	3800	101, 110,		T	
PHAS BOUR	FILANCENTOUS HEMAGGLUTIPHIN			1339-1310 (2003-211	17.683						
PFHAC BOADE	HAEMOLYSIN-LIKE PROTEIN FHAC PRECURSOR	USSIS	607-706					Ì			
PERTA ECOLI	FOUNATE HYDROGENLYASE TRANSACTIVATOR		3	30-784	877-100			Ī	T	T	
PERUA ECOL	FERRICHACHE-INON RECEPTOR PRECURSOR	ESCHENICHIA COLI	\$1.45					1			
The state	PROTEIN FHIM PRECURSOR	ESCHENICHIA COLI	227-254							T	
TOUR ELVIS		ESCHENICHIA COLI	587-614								
	FIRST PROTEIN	SPIROPLASMA CITRI	161.195	126.367			i		:		
2 2 2	CELL EN AVENTA TION PROTEIN FIC	ESCHERICHIA COLI	151-178								
	CELL EN AMENTA TION PROTEIN BIC	IINIURIUM	151-178								
1	-		201-235	\$40-567	618-645						ļ
THE BOOK	CUARREDUE PROTEIN	ESCHERICINA COLI	31-38								
Tallet Con		ESCHERICHIA COLI	(\$2.55	458.485	534.561	563-590					
	THE TANK THE PERSON ATTORNEY BEATERN FINE	ESCHERICHIA COLI	163-192								
300	THE LANGE A PARTY IN	SAI MONELLA TYPIIMURIUM	49.36								
TIMA SALTA	PUNBUAL V PAULIN	FCCHERICHIA COLL	\$	162.193	196.330			1			
L ECOL	I MORANE C TANIEN	CALLADARITA TYPHINIURIUM	135.200								
7	_	ECHERICHA COLI	145-172		L						
TING ECOL	_	STATES AND STATES	162-189								
		AND THE POPULATION OF THE PROPERTY	129-156								
PIXC AZOCA	FIXC PROTEIN	A COURT OF THE CALL OF THE CAL	71.5								
PFIXE AZOCA	SENSOR PROTEIN FIXE.	AZUGRICOBIUM CAUCIMODANS		341.360							
PFIXE, BRAJA	SENSOR PROTEIN FIX			331.208							
PFLA1 BONBU	LAGELLAR FILANES	BOILDELIA BURGUCARA	61.9								
PELA HALLA	LAGELLIN A! PAEC	A PRINCIPLIE VOI TAE	15.35	99							
MINI METVO	LAGELLIN BI PREC	WESTANDOOCHIE VOLTAE	78.66		L						
PILAS METVO	FLAGELLIN B2 PREC	MALONACTERINALIA COLLAR	199								
PFLA HALHA	FLACELLIN BI PREC	TALUBAL FAUM HALDERON									
PELA METVO	FLACELLIN BY PREC	ME INVICATION VALVA	8	13:19							L
PLAN MALKA	PLAGELLON BY PREC	DATOS ACTES IN CUAL OR INC.	16.61	=							L
PLAS MALKA		STANDARD STA	31.18	13.116							
PELAS BACSU	FLAA LOCUS 22.9 KD PROTEIN	CANANG DEACTER COLL	3	64.9	497.535						
2 YYL	PLAGELLINA	CANAN CALCARE RAIN	220-266	10.337	300.51	L					
PICK CALL		MACRIA MOCOCUE VOI TAE	31.63								
PRIAN METVO	PLAGELLIN A PRECU	PETITONA AFBIICINOSA	7	3	93-134						
PRIAN PSEAE	-	PALTONIAL MET IN OTI	181-219	228-265	160.391						
ארא גיספ		SPECCHAETA AIRANTIA	162.189								L
MLAA SPIAN	PLAGELLAL PILAN	TREPONEMA HYODYSENTENAE	53.19	219.285							
THAN INCH	CAUCALAN PRANCAL PROPERTY AVER PROTEIN	TREPONEMA PALLIDUM	243-270		L						
VILLA LIBERA	CACELLAN INC.	CAMPYLOBACTER COLI	144-191	497.535							
	TANCEL OF THE PARTY OF THE PART	CAMPYLOBACTER JEJUNI	230.266	110-311	\$00.538	L					
TAB CANGE		RUGZOBIUM MEL IL OTI	11.92	177.219	28.35	160-391					
		CLOSTRUDIUM NO	3								
A CANA		CAULOBACTER CRESCENTUS	391.318	551-578							Ц
	STAGET IN	BACELUS SUBTELIS	102-129	328-255							
DELA BACE	-	BACOLUS SUBTO.15	\$								
AT ICK SALTY	FLAGELLAR HOOK-	SALMONELLA TYPHINGRIUM	12.50	111.360	456-540						
PFLGL ECOLI	FLAGELLAR HOOK-	ESCHENICHUA COLI	\$01-19	339.366							
PELCE SALTY	т		6:0 03:0	36.266 28.266							
PELMO ECOL	FLAGELLAR TRANS		ŝ								
PFLIA PSEAE		PSEUDOMONAS AERUGINOSA	3								

HE ECON LYCETION WITE SYNA LYCETIN WOODNIA	107617124		a								
				Г	35.33	23-466					
		DOA COLI	1	T	Т						
		LERAE-SUIS	1	T	T	313 340	111.299	176-403			
			1	٦	Ŧ	Т					
	FLAGELLIN	A A MOMEST A PARATYPHI.A	17	٦	10-180						
	FLAGELLIN		<u> </u>		36-130						
	FLAGELLIN			\$4-115	136-200						
	FI ACEL I IN	SALMONELLA I I FRIENCE	Ī	15-43	53-89	103-130	37.164	176.572			
	1000	CBNS	77 57	100	160-187	116-291	Ş				
	THE PROPERTY AND A PROPERTY OF THE PROPERTY OF		T		L	\$(7.20)					
	711	HINDRICK	1	3	Т					L	
PILED SALTY IFL	FLACELLAR HOOK-ASSOCIATED PROTEST										L
THE BACKET FILE	AG HOOK BASAL BODY PROTEIN FLIE		137.361	391-418							L
200	COST AN MARKO PROTECH		Ţ	307.134	181-188						1
פאריים	A COLUMN TO THE OWN TH		Т					L			
ביות כאומ	ACELLAR M-RING FACTOR		484-326						L	L	
LIF SALTY IFL	AGELLAR M. RING PROTEIN	2 - 5 - 1 - 1 - 1 - 1 - 1 - 1	13-62								
IN BACKET FL	SI ACIELLAR SWITCH PROTEIN FLIG		14.31					_			_
100	ACELLA A CWITCH PROTEIN FLIO		ĺ	130							
	A CALL SO CHEST	DACILLUS SUITTILIS	1						_		
	PROBABLE PLINTED BAN	MACH LUS SUBTILLS	2.2								L
PFLU BACSU IFL	AGELLAR FLU PROTEIN	Military 1 A Tobally (1911)	13.118		1	:	:	•	: :	:	!
	AGELL AR FLU PROTEIN	SALMONELLA	•	11.							-
	PEONANT F FLIK PROTEIN	DACILLUS SUBTILIS	5	78.105	109-136						1
	National in the	BACILLUS SUBTILIS				L	_	_			-
┪	il TROISIN	ESCHERICHIA COLI									_
_	FLIL PROTEIN	CAL MONET LA TYPHIMURIUM	103-133								L
L	FLIL PROTEIN	a call no diment to	140-175								ļ
L	FI IM PROTEIN	BACILLUS SUBTINIS	341.378			_					1
-	ST THE OTHER	ESCHENCHIA COLI							-		
101	COST A DIVITOR CANTON PROTEIN	CAULOBACTER CRESCENTUS					_	_			
-7	PLACELLAS PROTECTION OF THE PR	ESCHEDICHIA COLI	34.80						L		
_		SALMONELLA TYPHIMURIUM	9.40	3			-	-			L
PFLIT SALTY FI	FLAGELLAR PROTEIN FLIT	PRETITION CONTACT AERUGINOSA	10.67	2			\downarrow			L	L
-		Pecural Col. I	5.32							-	L
	TYPE-1 FEMBRUAL PROTEIN, A CHAIN FILE CUASON	PSC INCIDITA COLI	11:38							-	ļ
	YPE-I FORBULAL PROTEIN, C CHAIN PILECURSUR	ACTINOACTER VISCOSUS	248-282	112-179	417.444		1		1	-	1
	FOABILAL SUBUNIT TYPE I PRECUISOR	Eschebichia COL	114-141				1		\downarrow	\downarrow	-
	FDORMAL PROTECN 917P PRECURSOR	h A CHEE ALINE MONORIIS	110-133							-	+
KIMAO BACHO F	FINBRIAL PROTEIN PRECURSOR	BACIES MODOSIIE	107-134	L	L					1	1
ELAN BACOO	INDITIAL PROTEIN PRECURSOR	BACTEROLLES MOCOSOS	107.134		L		L			1	+
STATE BACKED	PENAN BACKET FEMBLAL PROTEIN PLECUISOR	BACTEROLINES MOLOSOS	110.139		L	L	L		1	4	1
2000	NAME AND TECHNOOR	BACTEROIDES PRODOSOS	9				-		-		-
COLUMN TWO	PAGE AT PROTEIN PRECURSOR	BACTEROEDES MODOSUS			1	-			L		
TOWN WITH	A CHESTAL PROTECTION PRECINSOR	BACTEROLDES NODOSUS			1	-	-	-		L	
PINA BACK	STATE OF STA	BACTEROIDES MODOSUS	27.64			-	-			L	L
PENAH BACHOL	DOBLIAL PROFESS TACKSON	BACTEROIDES NODOSUS	111-143			1	 	-	-	-	L
PENAL BACHO P	DOUGH PROTEIN	BACTEROIDES NODOSUS	96-133		4		1	1	1	1	ļ
PENAN BACNO	DEBLAL PROTEIN	ASCITUTOTONIA CAPILICINOSA	70-97						1	1	\mid
BASS COLIN	PARILLAL PROTEIN	Participate Monorale	106-144	28:382	L						+
-	POSSIBLE FORMAL ASSEMBLY PROTEIN FOWD	BACIEROMES INCOSOS	106-144	155-382	_	L	L			4	1
DOM NOT	COSSIBLE FOODRUAL	BALIERUMES MUCOSUS	07.174			L	L	_			4
	117 STATE IN PROT	ESCREMICHIA COLI			-			L			_
1	OTHER PARTY	MEISSERIA MEMORITIDIS		1	+	-			L	L	
-	PURELLA PROTEIN PRECITAGE	NEISSENIA GONDRAHOEAE	66-90	\downarrow	1	+	1	+	-	-	L
	PURENTAL TROUBLE SECTION OF THE PERSON OF TH	MORAXELLA HONLIQUEFACIENS	103:140		-	+	$\frac{1}{1}$	-	-		-
	FDABILAL PROTEST PROTESTED	PSELIDOMONAS AERUGINOSA	10-67	호	+	1	+		+	-	\mid
7	FDABILAL PROTEIN PRECUESOR	PSELIDOMONAS AERUGINOSA	20.00		4	+	1	1	+	-	-
7		ESCHERICHIA COL!	\$	2	1	1		+	1	-	H
┑		ESCHEDUCHIA COL!	49.91				1	+		\downarrow	1
3	CS) FDGRIAL SUBURIS A FACCURAGE	HAEMOPIELUS INTLUENZAE	103-139		╗	T	Т		13.5	1	ŀ
	MAIOR FUNBILAL SUBURILI PALCONO	STAPHYLOCOCCUS AUREUS	41.13	<u>=</u>	<u>\$</u>	10		7	Т	-	ŀ
_1	FIBRONECT IN-BINDING TROILEIN THE	ESCHENCHIA COLI	133-159		4	4	+	+	1	-	+
PFOLC ECOLI	FOLYLOLYGLUI	LACTOBACILLUS CASEI	139.136		+	4	$\frac{1}{1}$	+	+	+	\vdash
PFOLC LACCA	FOLYLOLYGUIAMAIR STATINGS	BACH US FIRMUS	183-180			$\frac{1}{2}$	$\frac{1}{2}$	-		-	

PCT/US95/16733

		Pratarogic Sciences			F						
FILENAME			\square	AREA 3	ABEA A	AREA	AREAS	TABLE SABLA?	_	48544	AREAS
PFRDA ECOLI			≊	Ì		1	i	+	1	-	i
PFRDA WOLSU	UMARATE REDUCTASE FLAVOFROTEIN SURUNIT	NES		487-514	1	1	+	1	+	†	
PFRZE MYXXA	ALIDING MOTILITY REGULATORY PROTEIN		3	478-505		1	\dagger	†	+	+	
PETHS CLOTH	FORMATE_TETRAHYDROFOLATE LIGASE		16)-190		_		1	1	1		
PETTH METTH	FORMYLTRANSFERASE	IN THERMOAUTOTROPHICU	9-43		1		1	1	1	1	
PFTSA BACSU	CELL DIVISION PROTEIN FTSA		26-110			1	+	1	1	1	
PFTSA ECOLI	CELL DAVISION PROTEIN FTSA	ESCHENICHIA COLI	301-338	13:41	+	+		1	1	1	
PFTEJ ECOLI	INFIS		2			1	1	1	1	†	
PFTSL_ECOLI	INFIST.		8.5		1	1	1	1	1	t	
PETSN ECOL			131-18			1	1		1	1	
PFTSX ECOLI			278-305					-		1	
PETSY ECOL	CELL DIVISION PROTEIN FISY		330-260								
PEUCE ECOL	L-FUCOSE OPERON ACTIVATOR		7.45						_		
PETRAN NACKT	FIDAMENTE HYDRATASE CLASS I AEROBIC	THERMOPHILUS	790.317							_	
PELINOI BACKLI	INTABATE HYDRATASE		414.445		ı						
PETTS VERIE	NINE STATE BEGIN ATON PROTEIN		2	:	:			:	:		
100	CLAST SHORT SERVING SERVING A		103.129	İ		-		-			ĺ
	CI VA I SUDE DELIVERACIONA CE 3	F10.15	17.114	-			İ				
TANK THE	CLYC THOS DELYCOCKALCE 1		162.139		l			T		T	
VAVA CACO	G. I.C. S. THUS WELL UNDURANSE S		316.334		\dagger	t	T	-		l	
	STATE OF THE PROPERTY OF THE P	FRIEDA	Т	112.715		l				Ĺ	
POTE PACEL			Ι								
Oweve error		35	259-286								
AVENT BOS			290-328			l					
100		THERMOPHILUS	103-143	241-268		-	l		-		
DUJE CENT	TI INDER A PHOEPHATR I DEHYDROGENASE		301-328								
	TINDAG A BUDGEMATE 1. DEHYDROGENASE	1.15	165-192								
POACA PREFI	YANDE CONTROL PROTEIN	ESCENS	174-205			-					
POAL! SALTY			9F-13								
POAL? HAED	GALI-PHOS UND TATANSFERASE		П	239-269			H	H			
POAL? LACHE	GAL-1-PHOS UNIDYLYLTHANSFERASE		104-338							1	
PGALF_SALTY	GALACTOSE OPEAON NEPRESSOR		23-91						1		
POALR HAED	GALACTOSE OPERON REPRESSOR		62.20		1		1	1	1		
PGAL PSEFL	DEHYDROGENASE	JORESCENS	201-27		T	1	1	1	1	\dagger	
	GIF CYCLOHYDROLASE II	SCHEMENT COM	107.337	346.331	\dagger	\dagger	T	\dagger	Ì	t	T
ACE PROPE	GIF CYCLOHYDROLASE II		1		T	Ì	\dagger	\dagger		T	T
	ELACE		216.246			T	I	\dagger	T	T	Ī
TOUR ECON	GI YOME OF BAVAGE SYSTEM TRANSACTIVATOR		2.3					T		l	
PGENK ECOLI	PROTEINK	ESCHENICHIA COLI	24.51								
PGENI BACSU	SPORE GERMINATION PROTEIN!	8	49-83	182-216	350-384						
PGELU_BACSU	SPORE GERMINATION PROTEIN III PRECURSOR		193-525								
PGEME BACSU	GERMINATION PROTEIN GENE		13-40								
PGG12 STAHA	ANTIBACTERIAL PRO		3				1	1		1	
PGG13 STAHA	ANTIBACTERIAL PRO	HAEMOLYTICUS	6.))					1	1	1	
PGIDA BACSU	GLUCOSE DAMBITED		130-423			1	1	\dagger	†	1	
PGIDA ECOLI	GLUCOSE DAMBITED DIVISION PROTEIN A	ESCRIPCIONA E PITTOA	10.16		1	1		\dagger		T	
NAME OF THE PERSON OF THE PERS	CLICOSE INCIBILED		177		Ì			\dagger	T	Ť	I
POIDS BALSO	GLUCUSE INTERIED	VQ.	25-52			\dagger	\dagger	T		T	
LANAS AD IDA	GLUCOSE TRANSPOR		200-322			T	t			ľ	
PGLDA BACST	CLYCEROL DEHYDR	BACILLUS STEAROTHERMOPHILUS	20-79			İ	l	T			
PGLGA ECOL	CLYCOGEN SYNTHA	ESCHENICHIA COLI	156-283						T	T	
PGLGC ECOLI			114-141							Ī	
POLGC SALTY	GLUCOSE I-PHOSPHATE ADENYLYLTRANSFERASE	SALMONELLA TYPHIMUNIUM	114-141								
PGLMS ECOL	П		208-243			1	1	1	1	1	I
PCLN: METTL	GLNB-LIKE PROTEIN I	METHANOCOCCUS THERMOLITHOTROPHICUS	28-82		1	1	1	1	1	1]

		Probable Consects		П	п	П	דדו	П	П		
PCCENE 10711 /61			4	AREAZ	74384	2854	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4	7	4	7
THE DAY AND THE	CHANNE SYNTHETASE		₹	1				Ī			
TOTAL PROPERTY OF THE	TAKE	LICIS	-								
ארויים פרויים	MINE STREET	OBUTYLICUM	413-440					1			
PGLINA CLUAB GLUTA	Aline Straine (Asc		144-171					7			
PGLNA ECOLI GLUIA	MINE STRIFF I ASE	VOLTAE	92.00								
PGLNA METVO GLUTA	O GLUI AMINE STRINE I ASE		142-169								
PGLNA PROVU GLUTA	MINE STRING I ASE		127-165								
PCLNA PYRFU GLUTAL	MINE SYNTHETASE	Mile	2								
	MINE SYNTHETASE			:	i i	:					
PGLNA STRCO GLUTA	CLITAMINE SYNTIIETASE	_						:	:		
	HITROGEN REGULATORY PROTEIN P.II						T				
	GEN REGULATORY PROTEIN P.II	ULATUS	9								
	NITROGEN REGULATORY PROTEIN P.II	SYNECHOCOCCUS SP	2		1						
т	STATES A CO	ESCHERUCHIA COLI	120-147	2.5							
	AND ILLIAMORE AND AND AND AND AND AND AND AND AND AND	CAT MONELL A TYPHINGURIUM	151-171					1			
PCLND SALITY UDF UR	UDF UNDITLINANSERASE		00.00	÷.460	37.13	: 					
	LILIMANSFEMSE		ī	Ī							
	MINE-BINDING PROTEIN PRECURSOR	311				Ī					
	GLUTANDNE PENNEASE OPERON PROTEIN GLNQ										
	IIC CLYC.)-PHOS DEHYDROGENASE										
Г	AEROBIC GLYC.). PHOS DEHYTOROGENASE		9								
	CLYCEROL IPTAKE FACILITATOR PROTEIN	BACILLUS SUBTILIS	235-274								
300 1300 1300	CONCERNA SE		44.9]								
	CI VICEO E EDIACE		26.90								
7	STATE OF A SUSCESSION OF SECTION OF BEFORE ACTOR	ESCHERICHIA COLI	5.32								
◂		CONTRACTOR OF THE	397.334								
- 1	GLPX PROTEIN	ESCRIPTION COLD	307.174								L
	GLPX PROTEIN	SHOELLATERACA									
		EXCHENCIAL		Ī							
PGLTB ECOLI GLUTA	Ĕ	ESCHENICHIA COLI	5		I						
POLTP ECOLI PROTO	PROTON GLUTAMATE SYMPORT PROTEIN	ESCHENICHIA COLI									
	PHOSPHOTEANSFERASE ENZYNŒ TYPE-IIB	ESCHENICHIA COLI	2								
PCLYA BRAJA SERUN	E HYDROXYAGTHYL TRANSFERASE	BRADYRHIZOBIUM JAPONICUM	3								
	E HYDROXYMETHYLTRANSFERASE	CAMPYLOBACTER JEJUNI	176-40)								
PCLYA HYPLE SEUN	SERING HYDROXYNGTHYL I RANSFERASE	HYPHICARICROBIUM METHYLOVORUM	3	1							
PGMG) BACSU COMO	OPERON PROTEIN ?		9	?							
POWTH BACSU GLUCK	GL UCONORDNASE	BACILLUS SUBTILIS									
PGPID CIG.TR VIRUE	VIRULENCE PROTEIN PCP1-D		3	İ							
PGP2D CRETTE VIRUS	ENCE PROTEIN PGP1.D		2.	1							
PGP4D CALTA VIRUE	ENCE PROTEIN PGPS-D	٠	27.53								
PCPSO COLTR VINCE	ENCE PROTEIN PCM-D		8	0::0							
PGPTD CIRTH VIRUE	ENCE PROTEEN POPT-D	CHEAMYDIA TRACHONIATIS	8								
POPED CRETTE VIRUE	ENCE PROTEDY PGP1-D	CHLAMYDIA TRACHONIA 115	2								
PGREA BIOPR TRANS	TRANSCUPTION ELONGATION FACTOR GREA	RICKETTSIA PROWAZEKII	•								
PGINE BACSU CANE	CAPELIKE PAOTEDI	BACELUS SUBTRIS	=								
PCAPE BORBU CAPE.	CAPE LIKE PROTEIN	BORNELIA BURGDORFERI	2								1
PCRYE CLOAS CAVE		CLOSTRIBILIM ACETOBUTYLICUM	2								
-		BACELLUS BREVIS	? ?	38.62	20.03	1013-1062					_
-	CILALACCIDON S SYNTHET ASE II	BACELUS BREVIS	46.75	₹.	20.15	? ? ?	20.12	163.2 263.2	23.80.2386	7819-7840	98
_	CH LIT AMATE CYSTEDYE LIGASE	ESCHERICHON COLI	139-266	174-301							
Т		ESCHENICHIA COLI	100-134	110.002							
Т	CHITATHOONE REDUCTASE	PSEUDOMONAS AERUGINOSA	\$0-114								
+		BACOLUS SUBTILIS	14-101	365-296							
POSPO FRACA PROT	PROTEIN D PRECURSOR	EXWORA CAROTOVORA	258-285	\$16-543	\$10-616						
LOSA HUMAS GASON		ERWINA CHRYSANTIGENG	159.302	107.338	181.578	989-669					
POST KI EPN PROT		KLEBSELLA PNEUMONIAE	159-786								
т.	MOTENE	ERWING CAROTOVORA	119-367								
4=	PROTEIN E	EXWINIA CHILYSANTHEMI	136-367								
_	PROTEIN E	KLEBSTELLA PNEUMONIAE	3.76								
1	PROTEIN	PSEUDOMONAS AERUGINOSA	132-14	131-369							
1											

PCGENE		Sequentes	1	-			- 6-	1-	-	-
FILE NAME	PROTEIN		18:51	TY TO	77/17	PLA	MV TVIKE	AREA SONO!	3810	AMEAS
PCITT PSEAF	_	PSETDOMONAS AFRICINOSA				Ì		1	1	
PCSPI AERHY	PROTEIN I PRECURS					İ	1	† T	<u> </u> 	
PGSPI ERWCA			192			Ī		! T	<u> </u>	
PGSPJ KLEPN	PROTEIN J PRECURS	KLEBSIELLA PNEUNIONIAE	140-167			Ī			-	
POSFK ERWCA PROTECNIK	PROTEIN		3.5							
NOOK KLEPN	PROTEIN	KA PROBLIA PARI ALAMIA	6 8 6		1		+	+		
MOSTIC PSEAR	PROTEINK	SA	162.289		T	T	<u> </u> 	<u> </u> 	<u> </u>	
PCSPL EAWCII	PROTEIN		Т	740.78h	18:38	İ		T	<u> </u> 	-
PGSPL XANCP	PROTEDIL.	SIN		Ţ		Ī	-	 -	 -	
POSPIN EXINCA	PROTEDVIM		108-145			T		-	-	
PCSOD ERWCH	PROTEDN D PRECURSOR		359-302	446-475	346-573	537-684	-	L	-	
offi shoo	GLUCOSYLTHAMS/ERASE:! PRECURSOR		П	П		Ξ.	+-	495-1529		T
CIT'S STEDO	GLUCOSYLTRANSFERASE-I PRECURSOR		ī	106-211	450.485	1313-1413	1407.1414			
STATE OF THE STATE	GUCOSTLINANS ERASE.S	STREPTOCOCCUS MUTANS	٩		┪					
CTIC CTIVAL	CLINCOLAT PRANCE				T	П	113.347 592.627	2		
POTFS STREES	CLUCOS YL TRANSF		١	T	707		100.10	1	1	
PCTNA NETT!	POSSIBLE G-T MISMATCHES REPAIR ENZYME	ERAIOFORAIICICUM	Т	1		T	1	<u>]</u> T	T	
POUAA BACSU (ALP SYNTHASE		L	Т	471-505			<u> </u>	<u> </u> 	
POUAA ECOLI	SAIP SYNTHASE		105-132		Ī	İ		l		
MAGE BACCI	BETA-GLUCANASE P	BACILLUS CIRCULANS	164-191				L	 -	<u> </u>	
MOUS BACE!	BETA-GLUCANASE PRECURSOR	S	132-166							
100 A	BETA-CLUCANASE P	45	26-160							
CONTRACTOR OF THE PARTY OF THE	CANADA INTERNATE PROTECTION	DACELLOS ST	T							
PGUNI BUTTI		SOI VENS	20.00	10-40	1	1	+	1	+	
PGUPP BACSU	ENDOGLUCANASE P		T		T	Ì	+	1		
PGUNG THEETU	ENEDGL UCANASE I	NOSPORA FUSCA	201-228	Ì	T	†	+	1	+	
POUNT BACS	ENDOCLUCANASE (110-131	348.378	\$38.565	İ		-	1	Ī
	ENDOGLUCANASE PRECURSOR		П	П			-	<u> </u>	-	T
PGUND FIBSU	ENDOGLUCANASE 3 PRECURSOR	£\$	343-586						-	
	ENDOGLUCAMASE E-4 PRECURSOR		308-342						H	
	ENDOG! LICANASE	HELMOMOMOSTORA FUSCA	12.5		7					
PGUNA CLOTA	ENDOCT UCANASE A	RMOCELLIA	Т		1	1		1	+	
POUNA PSEFL	ENDOGLUCANASE A		763.789	T	T			+	+	
			394-331	Ī	T	T	1	+		
	CELLODEXTRINASE A	AVEFACIENS	176-303			Ť		-	+	Ī
L'ALLE BACK	EMDOGLUCANASE B PRECURSOR		П					-		
	ENDOCATIVATAGE BRECITE COR	CALLOCELLUM SACCHAROL YTICUM	7	44-478					H	
NGUNB CLOCE	ENDOCLUCANASE B	OVORANS	161 771	97. 77.		1		+		
PGUND CLOTH	ENDOGLUCANASE B		Т		T	\dagger	1	1	+	1
PGUNC CELFI	ENDOGLUCANASE C		801-908		İ	T		+		1
PGUNC PSEPL	ENDOGLUCANASE C		53-03			T			-	-
	ENDOGLUCANASE DIFFECURSOR	CLOSTRORING CELL ULOLYTICUM	П					$\prod_{i=1}^{n}$		
	ENOUGH TO ANA CE E PRECIDIO		Т	┪						
POINT GOT	ENDOG! IJCANASE H		اء	20.2	34.31				H	
PGUNS EXWCA	ENDOCEUCANASE PI			20.00	1	1	1			
PCUNX CLOTH	PUTATIVE ENDOGLU	ELLIM	٥		1	†		+	+	
PGUNZ CLOSA	ENDOGLUCANASE 2 PRECURSOR		1	133.540	T	\dagger	+	\downarrow	+	1
$\neg r$	ENDOGLUCANASE	LWWXA	194.225			\mid	+	$\frac{1}{1}$	1	Ţ
TO THE PLANT	EMBOGLICANASE PRECURSON		П	П					-	I
1	ENDOLUCIONES PRECEDENTE	HACILLOS SP	198.2%	301.538	137-664			H	H	

PCCFWE (197417914	Probaryotic Sequences	П	_		\neg		,,,,,		1301	
PILENAME PROTEIN	ORGANISM	4	V	4	1	T	7	┰	_	
PCUTD ECOLI SORBITOL 4-PHOSPHATE 3-DEHYDROGENASE	ESCREDENTA COLI	16.61		T			Ī	<u>:</u> !	:	:
POVPI HALJIA GAS VESICLE PROTEIN, PLASMID	TALCOACTERIOR INCOME.	3							-	
PGVP2 HALMA GAS VESICLE PROTEIN, CHROMOSOMAL	HALOBAC I ENGW HALOBIONI		79.0		Ī			İ	T	
PCVPA APHOL GAS VESICLE PROTEDY	SECULE A DIEI OCIETAN	1	8.6			<u> </u>				
FOVE THEM DAS VESICLE TROISIN	HALOBACTERUM MEDITERRANEI	17.64								
MOVED AND CAR VENCE PROTEIN	MICROCYSTIS SP	39.66							:	
POVPA PSEAN GAS VESICLE PROTEIN	PSEUDOANADAENA SI	£31	39-66					1		Ī
POVPC APPLI DAS VESICLE PROTEIN C	APHANIZOMENON FLOS.AQUAE	40						İ	†	
PRIVIC HALHA GAS VESICLE PROTEIN C	HALOBACTERIUM HALOBIUR!	150-749						-	İ	1
POVEC HALME DAS VESICLE PROTEIN C	HALOBACTERUM MEDITERIANEI	139.169						1	l	
PGVPD HALLIA GVPD PROTEIN, PLASMID	HALOBACTERIUM HALOBIUM	110.147							i	
VPD PROTEDA	HALODACTERIUM MEDITERRANEI	110.147						-		
PCVPF MAI HA CVPF PROTEIN PLASMID	HALOBACTERIUM HALOBIUM	13-47	135.169						1	
	HALOBACTERIUM MEDITERUANEI	13.47							1	
PCVPE HAI SA GVPS PROTEIN	HALOBACTERUM SALINARUM	8-49							1	
POVEC HATHA GOVE PROTEIN PLASMID	HALOBACTERIUM HALOBIUNI	39-65								
VPC PROTEDY	HALOBACTERUM MEDITERRANEI	11.72								
POVPH MAI HA GVPH PROTEIN	HALOBACTERIUM HALOBIUM	10.40								
PGVPI HALLAE GVPI PROTEIN	HALOBACTEAUNI MEDITERRANEI	\$.32							1	
POVPK HALKA GVPK PROTEIN	HALOBACTERUPA HALOBIUNI	45.76						1	1	
POVPK HALLAG GVPK PROTEIN	HALOBACTERUM MEDITERRANE!	12.39	2.74						1	
PGVPK HALSA GVPK PROTEIN	HALOBACTERUM SALINARIUM	11.31	50.17						1	
PGVPL HALAJE GVPL PROTEIN	HALOBACTERUM MEDITERRANEI	44.78								
POVPN HALHA GVPN PROTEIN	BIALOBACTERUM HALOBIUM	13.140								
FOVEN HALLAE GOVEN PROTEIN	HALOBACTERIUM MEDITEARANEI	3.50							1	
PGVPO HALLAGE GVPO PROTEIN	HALOBACTENUM MEDITERRANE!	7	103-132						1	Ī
DNA GYRASE SUBUN	BACILLUS SUBTILIS	7	429-439						1	Ī
35 85	CAMPYLOBACTER JEJUNI	287.310	181.408	452-479	663.693				1	T
DNA GYRASE SUBUN	ESCHERICHIA COLI	62.9	469.407						1	Ī
POYTA KLEPH DNA GYRASE SUBUNIT A	KLEBSIELLA PNEUNIONIAE	8	Q V						T	
PGYRA MYCPN DNA GYRASE SUBUNIT A	MITCOPLASMA TREUMONIAE	1.00	111 111	064 064	447.474	913 118			Ì	Ī
NA GYRASE SUBUN	SIAMILLOCUCIOS ADARCOS	108.310			2					
NA GYRASE SUBUR	RORRELIA BURGOORFERI	134.181						-	Ī	
POVER BOOK DAY OVER STRIPLING	ESCHENCHIA COLI	616.64)								
PCYEN HAT SO IDNA CYRASE STRUNGT 8	HALOFELAX SP	230-257								
DNA OYPLASE SUBUN	MYCOPLASMA PNEUMONIAE	249-283								
POYTH NEIGO DNA OYRASE SUBUNIT B	NEISSERIA GONORRHOEAE	524.558	011-045						1	1
POYRE PSEPU DNA GYRASE SUBUNIT B	PSEUDOMONAS PUTIDA	122-149	684-711							
POYTH SPICE DNA GYTHASE SUBUNIT B	SPEROPLASMA CITAL	40-74	189-238	283.310	34.364	\$60.530			1	T
DNA GYRASE SUBUN	٦	27.78	201-318						1	
PHONIA ECOLI 17-ALPHA-HYDROXYSTEROD DEHYDROGENASE	Ť	21-98							†	Ī
_	LACKEDICKIA COLI	61.00	374-330					1	1	
	Cid On On On the Color of the C	21.00							Ť	
PREMI CHLVI GLUIAMTE INTO TEXT STATE	SECURE OF THE COLUMN TWO IS NOT THE COLUMN T	71.00							†	T
GLUTAMYL-TRWA R	SCHOOL COLL SOURCE	9 6							1	
PREMI PHOSH S-ANDIOLEVILING ACID STRIPLYSE	CALLACAGE I A TYPHING BUILD	710.116	144.171						T	T
	Ť	8	160.177						Ť	
PREMI STREET GEOLOGATE TANDOL ENTERNO ACTUAL	T								T	T
PHENT MAINT DELIANGE TROUBLE CONTRACTOR STATES	T	16.91						T	T	Γ
PHEMA ECOLI ILEOPONEHYZINOGEN-III SYNTHASE	ESCHEDICHÍA COLI	211-238							İ	
PITEMAN ECOLI HEMAN PROTEIN	ESCHENCHIA COLI	147-174								
PHEMAL YEARN FREMEN NECEPTON PRECURSOR	YEASING ENTEROCOLITICA	234-261								
PHENOX ECOLI PUTATIVE METHYLTRANSFERASE	ESCHERICHIA COLI	86-13B	165-219						1	7
PIEMY BACSU HEMY PROTEIN	BACILLUS SUBTILIS	217-262								
	•									

PCCENE	10001354	Probactuals Commercial									
FILENAME	PROTEIN	DRGANISM	AREAL	ABFA 2	ARFAS	ARFAG	ARFA S	ABFAK	1011	100	10.0
PHEME BACSU	ERROCHELATASE	BACILLUS SUBTILIS	Т		_					т	4
META ANAS	ŒTEROCYST DIFFE	ANABAENA SP	184-211	357.198	\$21.565						
PHEXA STRUN	NA MISMATCH REP	STREPTOCOCCUS PNEUMONIAE	476-460								
WEST STORY	DNA MISMATCH REPAIR PROTEIN HEXB	/E	470-497								
	TI O TRANSACTIVAT	ESCENTUS	98.125								
A LUCA		ESCHENCHIA COLI	9			į					
PIEO COL	TOTAL PACTOR A PROTE	ESCHERICHIA COM	. 1. S	į						i	
PHIEC HAFIN	TAIL LATING BACKETER		2				 				
A CAL COLLEGE	A LCIA FION FAULT	TIMENOPHILUS INFLUENZAE	ž	\$	447-474						
PRISA ECOL			76-74								
V LV PARA	P.C. A CABBOYALINE SIBOTINE		22								
PHICE LIFTUR	P. P. CARBOVALLIDE RIBOTINE		9	181-228							
72 173 17311	T-A CAMBOANNIDE NEOTINE		115-142								
200	P->-A CAUGOXAMIDE MIROTIDE	UNUM	651-521								
MISS LACLA	ANDOTANSFERASE HISH		7.34								
- 4	TLO TROIEU		39.66	143.169							T
PHIS6 SALTY		IINUM	99-66	142.169							T
THISY ECOL.	IMIDAZOLEGI. YCEROL-PIIOSPHATE DEHYDRATASE ESCHEJUCHIA COLI	ESCHENCHIA COLI	161.199								Ī
PHIST SALTY	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE		161-199			Ī					Ī
PHISE ECO.	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE		710.06								
HUSE HALVO	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	CANII	174-201								ĺ
YHOSH LACEA	HOSTIDDIOL-PHOSPHATE AMENOTRANSFERASE		191-191								
LIDS SALIT	THE I LUNGL-PHOSPHATE AMINOTRANSFERASE		293.320								Ī
200	HISTORINE PERMEASE MEMBITANE Q PROTEIN	SALMONELLA TYPHIMURIURI	1.35								Ī
TOTAL COLUMN	HIS LIGHTON DEHYDROGENASE		•								Ī
V V V V V	HISTORICS DESTURBORNASE		П	264-303							Ī
A PLACE AND A PLAC	HISTORION DESTRUCTIONS	IS	П	199.430							Ī
PLU A CTAALI	ALEMANDE DE L'INCOMENANTE	2	393-434								
PHO.YI ECOLI	HEADI VINA CHROMOSOMA	STAMPLUCCCCUS AUREUS	<u></u>	П		П					
PHLY2 ECOLI	HAEMOLYSIN SECRETION PROTEIN CHROMOSOWA		┪	26.10 10	161-224	134-261	153.380	458.492	384-581	647.738	
PHLY4 ECOLI	HEMOLYSIN D. CHROMOSOMAL		T	T							
PHLYA ACTPL	HEMOLYSIN	2	=	٦	┪						
PHLYA ACTSU	HEMOLYSDA	T		7		╛	П	П	846-934		
PHLYA ECOLI	HEMOLYSIN A, PLASMID		T	_	T	7	Т	П	646.924		
PHILYA PROMI	HEMOLYSIN PRECURS		ě	101:0/	Т	Т	Т	7	╗		
			Т	Т	200 400						747.774
PHLYA SERWA	HEMOLYSIN PRECURSOR	SERRATIA MARCESCENS	Т	Т	1	_	8	77.02		_	2
			15	ī	Т	Т	Т	1		7071-6611	744-1780
MEYA VIBON	HEMOLYSON PRECURSOR			638.663		T		1	T	†	
THE ACTU	HAEMOLYSIN SECILETION PROTEIN	LEUROPNEUNIONIAE	197		T	Ī		T		1	T
THE ELOCA	HALMOLYSIN SECTETION PROTEIN, PLASHID		487.514					Ī	T	\dagger	Ī
TO SECURITY OF THE	MANUAL SUR ACTIVATION THOSE PARE UNSOR			499-547							
MA VIN CERVA	VENCE YOU ACTIVATION PROTEIN BECOME			487-514						T	T
	MENON YON RECEPTION PROTEIN BILLINGS	SEMANIA MARCESCENS	П						Ī		Ī
MG VC ACTE	HENDE VEN C		_	413-447	458-524						
A CALL	I HELLOL VAIN CECTETION PROTEIN A PRO	ACTUMOBACILLOS PLEUROPNEUNIONIAE	19-157							\dagger	Ī
HE YO ECOL	HEMOLYSDA D. PLASACIO		Т	7							Ī
MEY HALL	HALOLY SIN PRECURSOR		7	2 2	223-331						Γ
PHOACH DESYN	4) 2 KD PROTEIN IN HOAC OPEAGN		2		1						
PIOD METKA	HIZE ORNAND DESTYDROGENASE		2	1							
PPOS SEDAN	DNA-BINDING PROTEI					1					
PHOLA ECOLI	DNA POLYNŒÃASE IQ DELTA SUBUNIT		T	100	1	Ì	1				
PHOKA BRAJA	REG PROTEDY HOXA	JAPONICUM	1	1077	†	1	1	1	1	+	
WOON OR OTHER	PHONE NOOP HOXS ALPHA SUBUNIT		Т		 		T	1	1	\dagger	1
LUCAN ALLEN	HOAD PROJECT	ALCALIGENES EUTROFHUS	24-110				 	\dagger	T	1	
						1		1	1	1	7

374504	1102-110-4	Posts grante Consenses					l	-	-	\vdash	Γ
FILE NAME	PROTEIN		ABEAL	AREAL	AREA?	AREA!	AREA A	AREAS AREA?	IAT AREAR		1864
PHOXX BIXAJA	HOXX PROTEIN	ZOBIUM JAPONICUM	5.5			Ì		<u> </u>	1	-	i
PILL DEIRA	HEXAGONALLY SUR	URANS	<u>≃</u>	- <u>-</u> !		Ī		1	<u> </u> 	1	!
PIPRT LACLA	PHOSPHORIOSYL TRANSFERASE		ī	2		j				1	
PILLOD STRCO	SIGNA FACTOR IUDI		36.55							1	
PHOUSE BURSO	EGULATORY PROTE	EARUN	<u> </u>			Ì		1		+	Ì
PICUPH PSESY	OUTER NEWBRANE P		2.0	2			1		1	+	
PHOUS PSESH	ROBABLE REGULAT				1	Ť		1	1	+	Ī
PHS18 CLOAB	18 KD KEAT SHOCK PROTEIN			i	-	1	•	•	_		_
PISTO HALMA	HEAT SHOCK TO KD PROTEIN							_		_	
MISTO MYCLE	IN AT SHAKE TO KID PROTEIN					:	:	; 	:	-	i
FIISTO MYCPA	HEAT SHOCK TO KD PROTEIN	AKATOHI KU ULOSIN	T			Ì		+	1	+	
PHING ECOLI	HEAT SHOCK PROTEIN C62 S		i			Ì	+	+	-		1
PHTTA ECOL!	PROTEASE DO PRECL	-	ı				-		1	- <u> </u> 	
PHINE ECOLI	HTRE PROTEIN PRECURSOR		7	22.1%				<u> </u>	<u> </u>	<u>-</u> !	
MILE HALKA	SENSORY RHODOPSIN I TRANSDUCER		7			İ	<u> </u>		· !		_
PHTEL HALSA	SENSORY INCODOPSIN	ALINARIIN		5.5	13. CE				_		_
PHUTP BACSU	HUT OPERON POSITIVE REGULATORY PROTEIN		7	i			1	<u> </u>		<u>-</u> 	_
PHYT! LACIE	ELVETICIN J	ELVETICUS		<u>=</u>				-			Ī
PHYCA ECOLI	FORMATE HYDROGENLYASE SUBUNIT I		8	2		İ	-	-		•	
PHYDO ECOLI	TRANSCRIPTIONAL REGULATORY PROTEIN HYDG		1.5			1		+	1	1	
THYDO SALTY	TRANSCRIPTIONAL R	HINTOMORY	231-216		Ī				1		
PHYDH ECOLI	SENSOR PROTEIN HYDH		<u> </u>	ŝ					<u> </u>	1	Ī
PHYCE PSESN	HYDAMTOIN LITILIZA		ੂ	-		j				_ <u> </u> 	1
7	HYDANTOIN UTILLZA		П	≘				1		-	
ا ــ	DEDOLEACETATE -LYSINE LIGASE	RINGAE	,	37.31			1	1		1	
PIA ECOLI	ALK PHOS ISOZYNŒ CONVERSION PROTEIN	ESCHERICHIA COL!	Т	Т	╗	Т	╗	٦	╗	Т	
ACEN EXAM	ICE MUCLEATION PROTEIN		1	575-676	236.361	014.641	27 089 73	72 - 748 758	758-785 854-88	┪	170.077
			31	Т	1	Т	Т	Т	Т	+	T
PICEN ERWIE	ICE NUCLEATION PROTEIN		Т	Т	Ŧ	646-673	_	I	116-913 982-1009	8	1
אנבא גאוו	ICE NUCLEATION PROTEIN	PSEUDOMUMAS PLUORESCENS	B) (1)	T	23-625	┪	129.781	785-852		+	
	ILE MULEATION PROJECT		Т	Т	Τ,		1	4		+	1
PICEN XANCI	ICE MUCLEATION TROIEIN		10.00	20.00	POZ 1-20	174-1775	1	-	1	\dagger	T
200	ACTIVITY OF THE PROPERTY OF TH	313 1174 0144 35	T		1	Ì			1	1	
PIES BACK	INTERVIOUS ACTOR IS 3		Т	201.70		1	$\frac{1}{1}$	\dagger	†	\dagger	T
1	DOTIATION FACTOR 15.2		Т	38.5		Ť		\dagger	-	+	T
1	MITTATION FACTOR IS.2	ECIUM	Т		Ī	Ť		\dagger		\dagger	T
1	DATIATION FACTOR IF.3	OPHILUS	2.		T	ĺ	-	\mid		+	
L	DATILATION FACTOR IF-3		ž	16-01		Ī		\mid	-	ŀ	ĺ
PUT KLEPH	DITTIATION FACTOR IF.3		ž.	10-01		l	-	\vdash	-	H	
PUT MYCHE	DITIATION FACTOR IF:3	MENTANS	13:311				_	-		-	Ī
PLF3 PROVU	INITIATION FACTOR IF-3			70-07				L			
PD) SALTY	DUTIATION FACTOR UF.)	ממא	٦	76.97							
PIETS SERVA			7	П	┪		_			-	
104 ME100	IGA-SPECIFIC SELENE EMBOPEPTIDASE	HOEAE	2	П	┪	1024-1058	1377-1404 141	1483-1531		Ц	
PIGGS STREE	IGG BINDING PROTEIN PRECURSOR			╗						\dashv	
PICGO STREE	IGO BENDENG PROTEEN PRECURSOR			╗	25.23	170.797				$\frac{1}{2}$	
PRIM ECOL	ACETOLACTATE SYNTHASE		٦	2						-	
PEW SALTY	ACETOLACTATE SYNTHASE	URIUNE	7	200						Н	
A CAN	ACETOLACIA IE SYNTHASE		Š					_		-	
POGB SALTY	DATE PROTEIN		? ?				_				
PDG ACICA	INOSINE S-MONOPHOSPIKATE DEHYDROGENASE	ALCOACETICUS	<u>\$</u>			1			_	+	
THE BACK	POUNDE PARTICIPA A SECURICIO	BACH LIE TO BEAUTIONS	Ť						1	+	٦
PING A LISTO	INTERNATION A STECONOR		07:0	26-326	100	1	+	+		+	T
PENLE LISMO	INTERNALIN B PRECURSOR		1	Т		\dagger		+	$\frac{1}{1}$	+	T
PINVA YEKEN	PAVASIN		Ļ	Т		T	\dagger	+	+	+	T
	٦.			1		1				$\frac{1}{2}$	7

PCCFNF	147-130-4	3 :									
TILE NAME	PROTEIN	ORGANISAL	AREAL	ABFA 2	ABFAT	ABFAA	ABFAS	ADFAA			
PUPAY SHUFT	60 KD ANTIGEN	SHIGELLA FLEXMEN	T		_	1	_	Т	Т	┰	7 07.00
LINA SHOP	70 KD ANTIGEN	SHIGELLA FLEXMEN	98-136	\$17-160	493-557	396-630				l	Ī
A SEE	62 KD MEXIBAANE ANTIGEN	SHIGELLA DYSENTENIAE	28-55	691-14	100-001	\$22.554					
TILVE SHIPL	62 KU MEMBRANE ANTIGEN	SHIGELLA FLEXNERI	21.55	11.169		955-225					
	41 KD MENITRANE ANTIGEN PRECURSOR	SHIGELLA DYSENTENAE		113-161		324.378					
PIPAD SURV	11 FO PIEPERANE ANTIGEM PRECURSOR	SHIGELLA FLEXNEN	٦	13.161	373.300	114.373					
	A FO PERSONS AN HOEN UND	MUCELLA DI MENALA	1	П							
POCE SHIDY	POR PROTEST	SHICELLA PLEXNER	7	259-286	201-316						
Pipes sann	DCB PROTEIN	SHIGHT OF SERVENAL									
200 100	ICONCUTENCY SEASONS ASSESSED ASS.	SHIDELLA FLEXNER	<u> </u>								
L COS		PSEUDOMONAS SYNUNGAE		143-173						T	
TOTAL STATE	WORDANG TRUTHOSTIA I ASE	ESCHEDICHIA COLI									
DOWN ACCOUNT	WANTED THE THE THE CONTRACT OF	VIBRUO CHOLERAE	212-239	136-377							
2000	TRANSPORTER REGULATORY PROTEIN MUSE	VIBRIO CHOLERAE		67-97							
PICEN CUTTO	MON-MENULATED MOTEIN A	SYNECHOCOCCUS SP	167.19M					Γ			
מינות מינות	INSERTION FLEMENT ISOURING PROTEIN INSERT	SHIGELLA DYSENTENAE	16-113							T	Ī
	DISEASON ELEMENT INC. 1819 PROTEIN INSE	SHIGELLA DYSENTEMAE	6.33							T	Γ
	DISCOULS ELECTION 131 PROJEST INSE	ESCREDUCHIA COLI	122-149								
2000	INSENTION ELEMENT IST PROTEIN INSE	SHIGELLA FLEXNEN	11.9							r	
PISPI BACKI	MANDE DETRACTION AS SECOND PROTECT	SHIGHT A SONNE!	7	П		Ī				T	
PISP BACED		BACILLUS SUBIILIS	┪	197.724	253-210					l	-
PISTA FCOL	ISTA PROTEIN	BACILLUS POLYMYAA	⊋ 8								
PICTA CLICA	ISTA BROTTEN	ESCHENICHIA COLI	183-210							T	
PILITA ECOLI	FEBBIC ACOUNTY DECEMBED BATCHESON	SPUCELLA SONNE!									Ī
PIAG BACSU		ESCHENCHIA COLI	_	535-543	\$50.501						Ī
PK6P2 FCOL	A-PROCEROFFICTOR IN A SET TO NAME &		68.03								
PKAD BACSU	ADENYLATE KINASE	DACTI LIE ET DETTI LE	2								
PKAD LACLA	ADENYLATE KINASE	PACIFICA SUBILIES	2								
PKANU BACSP	KANAMYCIN MACL										
PKANU STAAU	KANAMYCIN NUCLEOTONL TRANSFERASE	ACCUS ALMERIS	8.00		1		j	Ì			
PKDGT ECOL	KETO-1-DEOXYG		1001	1	1	1	Ì	Ì			
PKDGT EAWCH	-KETO-J-DEOXYG	THEM	136.151	1	T		1		1	1	
PKDTA ECOLI	DEOXY-D-MANNO		164.1%		İ	T	1	T	1	1	1
PKGTP ECOLI	LIMA-KETOGLUTA		3	T	T	Ť	1	1	1	1	ĺ
PKGUA ECOLI	GUANYLA TE KIDAS	ESCHENCHIA COLI	162-189	Ī		T		1	1	1	
THISE BACSO	HOMOSERINE KINA		\$.76		T	T	\dagger	Ť	t	1	T
TANK TANK	AMMOCI VOOLING	HON	52.79			T		T	T	\dagger	1
PKORB ECOL	MANAGER COSTEE J. FROSTROI PARASPERASE	LMS.	66.21						T		Ī
PKPVI SPICE	PORTIVATE PRIACE	ESCHEDICHIA COLI	226.255					Ī		l	Ī
PKPYK BACST	PYRUVATE KINASE		2							-	Γ
PLACA STANU	ISOMERASE LACA SUBLINIT		Z								
PLACA STUMU			5 5		1	j					
PLACC STUM	TAGATOSE 4-PHOSP		T	287.116	†	Ť	1	1			
PLACG LACCA			ŀ		Ì	1	1				
PLACI ECOLI	LACTOSE OPERON REPRESSOR		١	1	1	1	1		1		
PLACI KLEPN	LACTOSE OPERON REPRESSOR		95.229	1	T	1	1	1	†	1	
PLACE STAND	PHOSPHOTRANSFERASE REPRESSOR	2	ē.	Ť	T	\dagger	†	†	1	†	7
PLACE STRAN	PHOSPHOTRANSFERASE REPRESSOR		2	T	\dagger	\dagger	\dagger	\dagger	\dagger	\dagger	T
ALACY LAGE	LACTOSE PERMEASE	==	٥		T	t	\dagger	t	\dagger	\dagger	T
A VIEW		US	62-89	311-415			t	T	\dagger	+	T
TANG PLEY	FUND 1 1/2 BETA CITICALE		337.364		l		\dagger	I	\dagger	\dagger	T
PLASI PSEAE	ORDEL SYNTHESIS PROTEIN LAST	2	133-159					T		+	T
	PROBABLE LEUCOCIN A DOMINITY PROTEIN	DSA	171-198					ŀ	-	\dagger	Ī
PLCNC LACLA	LACTOCOCCIN A SECRETION PROTEIN LCNC	LACTOCOCCUS I ACTUS	т	7							
			102-189	207-234		1			H	H	Π
											l

THE STATE OF	107,170,4	Sequences	T	T	1	AREA	ARCAS	AREAS	AREA?	AREAL	AREAS
LE NAME	PROTEIN			20.00					Г	Г	
CMD LACLA	LACTOCOCCIN A SF.CI			Т		Ī					
PLCRD VEREN	LOW CALCIUM RESPONSE LOCUS PROTEIN D	Colinea	Т	4 S 1 67							
CRD YEAVE	LOW CALCIUM RESPO		7	Т	240.767						
CRV YELVE	VIRULENCE-ASSOCIATED V ANTIGEM		Ţ	Т							
CRV YERPS	VIRULENCE-ASSOCIA	LULUSIS	T								
CTB BACCA	LCTB PROTEIN										
PLCTB DACST	CTD PROTEIN	MACILLOS SIEAROTHERANCTHI.OS									
DHD LACK	D-LACTATE DEHYDROGENASE	WYICHS	T	241-272	379.306						
DILP BACPS	L'LACTATE DEHYDROGENASE P			241.275	279.306						
DHX BACPS	L-LACTATE DELIYDROGENASE X		2								
PLDH BACKE	L-LACTATE DEHYDROGENASE	SCALLE LIE	Т	116.111							
PLDH BACST	L-LACTATE DEHYDROGENASE		T	740-767							
PLOH BACSU	L-LACTATE DEHYDROGENASE		T.								
PLOH BIFLO	L.L.ACTATE DEHYDROGENASE										
או שו ואסער	L.L.A.C.TATE DEHYDROGENASE	2									
PLDH LISMO	L-LACTATE DEHYDROGENASE		40.7								
PLDH MYCHY	L-LACTATE DEHYDROGENASE	EUMUNIAE	200								
PLOH THEAD	L.LACTATE DEHYDROGENASE	THERMUS AQUATICUS	2		717.007	140.000	119.414	337.364			
PLEF BACAN	LETHAL FACTOR PRECURSOR			5		Т					
PLEPA PSEFL	LEPA PROTEIN	ORESCENS	2 .								
	SIGNAL PEPTIDASE I		2								
PLEUI ECOLI	1.ISOPROPYLMALATE SYNTHASE		07.7	700 001							
	2-ISOPROPYLMAL ATE SYNTHASE										
PLEUS BACCO	3-ISUPROPYLMALATE										
PLEUJ CLOPA	3-ISOPROPYLMALATE	CLOSTADIUM PASTEURAMUNI	717.5								
PLEUD LACLA	ISOPROPYLMALATE	LACTOCOCCUS LACTIS	307.134	476.701	344.334	715-822					
PLEVR BACSU	TRANSCRIPTIONAL REGULATORY PROTEIN LEVE	BACKLUS SUBTICES	146-17								
EXA ERWCA	LEXA REPRESSOR	MORA VELLA SP	36.53								
PLIFI MORSP	LIPASE	MORAXELLA SP	156-383								
PLIFT MURSE	LIPAGE A		(6-9)								
IP BURCE	LIPASE PRECURSOR	BURKHOLDENIA CEPACIA	176-203								
PLIP PSEFL	LIPASE PRECURSOR	PSEUDOMONAS FLUORESCENS	2								
PLIP PSESS	LIPASE PRECURSOR	PSEUDOMONAS SP	176-203								
FLIP STANU	1	STAPHYLOCOCCUS AUREUS	101.330								
PLIVE SALTY	LEUALE/VAL/THOR-BIR	7	195.222								
PLIVE SALTY	LEUCINE SPECIFIC BI	KAI MONET A TYPHINGS IS	121-146								
INE SALIY	AMINO ACID INANSPORT PROTEINLIVE	ESCHENICHIA COLI	23-50								
PLAN ECOLI	LEIGH EVAL BROWNS PROTEIN PRECURSOR	CITROBACTER FREUNDII	195.222								
HIVE ECON	I FLUT EVAL BINDING PROTEIN PRECURSOR	+-	195-222								
PLIVE FCOLI	LEUCINE. SPECIFIC BINDANG PROTEIN PRÉCURSOR	-	195-222								
PLIVM ECOLI	AMINO ACID TRANSPORT PROTEIN LIVIN	Н					3				
PLKTA ACTAC		ACTINOBACILLUS ACTINOMYCETEMCOMITANS				217 007		1007	(17)	107111	151.036
PLKTA PASHA	LEUKOTÓKIN	PASTEURELLA HAEMOLYTICA	4	97.41	77.66	5					
PLKTB ACTAC	LEUKOTOXIN SECNE	ACTINOBACILLUS ACTINOMITE LEAK UNITERAL		3	313 187						
PLKTB PASHA	LEUKOTOKIN SECRETION PROTEIN	PASTEURELLA MAEMOLYTILA	6	9131							
PLKTC ACTAC	LTCPROTEIN	ACTINODACILLOS ACTINOMITACIONAS ACTINO									-
PLKTC PASIA	LKTC PROTEIN	PASIEURELLA MACMOLTINA		304.343	372.105	161.10					1
LKTD AGIAL	CLKTD FROTEIN	PASTEIMELLA HAEMOLYTICA									
TKIO LV	A LATIO FACILITY PROTECTED A	ESCHERICHIA COLI	21.148								
PLON ECOL	AIP-DEPENDENT PR		239-256								
100 X	I POPROTEIN SIGNA		6.33								
H SPA STAAU	LIPOPROTEIN SIGNA	STAPHYLOCOCCUS AURITIS	134-161								
HIRF STAN	LEIKOCIDIN F SUIL	STAMIVI, OCOCCUS AURILIES	161.195		:						
100	HILL S NICHT WORK	i	147.707								

A COLOR TO THE COLOR OF THE COL	6.4	Probate Consesses	Ī	Ī	ſ		l	ŀ	-	f	ſ
FILE MAME PROTE			IJ,	ABEA1	77387	PREAT	1 7780	ABEAS	AREA? AR	AREAL	AREAS
PLUXA KRYAL ALKAN	VAL MONOOXYGENASE ALPHA CHAIN		Т	100.00		1	1		+	\dagger	
PLUXB PHOPO ALKA	ALKANAL MONOOXYGEMASE BETA CHAIN	M PHOSPHOREUM	107:11	149-167		Ī	1	1	+		
PLUXB VIBHA ALKAN	AAL MONOOXYGENASE BEIA CHAIN				Ī	Ī			1		Ī
PLUXC PHOLE ACYL.	COA REDUCTASE	PROTOBACTEBUM LEICHMAIN				T		1	1	\dagger	T
PLINC WART ACVIL	COA BEDIKTASE		599				Ī			\dagger	Ī
PLUXC XENLU ACYL	COA REDUCTASE		19-66						-	\mid	Ī
PLUXD PHOLE ACYL 1	TANSFERASE	IM LEIOGNATIII	٦	216.245						Н	
PLUME VIBHA LUCIFE	LUCIFERIN-COMPONENT LIGASE		30-57							H	
PLUX PHOLE NON-FI	LUCKESCENT FLAVOPROTEIN							1	+	1	
PLUX PROPO NON-P	LUCKESCENI PLAVOFROIEIN	THOUGHACTERON THOSTHOREON		9			Ī	1		+	I
M. LYCL VIBER PROSA	PRUBABLE PLAVIM REDUCTASE					Ţ	T			t	Ī
DI IIVI VIDEI CANA	SOUTH DESCRIPTION OF THE PROPERTY OF THE PROPE			T				\dagger	+	Ť	
PLUXI VIBEI OLOGIA	OND SYNTHESIS FRUIEN LUXI		10.53		T			T	+		T
PLUX PHOPO LUNKA	LUMAZINE PROTEIN	INI PIIOSPIIORI, UNI	21:45	162-189			Ī		\dagger	t	Ī
PLUXX YISHA LUXX R	LUXX REGULATORY PROTEIN		91:0				T	T	\mid	t	Ī
	IAL MONOOXYGENASE BETA CHAIN	UNILEIOGNATHI	268.205								
	ALKANAL MONOOXYGENASE BETA CHAIN		271.255								
FLYB BACSU BENZYNIE			17-110					-		H	
PLYC CLOAB AUTOL	AUTOLYTIC LYSOZYAIE	IOBUTYLICUM	91.19							H	
PLYSP ECOLI LYSINE	LYSINE-SPECIFIC PERMEASE		142.176		П						
PLYTB BACSU AMIDA	ğ۱		<u>=</u>	2	467.513	23.313					
MYTB ECOLI LYTB	LYTB PROTEIN		┱					1	-	1	
PLYTC BACSU AMIDA	AMIDASE PRECURSOR		_	232.532					1	1	
PLYTR BACSU MEMBE	MEMBRANE BOUND PROTEIN LYTH		T	239.30)		┪	┱			1	
PALLY STRUT IN PROP	TEIN, SEKOT VPE 12 PRECURSOR	STREFTOCOCCUS PTOCEMES	2 2	116-136	191-300	105.342	30.45	100.404	+	+	
	FEN SEROTYPE 49 PRECINCOR		Τ.	349.133		Ŧ	Т			\dagger	T
1	TEIN SEROTYPE SPRECURSOR (T	\$6.763	106.133	193.410			+	+	T
PAIS STAPY MPROT	M PROTEIN, SEROTYPE & PRECURSOR			Γ	Т	14).401	Ī		+	\dagger	Ī
PHALE ECOL! MALTO	SE-BINDING PROTEIN PRECURSOR		Γ	Γ	Т		Ī		_	t	
PAIALE ENTAE MALTO	MALTOSE-BINDING PROTEIN PRECURSOR		10-47							H	
PLIALE ENTAE INNER	INNER MEMBRANE PROTEIN MALK	ROGENES	92.								
PMALT ECOLI MALT	MALT REGULATORY PROTEIN		١								
PMALX STRPN MALX	PROTEIN PRICURSOR	CUS PNFUNIONIAC	7	16-207						+	
PIANE DACSELLA-UET	PRIAND DALSA IN ALAMANA RESIDENCE A AND DIRECT	CALIDOCELLIBA SACCILADOS VVICINA	410-441	70,7			1	1	+	+	
PHINDY BACST MALAT	TE OXIDORE BUCTASE		Т				T	1		\dagger	
PAIACE ECOLI ANTIBE	ANTIBIOTIC RESISTANCE PROTEIN MAKE.		95-132			Ī			-	t	Ī
PARBER ECOLI MOBILI	MOBILIZATION PROTEIN MBFB			100-134					\vdash		
PARIETI, WOLSE! OUING	QUINONI-REAC NOFE-HYDROGENASE	NOCH:NI:S									
PAICES ECOLI MCBB P	ACBB PROTEIN	ESCHERICHIA COLI	7	132-163							
PACE ECOL METHY	METHY: ACCEPTING CHEMOTAXIS PROTEIN		90.27	120-131	36-343		1	+	+	+	Ī
PACE ECOLI METHY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN !!					1	1	+	+	\dagger	Ī
PAICPS SALTY METHY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN II	HINDROM	30.10	T	Ī	Ī	Ī		+	\dagger	T
PLACED ECOLS METHY	METHYL-ACCEPTING CHEMOTAXIS PROTEIN III		216.315	Ī	Ī	T	T	t	+	t	T
PAICP4 ECOLI METHY	A.ACCEPTING CHEMOTAXIS PROTEIN IV		\vdash	164-191	277.304		T	t	-	t	Ι.
PAICPA CAUCA CHEMIC	DRECEPTOR MCPA		160-287	П	\$16-543	Ī.	ľ	ŀ	-	F	
PMCPC SACTY CHEMC	CHEMOTAXIS CITILATE TRANSDUCER		Н	П	-					-	<u>-</u>
PMCPD EN'AE CHEM	STAXES ASPARTATE TRANSDUCER		20	П	П						Γ
PACPS ENTAE CHEMIC	DIACIS SEMINE TRANSDUCER	ROGENES	1	158-208	117.351	488-523				H	
PACEA ECULI SPECE	PACKA LATE SPECIFIC RESIDENCE A REDICTASE	METHANOGARCINA BARKERI	17.71	1	1	1	1	\dagger	+	+	
PINCRA METVA METHY	1. COENZYME M REDUCTASE		191-31	T	Ī	1	1	\dagger	\dagger	\dagger	T
PMCRA METYO METHY	PACKA METYO METHYL-COENZYME M NEDUCTASE		3)6-363	T	T	Ī	1	+	\dagger	+	T
				1		1	1	1	1	1	7

107,178,4	Prohibit Sequences	AREAI	AREAL	AREA 3 A	AREA	AREAS IAI	ARCA 6 AREA?	AREAL	ARGAS
THE NAME PROTEIN	METHANOTHERATUS FERVIDUS		П			1		1	
L-COEMY TAKE M MEDOC TAKE	METHANOCOCCUS VOLTAE	247-274		Ì	1	1	-	+	
L-COENT FRE FI ALCOCKAGE	ESCHENICHIA COLI	111-145		1	1	+	+	1	
TASE OPERON PROTEIN D	METHANOCOCCUS VOLTAE	74-91	1	1	1	†	1		
MAI ATE DEMYDAOGENASE	ESCHENICHIA COLI	23:13	1		1			 	
E DEHYDROGENASE	AIETHANOTHERARUS FERVIDUS	2.50	1	1	1	+			
MALATE DEHYDROGENASE	SALMONELLA TYPHINIUMUM	27.134		903,1019	İ	+	-	-	
	ESCHERICHIA COLI	7	Т			ŀ		-	L
BIOSYNTHESIS PROTEIN ADDIN	ESCHENCHIA COLI	1	1				-		
METHICILLIN RESIS REG PROTEIN MECI	STAPHTLUCUCCUS		I						
	ETIDELOMIDIS & AUREUS	419-495	26.53			-			
METHICILLIN RESISTANCE MECKI PROTEIN	SIAM TENCHOS	Т							
	EFIDERALIDIS & AUNCOS	214.248							
PMEMB METCA METHANE MONOOXYGENASE CONDONENT A	LOCATION OCCURS CAN SOCIALIZATION	321.34							
NE MONDOXYGENASE COMPUNENT A	WEIGHT CONTRACTOR OF THE PARTY	133.167				-	-		
	STREET DAY CO.	159.186							
PROBABLE HG TRANSPORT PROTEIN	SINCE IONITIES LINES.	144.165		Ī	-			L	
INIC REDUCTASE	SACILLOS SE SESSENDI OCOCCASE ATTRETAS	192.147	332.386						L
MERCURIC REDUCTASE	SIAMILLOCUCIOS AUREOS	14-111							L
MERCURIC RESISTANCE OPERON REG PROTEIN	SIAMILUCULUS AUREUS	146.181	Ī	Ī	Ī		-	-	
CYSTATHIONINE CANONA-SYNTHASE	ESCRETURING COL	163.380							
THIONING BETA-LYASE	CALLACAGE I A VOCUMENTA	3.29					-		
CYSTATHIONINE BETA-LYASE	SALMONELLA LITHIMOROM	441.412						_	L
METHIONINE SYNTHASE	ESCREAUTH COL	371.398	647-676						
ONINE SYNTHASE	Countries Chita Coll	185.212							
TRANSCRIPTION REPAIR COUPLING FACEOR	ESCHEDICHIA COLI	63-89	313.380						
GALACTOSIDE BINDING PROTEIN	PACITALIS SUBTILIS	65-122							
	ESCHELUCHIA COLI	103-129				1			
13 KO VEMBRANE PROTEIN PRECURSOR (CHEAMYDIA TRACHOMATIS	41-75				1	1		
MEMBRANE PROTEIN MIP PRECURSOR	LEGIONELLA MICDADEI	106-133							
ADENINE N4-METHYLTRANSFERASE	ENTEROCOCCUS FAECALIS	4.01	×				1	1	\downarrow
RENA ADENINE NAMETHYLTRANSFERASE	STAPHYLOCOCCUS AURIEUS	•							
ADENINE NÆMETIIYLTRANSFERASI	ENTEROCOCCUS FAECALIS		2			1			1
RANA ADENINE NAMETHYL TRANSFERMSE	BACTEROIDES FRAGILIS	16-43	1			1			ļ
ADENINE N-E-METHYLTRANSFERASE	ESCHENICHIA COLI		2			t		+	
ARMA ADENINE N-6-METHYLTRANSFERASE	STREPTOCOCCUS PNEUNIONIAE	=	200			1	-	 	
	STREPTOCOCCUS SANGUIS		\$2.5					<u> </u>	ļ
	BACTEROIDES FRAGILIS					T			
	METHYLOCOCCOS CATSOLATOS	40.34				T	-	_	L
MOLYBD COFAC BIOSTM PROTEIN B	PHIORACHITIC BERROOMIDANG	94-121	31.338			T			
MOBA PROJEIN	THEORACH LIS FERRODXIDANS	100							
MODEL TROCKIN	THIORACTITUS FERMOOXIDANS	95.132							
MOSIO PROTECTION	ESCHENCHIA COLI	45:73							
AND VARIOUSTERIN BIOSYNTHESIS MOCA PROTEIN	ESCHEDICKIA COLI	243.170							\downarrow
i i tai	CLOSTRIDIUM PASTEURIANUM	16-53							
MOLYBDENUM-PTEMN BINDING PROTEIN II	CLOSTRIDIUM PASTEURIANUM	26-64				1		-	
ANOL UTIL CONT PROTEIN MOXY	PARACOCCUS DENITIUFICANS	200-234	307.334			1			+
BILDN BIOSYNTHESIS PROTEIN MEU	SYNECHOCOCCUS SP	2.36	10-103	1911-223		1	1		
BILIN BIOSYNTIESIS PROTEIN MPEV	SYNECHOCOCCUS SP	<u>:</u>	175.216	-		1		+	1
MURA PROTEIN	ESCHENICHIA COLI	136-163				1		+	
WEPTIDE-TRANSFERASE	BACILLUS SUBTILIS	2	247.28			1		+	\downarrow
HAPE-DETERMINING PROTEIN MILES	BACALUS CEREUS							+	-
ROD SHAPE DETERMINING PROTEIN MUET	BACOLLUS SUBTILIS	106.901				T	-	+	1
PROPERTY MAKES PRECURSON	KLEBSIELLA PREOMOTIAE								

PCGENE	107317814	Preherzeite Sequences					$\overline{}$	П		п	П
THE WALL	ROTFIN		AREAL	AREAL	AREAL	AREAs	AREAS	AREA 6	AREA?	AREAL	AREAs
PACKD KLEPN	FINGRIA ADJESIN PROTEIN PRECURSOR		207.777	T			Ì			1	
PMAKE KLEPN MAKE PROTEIN	ł	KLEBSIELLA PREUMUNIAE	277.6	611.00	1		1	Ī			T
PARCE STREY		SINETIOCOCCOS TYCHENES	101	Τ.	341.301	431.448	403.414	(11.43)	W. 1.4.	3001.0301	T
PAGE ECOL	MUNAMIDASE-INTERASED PROTEIN PRECORSON			Т	Т	Т	Т	Т			Ī
PHISTA STAFF	ER YTHOROMYCIN RES	EPIDERAIIDIS	Г	333-150							
PAISTB ECOL!	ACIDIC PROTEIN MSYB		П								
PMT37 ECOLI	MODIFICATION METHYLASE ECOSM		П	474.544							
	MODIFICATION METHYLASE ACCI	ACINETOBACTER CALCOACETICUS	503-540								
			T								
	MODIFICATION METHYLASE BEP!		Т	309.336							
PATTBI HERAU	MODIFICATION METHYLASE HGIBI										
PMTB3 BACAM	MODIFICATION METHYLASE BAMMII	ž	200	1			1				
PMTB) BACAR IN	MODIFICATION METHYLASE BANIII		Т				1				
PMTBA BACAR IN	MODIFICATION METHYLASE BAM	OLYTICUS	ı	60+286			1	Ī			
PMIBB BACSU	MUDDIFICATION METHYLASE BOURT	BACILLOS SUBTILIS	71.00	RKT/D			1				
PATE DATE	ACCURATION METHODS BOOK		Т	9	00000		1				
A LIVERY IN THE	MODIFICATION METHOD AGE MAIO	THACHE	-	T				Ī			T
PATCI VERAL	MODIFICATION METHY ACE MOICH		111.111	T	T	Ī	\dagger				T
	MODIFICATION METHYLASE ECORI		Π	165-172			T	Ī			T
7	AODIFICATION METHYLASE HGIEL	URANTIACUS	L								
	MODIFICATION ACTHALASE ECONI		197								Γ
PNITES ECOLI IN	MODIFICATION MET		23.100								Γ
PMTEC ENTCL N	HODIFICATION MET		418-445								
PMTFI FLAOK A	NODIFICATION MET	ITES	164-211	379-306	337-366	398-425	355-646				
PMTFI FUSNU P	HODIFICATION MET	М	33-49								
PMTG2 HAEGA	AODIFICATION METHYLASE HGAL:	-	╗								
WING HAEIN	MODIFICATION METHYLASE HINCH	MAEMOPHILUS INPLUENÇAE	202-181	304.131		Ī					T
PATK! KIEPN	ADDIFICATION METHYLASE KPNI	and connection	Т		T		T	Ī			
NUT STIME	PATED STRAU MANNITOL I. PHOSPHATE S-DEHYDROGIZMASE	CUS MUTANS	Т	224-258	349-376		Ì				
PHTM! MORSP N	MODIFICATION METHYLASE MSPI			Т			Ī				
PMTN) WEILA	HODIFICATION MET	ICA	П	183-210							
PATES PROVU IN	MODIFICATION MET		108-335								
	MEMBRANE-ASSOCI	LDARIUS	9-67								
PMTPS PROST N	MODIFICATION METHYLASE PSTI	ARTII	736-264								
	TAYPIOPHAN-SPECIFIC TRANSPORT PROTEIN	ESCHENCRIA COLI	Т	Т							
WISS SHISO			10.10	103-401	600-000	Ĭ	1				Ī
_		SAUREUS	335.274			T	T	Ī			T
PMTSA LACLC A	MODIFICATION METITYLASE SCRFLA		#: E	187.214						T	
	MODIFICATION METHYLASE SCRFI-D	ACTIS	17-61				ļ				Γ
PMTSI SPISQ C	PO DNA METHYLAS		٥	256-290							
PMTSM SERMA	CONFICATION METI	45	91.19								
PMTT8 THETH	CODIFICATION METH	AQUATICUS	120-157								
	MODIFICATION METITYLASE VSPI		266								
PMUKO ECOLI			30.38	1014-1048	1216-1252						
PMULI ERVAN	PHULI ERWAM MAJOR OUTER MEMBRANE LIPOPROTEIN PREC	ERWINIA AMYLOVORA	ž		1						
PHULI MULMUL			× :	1	7		1			7	
PACE PROPE	AAJOR GUTER MEMB	PROTEUS MIRABILIS	┱		-						-
THORD BALSO	UNI-LIVASE	BACKLUS SUBTILIS	261-101	927.46	1						
PARTIE ECOL	UDP-MURNAC-PENTAPEPTIDE SYNTHETASE		407.417	1	1			Ī			
PAURZ ECOLI	HOYLPYRUVATE TH		197-419	T	T		1			1	T
PLAUNZ ENTCL			392419	T	Ī	Ī			Ī	\dagger	T
PMUTA STRCM	PAUTA STRCM METHYLMALONYL-COA MUTASE BETA-SYBUNIT	NENSIS	31.58				T	Ī		T	Γ
			ļ		١					1	

	Probaryolic Sequences	П		_	A 400 A 400 A	ANTAG	AREA?	AREAG	AREAS
NI JANUAR		0 15:50	To Topico	7000	τ		7	,	
LINE CACHE LATER THAT COM ANTASE ALPHA-SUBUMI		276-486	+	-					
A CORCIGIO ADENINE	г	8	1	+		L			
בייני לייני לייני	A. SIMILMIT STREPTOMYCES CHNAMIONENSIS	100.130	1	1			-		
PRIOTE STREM NE MICHAELON IC CONTRACTOR OF THE PROTECTION AND THE	7	2	$\frac{1}{1}$	+	+		-		
JNA MISNIA ICH PET		\$ 1.0		1	1	1			
JAA MISMAILTI ALI		134-169	$\frac{1}{1}$	1	+		-		
PAIUTL VIBCH PROJEIN MOSE BEBAIR PROTEIN MAITS		118-153	1	+	1				
JAA MISMATCH ME		60.87	1	1		1	-		
AUTT-LIKE PROJEIN	PCF I DOMONAS MEVALONII	341-368	╗	╗					
OENZYME A MEDUL	CTREPTOCOCCUS PYOGENES	5-129 141	48-182 190	190-217 34	240-301				
	ETH EPTONIVER CACADI	100-152							
AYCOLYSIN PRECUR	STATE OF STA	210-237	_		_				
PMYSC YEAEN MYTC PROTEIN PRECURSOR	_	L	255.289	-	_	-			
PALANCE AND THE MICOTONATE MUCLEOTIDE PYROPHOSPI		T	+	-	-				
ALLEGATION NAME OF CITY AND PARTIES OF THE PROPERTY OF THE PRO	-	297-162	1	†				L	
PRADE SALIT TRANSCRIPTION TO THE PROPERTY OF T	-			1	$\frac{1}{1}$				
TAGO ECOLI ITAGO PROTESI	CLOSYMDIUM PENFINGENS	╗	200-1017	1	1				
HIALDRONDLOCO	E SCHEDICHIA COLI	119-153		-					
PINGR ECOLI INACR PROTEIN	C. Octaining CENTICIDA	Г	289-330 922	933.988					
PHANH CLOSE SIALIDASE PRECURSOR	CLOST NOTION SCI TICON	,		-			_		
PHANN CLOSO SIALIDASE PRECURSOR	CLOSTRIDIUM SORWELLIN			ł			-	L	
BANANA CALTY C'ALIDASE				+	-				
STATES AND AND THE RESTREET OF THE PARTY OF	ENTEROCOCCUS HIRAE	19:130		+	1			ļ	
PRACE ENTER PROPERTY OF THE BENIET AND ALPIN CHAIN	PILA CHAIN ESCHERICHIA COLI	186-420		+			+		
PNARG ECOLI RESPIRATORI MITALE RESOCIATION		16.103		_					
	COCHEDICINA COLI	155-189							
REGULATOR PROTEIN	Country Con	Т	158.365	431.458	\$65-508				
PHARK ECOLI NITRATEMITRITE SENSOR PROTEIN NARK	1	Т	Т	Т	-			L	
١				\dagger					L
MEDILACIN RESISTAN		Т		t	$\frac{1}{1}$	 		-	
+	Г	7	208-298	1			-		
NA ANCORPTION PRO		=	Т	+		1			
Т		╗	186-220	11:31		1	+		1
т	ESCHENCINA COLI	115.342	-	1	+				1
TATAL STOCK AND	ENTEROBACTER CLOACA!	9:30		1	+				ļ
TANKS OF THE PROPERTY OF THE PA	ESCHERICINA COLI	106-233	1	1			-	+	
PRIAN ECOLI MAINTENANCE STATES A	ESCHENICHIA COLI	171.305							
MAINT I AND IN THE	- PSEUDOMONAS CIRLORORAPHIS	101-12					-		
PINIAB PSECL NITULE HTDRATASE SUBURITURETA	RHODOCOCUS RHODOCUROUS	16:19							
NITRULE HYDRATAS	10000000000000000000000000000000000000	3.5			\mid	L			
PHIFA AZOBR MIF-SPECIFIC REGULATORY PROTEIN	AZOSPIRALLOM BRASILENSE	30.33		T	-		_		
	The second secon	T	102.501	25.55					
PHIFA HERSE NIF-SPECIFIC REGULATORY PROTEIN	INTERPORTEDITION SERVICES	Ī	Т				_		L
NIS-SPECIFIC NEGUL	, RHIZOBIUM LEGUMINOSARUNI		\dagger	T	+			-	
NIF-SPECIFIC REGUL	RHIZODIUM MELILOTI		1	Ì	1				
PRIETA BINGCA INIF.SPECIFIC REGULATORY PROTEIN	RIIODOBACTER CAPSULATUS	240.287	+	1	1		1		
MIST PROTEIN	7 AZOTOBACTER VINELANDII	342-369		1	1	1			-
Т	KLEBSIELLA PNEUMONIAE	154-181							\downarrow
Т	ANABAENA SP	174-401		1				-	\downarrow
MITO ANAST MITTERS NO. VED. IRON PROTEIN	AZOSPIRILUM BRASILENSE	117.404							
MILKO MOCIONA	IPLECTONEMA DORYANUM	387.414							
NI KO MOLTBOTA	THIODACII LUS FERROOXIDANS	33.410							
MI RUG MUC 180-18	CLOSTBIDIEM PASTEURIANDA	159.366	-						
-	SEANCIA CP	19-83		=	-				
PHISH FRAME MIROGENASE INCH TROICEN	BI SCHOOL BOOK AND A	267.294		-	-				
NITROGENASE INCH	A-A-Companie - Total Day A-CT CLOCK	410417	l		-	-			_
MITROG MOLYBO-IR	BA ANGELIA DE LA PONICIONA	411.510	t	İ	-				
NTROG MOL YBD-8	DE A DYNAMI PORTO CO	478.505					_	L	
т	C OCTAINING PACTEURIANING	111.154							
NITROG MOLTBO-	THIOBACII LIS FERRONIDANS	479.506		l		_			
MITROG MOLYBO-	A POTOBACTER CUROCOCCINA MCD 1	265.292						L	
PHIFM AZOCH MIFM PROTEIN									

1000	102-136-4	Prohestoric Sequences	1		1	1				Γ
FILE MANIE			7 17387	ATCA L	ABGALA	AREA AR	AREA S AREA S	A AREA?	AREAL	AREAS
PHIF BRAJA	BIOSYNTHESIS PROTEIN NIFN	BRADYRHIZOBIUM JAPONICUNI	139-366	1			1			
PNIFS ANASP			<u>2</u>		1	1				
PHIFS LACDE	MIFS PROTEIN HONOLING	CKII	20.16		1	1	-			1
FNIFT AZOVI		AZOTOBACTER VINELANDII	- -	-	1		$\frac{1}{1}$		1	
PNIFU ANASL		ANADAENA SP	8		1	+		1		
PNIFU ANASP			2/1/2	\dagger	†	+	1	+		1
PNISO KLEPN		MUNITE	97.6	20, 100	1177	+	+		1	
PNIKA ECOLI	PROTEIN NIKA PRECURSOR	ESCRETCHIA COLI	┰	T		+				Ī
PNIKE ECOL!	PROTEIN NIKE	ESCIRENCIA COLI	Т	11. 11.	t		+	+	†	
PNIRB ECOCI	CTASE		وا	77,506	\dagger	+			+	Ī
PNIRC ECOLI			40.71	1	†	\dagger		1	1	T
PNIRS PSEST	OCHROME OXIDASE PRECURSO	2	Ť	Т			1		1	
PMSB LACLA	ASSOCIATED PROTEIN			Т	Т	074-0				Ī
PMISC LACLA	S PROTEIN MISC	LACTOCOCCUS LACTIS	Т	Т			+			
PHIST LACLA	ROTEIN MIST		Т	7	476-470	1	1			
PNIVA CLOPA	HASE, ALPHA SUBURIT		_	Т	Т					
PRIVO CLOPA	HOMOCITICATE SYNTHASE, OMEGA SUBUNIT	TEURIANUM	1	٦	T	283.310				
PINGEC ECOLI	PORIN PROTEIN NAPC PRECURSOR		\$	28.89	115-362					
PHODE BRASP	NODULATION PROTEIN C	JN SP	ĕ							
PHODE RUFLO	NODULATION PROTEIN C		216-313							
PNODC MILLT	NODULATION PROTEIN C	NIIZOBIUM LEGUMINOSARUM	10.01							
PHODE MILLY		OSARUM	25.52							
PNODE RHIDMS	NODULATION PROTEIN F		39.66				-			
PNODG NUMBER	NODULATION PROTEIN G	KHIZOBIUM NÆLILOTI	=				-			
PNODG RHILKS	NODULATION PROTEIN G		Ē			-				
PHODE, RHILV	NODULATION PROTEIN L	N.	26.53							
PHODO, AZOBA	NODULATION PROTEIN Q		- 1	7	1					
PNODT RHILT	NODULATION PROTEIN T		T	155-382 42	420-454					
PRODT RHILY	NODUL ATION PROTEIN T	AINOSARUM	7	16-44)	1		1			
PNODU RHIFK	MODULATION PROTEIN U	AMIZOBIUM PREDII	200.	77, 91,	1	\dagger		+	1	
2000	MODULA INDIVIDUAL VIOLENT VIOL		Т	80.46	1	1	1	+	1	
PACH B BHISE	MODULATION PROTEIN AND PARTY AND PAR	ANIZORION LECOMINOSANONI	111.16	†		+	1	+		
1000 M	MODEL A TION BEOTER MOTE	011	3	+	t	1	+	+	1	1
PHOCH PORT	NOSO PROTEIN PRECIESOR	103/	10.14	\dagger	1			+	1	T
PHOSE PSEST	REGIL ATORY PROTEIN NOSE	PSEUDOMONAS STUTZERI	31.5	\dagger	T	\dagger				Ī
PNOSZ PSEAF	NITROUS OXIDE REDIKTASE PRICIESOR	PSELIDONONAS AERIGINUSA	20,79		1	$\frac{1}{1}$	<u> </u>	<u> </u>		Ī
PNOSZ PSEST	IN IANE PRICORSIN		147.391			:		<u> </u>		1
PNPRE BACAM	BACILLOLYSIN PRECURSOR	ACIENS	Т	217-244			-			Γ
PNFRE BACPO	BACILLOLYSIN PRECURSOR .		19.65	187-228	l	ŀ	_			
PHPRE BACSU	BACILLOLYSIN PRECURSOR	BACILLUS SUBTILIS	116-146	107-134						
PAGOS PAILDE	NADH-UBIQUINONE OXIDOREDUCTASE 21 KD CITAT	PARACOCCUS DENITRIFICANS	3	j						
PNOW PARING	CXHAMETON: 20 KD CHAIN	:	2							
PNRING LCGLA	ANAER RIBONUCTRIPHOS REDUCTASE		<u>د: :</u>							
MAY ECOL	CYTOCHROME CSS2 PRECURSOR	ESCHENCHIA COLI	36.							
PRING ECOLI	MU O PROTEIN	EXCREMICHIA COLI	<u> </u>							
HANDEN THAN	ALIMATIC MITULASE	RADDOCOCCUS RADDOCHROUS	٠		1		-			
S T Y	INDIAL STANKE THURSON		1	7-107						
TAICA ARAN	MA-HINGING FROIT	ANAIMENA ST	7	+	1			$\frac{1}{1}$]
	CONT. MITCHEST ATON			+	†	1			1	-
THE WILL	ATTACKE BEGIN ATTON BROTTEN ATTACK	2000			1	1		1		·
THE PERSON	TROCEN RECUE	PROTEIN OF CARIS	37.	+	\dagger	+	+	+		Ī
PINTRO RUIDAE	ITROGEN ASSIMILATION REGULATORY PROTEIN	RHZOBIUM MELILOTI		+	T	+	1			T
PNU3C SYNP3	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN	SYNECHOCOCCUS SP	10.101	1	\dagger	\dagger	+	+		I
PACHE SYMY	NADH-PLASTOQUINONE OXIDOREDUCTALE CHAIN	SYNECHOCYSTIS SP	17.54		-	T	-			T
PHUSC SYMPS	HADH-PLASTOQUINGNE OXIDONEDUCTASE CHAIN		199-919	t	T	╁	\perp	<u> </u>		T
				1		1			1]

PUCENE	107517854	Proharyoile Sequences	17387	ABEAT	AREAS	AREA	AREA3	ABEAS	AREA?	ABEAT	AREAS
FILENAME	PROTEIN		1		_	П					
PHUJC SYNYS	PROB NADH-UBIQUIN		160.199								
PNIKE SYNY	PROB NADH-UBIQUIN		46.10								
PALL X SYNY	NADH-PLASTOQUING		160.402								
PASION FOOL			T	167.407							
PATION FCOLI	NADIS DESIYDROGEN		Į.			T					
NO PCOL			Ť	77	146.133						
PACE ECOL			T	Т							
PAUSA ECOLI	MUSA PROTEIN			70.07							L
PNI ISO ECOLI	NUTILIZATION SUBSI					ŀ					L
1003 0000	TRANSCRIPTION ANTI										L
200	TA MUTE IN THE	NIA	200								L
יייייייייייייייייייייייייייייייייייייי	A AVEN-CARE VANOATE		22.20								L
PATE PLAS	PANISONE AND A PORTE		223-250								
PNYLC PLAST		i	101-128								ļ
POING BACCE		TUNIFACILIN	133.202								
POCT ACATIO	OCIOAL MANAGEMENT OF THE PROPERTY OF THE PROPE	AZOTODACTER VINTLANDII	129.856								
P000 A20VI	OXULUIANA E	BACILLUS SUNTILIS	487.524	809-830							\downarrow
PODO! BACSU	OXOCLUTARATED	FSCHERICHIA COLI	6.13								\downarrow
1000 ECGE	OXOGLUTAMATEU		3.6								
PODO1 BACSU	DIKYDROCIPOANIDE	PCEI MONANAS PUTIDA	223-254								\downarrow
PODOB PSEPU	2-OXOGLUTARATE U	ECCIEPICINA COLI	624.651								
PODE L'COL	PYRUVATE DELIYORING NASH ET CONTONIN	AND!!	\$18-545								1
PODE AZON	DISTURBULING ACETICANS CONT		1971	117.144							
PODP1 ECOL		ESCREDONIS COCI	100.111				L				
POOPA BACST	PYRUVATE DEHYDRO	BACILUS STEARGINE MOUNICO	100						L		
PODPA BACSU										L	L
POOPS BACST	PYRUVATE DEHYDA	MERNIORIALUS									L
POOM BACSU	PYRUVATE DEHYDRO	BACILLUS SUBTILIS	2							L	L
1 00 and 0	IS KD CYSTEME-IUC	CIE ANYDIA TRACHOMATIS									
90132		NEISSERIA GONORUIDEAE	9								
POVIAL MEDA	OUTER ASEASBRANE	NEISSENJA MENINGITIDIS	2								-
PONTA NEIME		MEISSERIA MENINGITIDIS	Par :					ļ			L
POKEN METCO	CHITER NEMBRANE PROTEIN P IS PRECURSOR	NEISSERIA GONDAUDIOEAE	8					1			1
	CHITER LIFTINGANE	NEISSENIA MENINGITIDIS	8					\downarrow			\downarrow
COLUMN TO SELECT	DITTER LIFFABRANE	NEISSERIA CONORMIOEAE	8.6								-
2010	CITER MEMBRANE	NEISSENIA MENINGITIDIS	8.5							\downarrow	-
PONES ACTIVITY	CHECK MENTINE AND	NEISSERIA MENINGITIDIS	65.80								1
DAIB) PETING	OUTER MEMBANE	NEISSERIA MENINGITIDIS	34-51	63.90							1
PONB NEIME	-	NEISSENIA LACTAMICA	116-143								4
200		NEISSERIA SICCA	24-51	6).90			1				-
TOWN TOWN	COTTER MENTINANE	ACTINOBACILLUS PLEUROPNEUMONIAE	114-131								\downarrow
TO THE PARTY OF TH	CHITER MEMBRANE	HAEMOPHILUS INFLUENZAE	24.	Š	24.36						1
	DITTER MEMBRANE	PIAEMOPHILUS INFLUENZAE		200	200						1
	OUT THE MINERANG	NEISSERIA GONORRINOFAE	=					\downarrow			+
SALES CALLED	TO WOOD THE MEMB	STAPHYLOCOCCUS AUREUS	53-10	<u>=</u>							\downarrow
TONE STATE	THE LEVEN AND AND	THERMOTOGA MAUTIMA	100-138	131-170	183.249	255-292		2			4
VOID V	DOLER MEMBERS	ESCHENCILIA COLI	10-47	2.50							4
POWE ECOLI	COUNTRY MEMBRANE	NEISSEALA CONORUNOEAE	89-133								1
S S S S S S S S S S S S S S S S S S S	COLLEG MEMBRANC	SALMONELLA TYPHI	166-193								4
PONINC SALTI	OUTER MEMBERSHE	ESCHERICHIA COLL	<u> </u>	20.50	L						+
HWIT IC	OUTER MEMBRANE	PHOTOBACTERUDA SP	292-319			Ŀ	Ц				=
SONIPH PHI S	_	ESCHEDIONA COLI	2.5	L							_
OP ECO	PROTEASE VII PREC	MEISSERIA COMORALIDEAE	===								4
POP65 NEIGO	_	MERCERIA COMORRIOGAE	73.100			L					
POPO, NEICO	OFACITY PROTEIN OFAST	NEISSERIA GONORRHOEAE	3:13	140-167	L						4
SOLVE SELECT	OPACITY PROTEIN	NEISSENIA GONORUIOEAE	10-103	140-163							4
DOVAC NEIC	CACITY PROTEIN	MEISSERIA GONORAHDEAE	10-103	L					4		4
SOLA REISO	OPACHY PROTEIN	MEISSENIA GONORURIDEAE	11.105								4
707 AU	DEACHT PROJECT						İ	1			

Period A	1102017814	Proharyolit Sequences			7	-		_	_	7	
FILE NAME	ROTEIN		7	3	1	1	2011		70100	1	4
POPAK NEICO	OPACITY PROTEIN OPAS?	NHOEAE	6			1	1	\dagger	$\frac{1}{1}$	\dagger	
POPDA ECOL	OLIGOPEPTIDASE A		147.174					1	1	1	
POPDA SALTY	OLIGOPEPTIDASE A		2			1	1	1	1	1	
POPDE PSEAF	TRANSCRIPTION FACTOR OPDE	RUGINOSA	2				†	1		†	
POPPA FCOLI	A ICOPEPTIDE BINDS		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~			1	1	1		†	
YT IAS RAGOS	OLIGOPEPTIDE PERME	SALNIOWELLA TYPHINIURIUM	265-299			1			1	1	
POPE NEING	DPACITY-RELATED PR		108-135		1				1	†	
POPR 1 ME IAM	OPACITY-RELATED PR		94-135				1	1	-	1	
שמנות בנסו	DAMOTICALLY INDUC		П	٦	П		1	1	$\frac{1}{1}$	1	
1000	CHES CHISTACE PROT	AFERI	001-19	112-139	153.204	112-221				1	
SOLVE BORBO	SULER SURFACE PRO		Π	162.796							
POSPB BOKBU	DUTER SUMPACE PAU		Т						-	l	
POTC2 BACSU	DRIVITHINE CAUDAMOYL TRANSFERASE				Ī		Ì		-	T	
POTCC PSEAE	ORNITHINE CALBANOYL TRANSFERASE	PSEUDOMONAS AERUGINOSA					1	1		T	
POTCC PSERU	ONNITHINE CANDAMOYL I MANSFERASE	PSEUDOMONAS PUTIDA	6					1		1	
POLITIC RAPICES	CHOSE DITICEDWITH FACTOR B	BACILLUS SUBTILIS	118-151							1	
	TANES SCHOOL	ERWINIA CAROTOVORA	119-216								
NAME OF THE PARTY	LEADER FOR HUMBS	CYBESTOCCOLOG BAB ACANCIDE	115.140					-	-		
PPICK STRPA	I KD PROTEIN IN FLA	STREET COCCOST TOWNS TO STREET		271.711				ľ			
PPINK STRSA	IS KD PROTEIN IN SSA	STREPTOCOCCUS SANGUIS	7							T	
PPIP LACLC	PI.TYPE PROTEINASE PRECURSOR		2	┑	211.0	0071-077	-			1	
PP79 MYCHOL		MYCOPLASMA HYOMINIS		7	202-200		-			1	
A LUT A COR	PHI. TYPE PROTEINASE PRECURSOR		107-155		1073-1100	1223-1250	-	1625-1649		İ	
Va. V	BIL TYPE BENTENAKE PRECIESOR	LACTOBACILLUS PARACASEI	107-155	196-90	1033-1100	1223-1250	1446-1496	1628-1655			
1000		ESCHENCHIA COLI	29-62					1			
	The state of the s	HSII	676	135-173							
2	TRUICIN TO	ACCOUNT ACTA DOCUMENTS	36.35						-		
PP)7 MYCHOR	PROTEIN PAT PRELUKSOR	STATE OF THE PARTY	101,166	074.050	1071.1100	1223.1250	1446-1496	1628-16551		l	
PPIP LACIC	PIII-TYPE PROTEINASE PRECUASOR	LACIOCACOS CACIOS	Т				-		-		
PAIK PSECL	47 KD PROTEIN	PSEUDONOMAS CHEUKUMATHIS		1			Ī			T	
PPS4 ENTFC		ENTEROCOCCUS PAECIUM						Ì		T	
PP40 LISGR	PROTEIN P60 PRECURSOR		9	701-107				1	$\frac{1}{1}$	T	
PP60 LISIN	PROTEIN P60 PRECURSOR		07-70	107:101				1	$\frac{1}{2}$	†	
	PROTEIN PIO PRECURSOR	LISTERIA IVANOVII	01-10	113-139						1	
_	PROTEIN P60 PRECURSOR	LISTERIA MONOCYTOGENES	10)-144			***		1		1	
1	PROTEIN P60 PRECURSOR	LISTERIA SEELIGERI	9:-	_	31.365	2		1		1	
١.	PROTEIN P40 PRECURSOR	LISTERIA WELSHIMEN	٦	7	186.423					1	
L	PROTEIN PAG	MYCOPLASMA HYORHINIS	264-295	421-464	487-517	\$44.575				1	
PPABA BACSU		BACILLUS SUBTILIS	17-21								
PPART BACK	4. AMINO 4. DEOXYCHORISMATE LYASE .	BACILLUS SUBTILIS	150-117								
LOUI DAVAG	4. AMPHO 4. DEOXYCH	ESCHENICHIA COLI	140-167								
STORY STORY	PROTEIN Y	STREPTOMYCES GRISEUS	87.78						_		
TOWN TOWN	PENICH IN ACY ACE PRECINSOR	ARTHROBACTER VISCOSUS	130-197	13.36)	931.606	640.674			-		
77.		BACRILUS SPHAERICUS	332.359						-		
100000	PAC PROTEIN PRECIDENCE	STREPTOCOCCUS MUTANS	146-276	281-465	136.565	376-630	1075-1102	139-1116	1381-1434		
	PECCHANON PROTEIN PALL	MACTILITY SITUATION	103.137	Т						T	
200	PECIA ATORY PROTEIN PALS	BACH LUS SUBTILIS	163.172						-	l	
יייין אויי	┰	FSCI GELICHIA COLI	69-79	16:123				ĺ			
	AND FRENCH PR	ESCHERICHIA COLI	5							ľ	
100	Ť	ESCHEDICHIA COLI	262.316						-	Ī	
אים בינתר	TOWNS AND THE PARTY OF THE PART	ACRODACTERION TIMERACIENS	60-03					Ī	-	T	
1 V V V		ESCUEBICHIA COLI	,	146.361				T	\dagger	T	
PAND ECOL	PLASMID FALLITON	ESCUREICHIA COLI		137.76				T	$\frac{1}{2}$	ľ	+
PPANE ECELI		ESCHENCIA COLI		100.076	1				$\frac{1}{2}$	1	
PARE SALTY	-	SALMONELLA I TRIMORIOM							+	T	1
PPA BACA	PROTECTIVE ANTIGE	BACILLUS AMINGALIS	76.41	20.02	e i	200	1000		+	1	
PPBP2 ECULI	PENICELIN-BINDING	ESCHENCHIA COLI	221-64	S - 103	207-707				1	1	
PPBP2 NEICO		NEISSEAJA CONDUCHOLAI:	193.220						1	1	
PPBP2 NEIME	PENICILL'IN BROING	NEISSENJA MENINGITIDIS	- 1		3				+	1	
PPBP2 STRPN	PENICILLIN-BINDING	STREPTOCOCCUS PNEUMONIAE	-	2	239.286	20,50			+	1	
PPBP) ECOLI	PENICULIN-BINDING PROTEIN 1 PRECURSOR	ESCHENICHIA COLI	224-251	34-36					1	1	

PER ACCUING PER ACCOUNTS FOR AC										
PPBPA BACSU PPBPA ECOLI PPBPA ECOLI PPBPA STANU PPEAB STANU PPEAB STANU			Г	ſ	Т		-			
PPBP4 ECOLI PPBPA ECOLI PPBPX STAPH PPBP STAAU PPCAB PSEPU		BACILLOS SUB ILLIS	136.363							
PPBPA ECOLI PPBPX STRPN PPBP STAAU PPCAB PSEPU			145-172							
PPBPX STRPN PPBPX STRPN PPBP STAAU PPCAB PSEPU	PENICILLIN-BINDING PROTEIN IA		٢	263.290						
PPBP STANU PPBP STANU PPCAB PSEPU	PENICILLIN-BINDING PROTEIN IB	SCHEMENIA COLI	l.	304.733						
PPBP STAAU PPCAB PSEPU PPELS ERWCA	PENICILLIN-BINDING		T	Т	263.324 503.	\$01.529				
PPCAB PSEPU	PENICILLIN-BINDING PROTEIN	STATISTICAL OF A PRINCIPLE OF A PRIN	L	Т	T					
PPEL) ERWCA	CYCLOISOMERASE		Τ		-					
			110-133	-						
PPELA ERWCA	PECTATE LYASE A PRECURSOR	ENWINE CAROTOVORA	110-133							
PPELB ERWCA	PECTATE LYASE B PRECURSOR	ERWINE CAROLOGIA	110-137							
PPELC ERWCA	I PECTATE LYASE C PRECURSOR	ELWINIA CANOLOVOIS	٢	200.343			L			
PPELF ERWCH	PECTATE LYASE E PR	ERWINIA CARTONIO	2	+	-	-	_			
PPELP ERWCA	PERIPLASMIC PECTATE LYASE PRECURSOR	Sin Offic	047.657							
PPELP YENS	PERIPLASMIC PECTATE LYASE PRECURSOR	KCUCU313		+	\mid					
PPELX ERWCA	PUTATIVE PECTATE LYASE X PRECURSOR	ERWINIA CAROTOVORA		+		 			Ī	
PPELX ENWCH	EXOPOLYGALACTURONATE LYASE PRECURSOR	ERWINTA CHRYSANTICENII	(A-00)	+	$\frac{1}{1}$			Ī	Ī	
	AMINOACYL-HOSTIDINE DIPEPTIDASE	ESCIERUCIIIA COLI	264.314	+	+	+	1			
PRESC ECOL	Y.PRO DIPEPTIDASE	ESCHENICHIA COLI	221-278	+	+					
PPERT BORD	PERTACTIN PRECLIRSOR	BOXDETELLA BRONCHISEPTICA	617-644						Ī	
Vestor a vestor		BORDETELLA PARAPERTUSSIS	628-655		1			1		
BACAT BORDE	PERTACTON PRECURS	BONDETELLA PERTUSSIS	616-643					1		
TO COLUMN	PHOSPHOGL YCERATE KINASE	CORYNEBACTERUM GLUTNICUM	1	1						
יייייייייייייייייייייייייייייייייייייי		ESCHENICHIA COLI	116-216							
SECT ACTOR	PLOCEHOCI YERATE KINASE	METHANOBACTERIUM BRYANTII	36-63			1				
TOTAL DE	PANCENCE VERATE KINASE	THERMUS AQUATICUS	323.249			1				
100	ENTO POLYCAL ACT	ERWINIA CAROTOVORA	233.271			1				
מונים בעיירי		SALMONELLA TYPHILAURUNI	(6-93				-			
Trois sale	C BUYCOCYANIN. I ALPHA CHAIN	FREMYELLA DIPLOSIPHON	21.48					$\prod_{i=1}^{n}$		
יייייי נייייי	C. PHYCOCYANIN. 3 ALPHA CHAIN	FAEMYELLA DIPLOSIPHON	31.48		1	1	+			
DESCRIPTION OF THE PARTY OF THE	POLY(1.HYDROXYALKANOATE) POLYMEIASE I	PSEUDOMÓNAS OLEOVORANS	204-291		1	1				
PPHAR ANACY	ALLOPHYCOCYANIN	ANABAENA CYLINDRICA	7.	1		1	1			
PHAB ANAVA	ALLOPHYCOCYANIN	ANABAENA VARJABILIS	7		+					
PPHAB FREDI	ALLOPHYCOCYANIN	FREMYELLA DIPLOSIPHON		1						
PPHAB MASLA	ALLOPHYCOCYANIN	MASTICOCLADUS LAMINOSUS		+		-				
PPHAB SYNP6		SYNECHOCOCCUS SF		\dagger		+	-			L
PPHIAC SYNP6	ALLOPHYCOCYANIN ALPHA-B CHAIN	SYNECHOCOCCUS SP	3	+		+		-		
PPILAG FREDI	ALLOPHYCOCYANIN GANDIA CHAIN	FREMTELLA DIPLOSIPHON	36.58	\dagger	+	1	-			
PPHB) FILEDI		FREMYELLA DIPLOSIFICA	000	\dagger		-	1			
PPHBD ALCEU	ACETOACETYL-COA	ALCALIGENES EUTAUTIUS	33.65		+	+				
PPIKCA SYNYI	C.PHYCOCYANIN AL	SYNECHOCTS(IS SY	33 86		\dagger			-		
PPHCB SYNP6	C.PHYCOCYANIN BET	STRECHOLOCOS ST			-	1				
PPHCB SYNP?	C.PHYCOCYANIN BE	STRECHUCOCCOS SP	1		+	+				
PPHCB_SYNY!	_	STRECHUCTSHS ST		\dagger		-				L
PPHEA ECOLI	CHORUSMATE MUTAS	ESCREMONIA COUR		140.164	243.786	-				
PPHEA ERWHE	CHONSMATE MUTA	EXWINIA PERMICOLA	Ţ	Т	777.517		-			
PPHEA PSESP	PIENOL 1-MONOOX	PSECENCIAL ST.	Т	Т		+				
PPIEB MASLA	_	MAS FIGUELATUS LAMINUSUS				+	+			
PRIED PSESP	CATECHOL 1,2-DIOX	Tacological at								ŀ
PPIEG SYMY		STREETHOUGH CONT.	384.111		Ė	1	 			ł
PPHEP ECOLI		ESCRETCIA COLI			+	-				Ĺ
PHE! CLOSA		CLOST MINION PASTEUMANON			\dagger	+	-	-		
PHO. BACKE	_	DACH LIN CEREIK								
PPHE 2 BACCE	SPEINCONTELINASE C PRECIOSOR	MACH LUC CEREUS	2			-				L
TO SALLE	┰	BACILLUS CEREUS	32.59	179.206						
PHAC CLOSI	PHOSPHOLD ASE C PRECURSOR	CLOSTRUDIÚM BIFERMENTANS	П	335-365	П					
PPHI C CLOPE	7	CLOSTRIDIUM PERFRINGENS	110-117	169.368			-	_		

LUCIONE	1,007-178-4	Prohamette Sequences	П	\mathbf{I}	_		_		П	П	Π
FILENAME	PROTEIN			17317	723	AREAA	AREA S	AREA AREA?	10.10	7787	기
PPIG C LISMO	PHOSPHOLIPASE C PI		2			1	1	1		+	Т
PPIC PSEAF		¥	685.722		1				1	1	7
PPILC STAND	PHOSPHOLIPASE C PI	AUREUS	3		1	1	1			-	7
PPHLD BACCE	PHOSPHOLIPASE C PI	BACILLUS CENEUS	179-206							-	1
PPIC LEPIN	SPHINGOMYELINASE C PRECURSOR	ROGANS	20.53	384-428		1		1		-	1
PPIND ECOL!	PHIND PROTEIN		206-326					1	1	-	1
PPIINK ECOLI	PIINK PROTEIN		178-205				1	1	-	-]
PPINNI ECOLI	PHINM PROTEIN		١			1	1			-	7
PPHOE CITER	OUTER MEMBRANE PORE PROJEIN E PRECURSOR	UNDII		÷	╗		1			-	T
PPHOE ECOLI	OUTER MEMBRANE PORE PRUTEIN E PRECURSOR		٦	\$ 0	20 100	226-253	1	1		1	1
PPHOE KLEOX	OUTER MEMBRANE PORE PROTEIN E PRECURSOR			64.91						-	7
PPHOE KLEPN	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	KLEBSIELLA PNEUMONIAE	13-40	64-105		1				-	1
PPHOF SALTY	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	¥	POI-(9	130-347							
TOVE BUILDS	ALK BUCK CONTHESIS TRANS REG PROTEIN	BACILLIS SUBTILIS	185-219					 	-	_	
DE COMPA	CENTOR PROTEIN PH	ESCHERICHIA COLL	244-278				ľ	-	L	L	Γ
מפונים ביינו	TOPIN CHUE CENCUR	PLU FRITAL	236-260			T	T	-		L	ĺ
	ALM BLOCK CONTINES		10.145	107-111		T	İ	-			Ī
ביים מעראם	ALA FROS STRINGS		8	201.341		Ī	Ì			+	Τ
יייים ביטרו	PHOTOGRAPH PROTE		1			Ī	T			+	Ī
THINK STREET	R-PHYCUC YANIN II A	STATE CHOCOCCIIS CO				1	T	1		 	Ī
PPICKA STRPE	R-PHYLOCIANIN II A				T		Ì	+		1	T
LANSO ECOL	ULTCOCEN PROSMICA TLASE					Ť	İ	ł		1	Ī
PHSM ECOL	MIAL TODEXTRIN PROSPROXYLASE	ESCREMICITAL COLI			Ì	1	1			+	Ī
PPILA NEIGO	PROB SIGNAL RECOGNITION PARTICLE PROTEIN	MEISSENIA CONURACIOEAE	90.				1	+		+	1
PPILB PSEAE	FINDRIAL ASSEMBLY PROTEIN PILB	PSEUDOMONAS AERUGINOSA	999					1		+	T
PPILC PSEAE	PILC PROTEIN	PSEUDONIONAS AERUGINOSA	0.1.[0]					-		4	1
PPILD NEIGO			-0-1				1		-	$\frac{1}{1}$	1
PPILQ PSEAE	FINIBRIAL ASSEMBLY PROTEIN PILO PRECURSOR	PSEUDONIONAS AERUGINOSA	==	99.666			1		_	4	7
PPILS PSEAE	SENSOR PROTEIN PILS		9.46							+	
PPIR ECOLI	PI PROTEIN		200							1	
PPIV AIORBO	PILIN GENE INVERTING PROTEIN		43.69	152 182			1		1	1	1
PPIV MORLA		MATA	27:115			1				+	Ī
PPLC BACCE	PHOSPHODIESTERASE PRECURSOR		\$17.70			1			$\frac{1}{1}$	+	7
PPLC BACTU	PHOSPHODIES LERASE PRECURSOR	BACILLOS INDIGNOIS				1			1	1	T
TPLC LISKID		ESCUEDICUIA COLI	607-067			T	T	1	1	1	T
200	ALTLINAMS ENASE	ECCIENCIA COLI	0(1.1)							+	Τ
ANI AD COME	PETTINI VACE	EPWINIA CABOTOVORA			Ť	Ì	T		<u> </u>	+	T
TTL TO CAMEA			, ,				1	+		1	T
PANA ELOC		THEN	20.00			Ì	1			+	T
TOUR CANCE	MORMOCI VERMENTE		Y S				T			+	T
	PANCELLOCK VERAT	114	5	911.0			T			+	T
1000	THE PROPERTY AND INC.	E CLIEBICITA POL	706 976		Ī		İ			+	T
PENN SALTY	MINICAL PROPERTY	SALMONDE LA TYPHIMURIUM	70.70				;	-	-	!	•
PRODE DACKY			11.78		T	Ť	T	-	+	\downarrow	Τ
PPORT PSESY	OUTER MEMBRANE P		10:11							+	T
PPORO PSEAE	PORIN O PRECURSOR	PSEUDOMONAS AERUGINOSA	190-424			ľ		-	-	\mid	Γ
PPORP PSEAE	PORIN P PRECURSOR	PSEUDOMONAS AERUGINOSA	139-181	160-187	366.996			L		-	Τ
PROTO ECOL!	RINDING PROTEIN PR	ESCHERICHIA COLI	130-147				ľ	-	_	H	Γ
Profit (CQL)	FUINESCIPIE-DRINLING ANTIFURIER		911:16							-	Γ
FPOXO ECTL	PYRUVATE DEHYDRO	ESCHENCHIA COLI	11:1							<u> </u>	Γ
PPPB) BACSU			109-150	433-460						L	
PPFB4 BACOU	ALKALINE PHOSPHATASE IV PRECURSOR	8	15-123	136-363							
PPPB ECOU	ALKALINE PHOSPHATASE PRECURSOR		115-262				7				
PPO ESCRE			236.263				1			+	٦
TIPLE ILANE		I LA VOBACTERIOM MENINCOSETTICOM	£ 2				1	1	+	+	Т
מוני בינים	PROCEED ENDOFER HOUSE PRECORSON	Ī				1		+	1	4	T
FFICE CLUC:	I'MOSTINGENCE INCENTION IN THE				1	1	1	- -	$\left \right $	$\frac{1}{1}$	٦

PCGENE	107117014	Preharyette Sequencer	AREAL	AREA1	ARIA.	जाराज्य जि					
	PROTEIN	ORIGARIAN SERENCENE	Γ	Г				1	+	1	۱
			49.76					1	1		
•	PHOSPHOEMOLPYRUVATE SYNTHASE	ESCREDURIN COLI	40.74			-				1	۱
			171.198	Ī							
****	CALCILIN DEPENDENT PROTEASE PRECURSOR			T				-	_		
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BEATER SOME ALPHA	ACIDOPHILUM		1	Ī		T		1		
V. V. V. V.	PAUL SPECIFIC PROTEA		74.	T			T				
בי בי	THE STREET STREET STREET	STAPHYLOCOCCUS AUREUS	11.11	7	Т		Ī		t		
REI STAND	LASKIID RECORDING		44.75	٦	110-361	16.68	1	1	†	T	ļ
RE2 STAAU	PLASMID RECOMBINAL	2	17.76	391-316					1		
FFA LACPL	PLASHID RECOMBINATION ENZYNIE		5						-		
111111111111111111111111111111111111111	RECTO ATORY PROTEIN	BACILLUS LICHENIFORNIS		,,,	Ī						
	AL ASSESSMENT OF THE BAY YAS			٦							
٦	PLASMID ACCOMONANTION ENGINEER	CHIS AGALACTIAE	285-319	332-359	420-434			1	1		
PRE STRAG	PLASMID RECOMBINATION ENGINE		36.110	133.204					1		
L	LISTERIOLYSIN REGULATORY PROTEIN	2000									
Т	STATE OF STA	ESCHENICHIA COLI	211-243			1	Ī				
			117-11					1	1		١
_	DNA PRIMASE	TOUGHT , THE COLUMN TO SERVICE AND THE COLUM	17-61	282-319							
Т	DNA PRIMASE										
7	100000000000000000000000000000000000000	CLOSTNIDIUM ACETOBUTYLICUM	17-114					T			
_	URA FRUMASE		269.296						1		١
	DNA PRIMASE		10.17	245.286	477.504	\$26-593		_			
Series Vines	DNA PRIMASE	RICKETTSIA PROWAZENII									
•		DESULFOVIBRIO DESULFURICANS	2					İ	l		
אינים האיני		ACHIOMOBACTER LYTICUS	317.344					1			
ALB ACKLY	BETA-LYIIC MEI ALLO	S CACA A CACA ENZYALOCENE	121-148								١
PPRLB LYSEN	BETA-LYTIC METALLO	LI SOUNCIEN ENCINEERS	3717111	375.316					_		
POL LISMO	ZINC METALLOPROTE	LISTERIA MUNOC TIOURINES				Ī					
0,101	POSC MEYALLOPROTE	LISTERIA MONOCYTOGENES					Ī		İ		
201	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SERRATIA MARCESCENS	309-336						1		
ROA SERMA	CAMMA-GLUIAMIC	ATTENDED OF COLUMN ATTENDED	3.29								
ROA STAAU	PROTEIN A PRECURSOR	SI AMILIANOS MOITO	7.7								
PPROR SFRMA	GLUTAMATE S-KINASE	SERRATIA MARCENCERS									
CA STRACE	PROTEIN	STREPTOCOCCUS AGALACTIAE									
200			5								
TAKE TAKE			200.227						Ì		
KOH BALSO	THE PROPERTY OF STREET		460-487								
PPROP ECOLI			24.54						1		
ROV ECOLI		PALADOMETE A TOMINATION	14.54								
PPROV SALTY		SALMONELLA TOTAL	130.167								
PRE ECOLI	PRAB PROTEIN	ESCRETOCION							ŀ		
LICUS James	ANTICODOM MUCLEASE	ESCHERICHIA COLI	1								
1200		ESCHENICHIA COLI	278-305						Ì		
200		INACILLUS SUDTILIS	52.87	95-137					1		
MSA BACSO		CYREPTOMYCES GRISEUS	36-110								
PPRIA STRGR	PROTEASE A PRECUI	County And Verbrien	01.130								
PPRTC ERWCH	SECRETED PROTEAS	ERWINIA CONTROL									
PRITE PORCE	COLLAGENASE PRECURSOR	PORPHYROMONAS GINGLYALIS									
TUMBS CLOSE	PROTEASES SECRETIC	ERWINIA CHRYSANTHEMI	328-333								
	COTT ACTIVITY AND REMINE PROTECTS PRICURSOR	DACTEROIDES MODOSHIS	5	219.245	146-114						
PFRIE SACRO	A I MAL CLES COLOR	ENVINA CHRYSANTHEMI	106-135	158-192	331-390						
FRIE ERWCII	PROTEASES SECRETION FROIE IN TRIE	CONTRACTOR OF A MATTER AL	280-310		L						
PPRTF ERWCH	PROTEASES SECRETIF	EAWINE CONTROL OF THE	16.191	113,130	L						
PRIM LACLA	PROTEASE MATURAT	LACTOCCCO PACTIO		100	91						L
PPRIM LACIC	PROTEASE MATURAT	LACTOCOCCUS LACTIS	66.53								L
AGTA I MEDA	PROTEASE MATURATION PROTEIN PRECURSOR	LACTOBACTILLUS PARACASEI	9						Ī		
AND TO STOME	FYTRACE LIBAR SE	SINDATIA MARCHISCHINS	Ē	3.04.00	100 - 104)	-					
THE STATE OF THE S	S AV DI I DE VENE	SIERATIA MARCESCENS	34.33	464-401	1007-1041				1		†
TINE SING	SATENCE AND TEACH	FRWINGA CHRYSANTHEM!	114.341			•					-
PRIX EX	SELNETED TAULEAS	KYNECHOCOCCUS ELONGATUS NAEGEL	120-147		-						
PPSAA SYNEN	CHICKETEL A APORTURE A	CANE CHOCOCCIS SP	109:136	336-356							
PPSAA STAT	CILCINORNALL A APOPROTEIN A	RAMECHOCOCCUIS VIAI CANUIS	120-147								
PSAA SYAM	CALOROPHYLL A APOTROLEUP AL	CONFIGURACIA CP	<u></u>	130-143	338.364					-	
PPSAA SYNYI		VEDELLIA POCTIC	144.231								
PESAN YEAR	CHAM: KONI: FROIT:	COMECHICATION OF THE COMECHINA COMEC	=	L	L						
PPSAD SYNP	PHOTOSYSTEM I REACTION CENTINE SUBORIT IS	SI DECONOCIONE		-							L
				_	_	Ļ	_	_	_		_

PCGENE	10011764				48641	ABEA ABEAS	_	AREA AREA	┰	ARFAB	ARI'A 9
TITETATE	PROTEIN	ORGANIX	20.00	12.00			1		1-		
PPSBO ANAM	STABIL IZING POL TPC		23.53	-			-				
PPSPA ECOLI	PHAGE SHOCK PROTE	Post vice	114.141	T		T	-				
PPSRA WOLSU			2.0		<u> </u>		-	ļ			
rrsrs ccoul	PIIOSMIATE RINDING	I.M. HERMANIA CO.	97.2			-		İ			
FF11 DACSU	PHOSPHOTANIST INST		,	977-001	H						
	PHOSMIOTRANSFERANE	17:10.10	Ť	300-426	-		-				
PP I SALTY	PHOSMICH AND ERASE		14-61		-		-				
V	PIROSPIO I KANSPERA SE	STREPTOCOCCUS SALIVARIUS	Γ	108-333							
SH SH	PROSMICI KANSTERASE	EBWINIA CHEVANTILING	127-154	-	-						
THE STATE OF	PROSTILITIES AND THE ACT OF THE IS		670.697		 						
PF12G BACSU	PROPRIOTEANSFERANCE COLUMN II	199	\$17.564				-				
אומר רעכנא	PHOSPIOI MANSFERANCE ENGINEER		T	409.436							
אוור ראכנא	PROSPHOTECASE EACTINE II	11.14	T	530-557							
PPT2L STAND	PROSPINOTANA ENA ENA TALE II		445.410				-	T			
PPTIN ECOLI		CABSORIA	188-415					Ī			
PT:N STACA			170-400								L
LIN ECOL	MACE I TLULUCUSAN	MITANS	600-627	 							
2016	THUSTROING ANGERTA OF THE THE TH	SAL MONTH A TYPHINGUALIN	107.134	-							
1 3 3 4 T 1	PILOSPILOTE ANGERERACE BACTOR III		40-67								
יייי ניעניע	-	FSCHERICHIA COLIA	31-65								
2002	THUSTHUCKNEE	SALMONELLA TYPHIMURIUM									
743 17 67	PHOSPHOL ARRISE PROTEIN HPR	KLEBSIELLA PNEUNIONIAE	31-65								
200	PROTEACE II	ESCHENCHIA COLI	94-121 2	317-251							
200 4 6 6 6	-		194-928		H						
Nag 12 V Line			804-918								
Neg IX O Diag		KLEBSIELLA PNEUPIONIAE	178-205								
PMG S KLEPN	PUTS PRECUTSOR			П				1			
PPLEA PREPU	UPTAKE PROTEIN PRECURSOR	IDA	_	210-237 42	429-463 73	136-763	1	1			
PPURI BACSU	AMIDOPHOSPHONBOSYL TRANSF PREC	BACILLUS SUBTILIS	184-431		1	1	1	1			
PPUR BACSU	PHOSPHORUBOSYLAMINE-GLYCINE LIGASE	BACILLUS SUBTILIS	349-376		1		1	1			
PPURD BACSU	FORMYLTRANSFERASE	BACILLUS SUBTILIS	149-176	+	1		†	1			
PPURD_ECOLI		ESCHENICHIA COLI		1	+	1	t	1			
PPUR BACSU		BACILLUS SUBIILIS	701	\dagger	1	T	T	T			
PPURS BACSU	_	EACHLUS SUBTILIS		\dagger	\dagger	T	+				L
PPUTE ECOCI	_	PACIFIC COMPLETE	7	Ì	T	T					L
PPURY BACSU	SAKAN STATINETASE	BACILLIS SIBITUIS	9	136-353	T	1					L
PPURE BACSO	ADENTLUSALLINATE LI ASE	ESCHERICHIA COLI	L	211-372	Ī						
PPIN BACKU		BACALUS SUBTRIS	19.53	348-372							
PPLING ECOL.	AICAR TRANSFORMYLASE	ESCHENICHTA COLI	339.364								
PPURS SALTY	AICAR TRANSFORMY	SALMONELLA TYPHIMURIUM	118-247				1				
	SYNTHASE II	BACILLUS SUBTILIS	609-636		1	1					
PPYGI ANASP	LINKER POLYPEPTID	ANABAENA SP	19.115		1						
PYGI MASLA	LINKER POLYPEPTIDE CPCGI	MASTICOCLADUS LAMINOSUS	9	1	1	1	1	1			
PPYG2 ANASP	LINKER POLYPEPTIDE CPCG2	ANABAENA SP	2	1	1		1				
PPYG2 MASLA	LINKER POLYPEPTIDE CPCG2	MASTIGOCLADUS LAMINOSUS	9		1	1					
PPYGJ MASLA	LINKER POLYPEPTIDE CPCG)	MASTICOCLADUS LANIMUSUS	7		1	1	†				1
PPYCA ANASP	LINKER POLYPEPTIDE CP.CA	ANABAENA SI		1	†	1	1	T			-
PPYR! AN/SP		ANABARNA SP			†	1	1	T			1
PYTE PED		FREM FELLA DIFLOSIFICATION		\dagger	†		T	T			
PPYRA FREDI	11.4 KD LINKER POLYTEPTIDE	FREMTELLA DIPLOSIFIFON	8 2	1	†	Ţ	T	Ī			
2	37.5 KD LINKER POLITICALIDE	REEVYELLA DIPLOSITION	Ť	11.146	T	Ī	1			ŀ	
A LA	ASSAULTATE CARRAMON TRANSFERASE	BACH LUS SURTH 18	T			T	T				
PEYER CERIA	_	SERVATIA MANCESCENS	160								L
	_	ESCHENCHIA COLI	115:143		T		T				L
11.12	٦.										

	Prohoryaile Sequences	П	_				***	ABFAS
PCGEME 10711 419	DRGANISM	7	A SEAL	1000	т			
THE CASE OF THE PRIVILED PRIVILED BEINDROGENASE	SALMONELLA TYPHINDRIUM!	T	2 2					
TAB POSTUACE	BACILLUS SUBTILIS	273-302 327-349	2					
PPYRU BALSU LLIF STRIMASE	FREMYELLA DIPLOSIPHON	171						
PHYCUGILISORIE V P	ESCHERICHIA COLI	160-218				+		T
QUINONE OXIDORED	ESCHERICHIA COLI	194-361						Ī
POUEA ECOLI QUE DOSINE BIOSTATIAE SISTROTESIA COLE	CLOSTRINITA PASTEURIANUM	23.50 157.233	133			1	1	
34 2 KD PROTEIN IN A	ECCUEBICHIA COL	21.3						
PRACE ECOLI PRACE PROTEIN	French Court Table MOPHILLIS	152.189						
PRACO STRTR ASPARTATE RACEMASE	STACT TO COUNTY IS	132.162						
PROBABLE AMINO A	BACILLOS SUBTILIS	1116						
	ESCHERICHIA CULI	****				-		
RAFFINOSE INVERTA	ESCHERICHIA COLI							
PIBORE TRANSPORT	ESCHENICHIA COLI	65.99	1					
Manager I Account	ESCHERICHIA COLI	200-239	-	1			1	
PROSK ECOLI INBORINASE	WI PROPERTY A APPROCEMENT	6.47	_	_		-		
PRETA KLEAE AUBITOL (RBT) OPERON REPRESSOR	ALEBSIELLA ACADOCIALS	130,167						
PACTA FCOLL BIOSYNTHESIS ACTIVATION PROTEIN A	ESCHENCHIA COLI	141.57	150	 -				
AND THE WAY BEING WATER SIS ACTIVATION PROTEIN A	ERWINIA AMYLOVORA	1	2					
THE TANKET STORY OF THE PROTEIN A	ERWINIA STEWARTII	174.20						
PRESA ERWS1 BIOSTRIPES ACTION INC. TO SECOND ACTION	KI FRSIELLA AEROGENES	164-205						
PRCSA KLEAE BRUSTNINESIS ACTIVATION PROFILE	ESTIMENTINA COST	14-41 159.	159.186					
PRESS ECOLI CAPSULE SYNTHESIS D'COMPONENT	ESCHEROCHIA COL	ļ						
PRECY LEGIN RECA PROTEIN	LEGIOWELLA PREUPIOFILIA							
	ACHOLEPLASSIA LAIDLAWII	•	Т					
	AGROBACTEMICAI TUNIEFACIENS	┪	132-139 281-303					
	ANABAEM VARIABILIS	22.74						
PRECA ANAVA RECA PROTEIN	ACARTERY DANCEMENT	971 06-19	136-153					
PRECA AQUPY RECAPROTEIN	ACCURACION OF THE PROPERTY OF	104.135	-					
	BACTERODES TANGETS	701.70					F	
PRECA BACSU RECE PROTEIN	BACILLUS SUB IILIS	Ť	100 000					
PERCA PROTECT PROTECT	BRUCELLA ABORTUS	Ť	74-13v 740-74					
SPECA BITCE BECAPBOTEDA	BUTKHOLDENA CEPACIA	75.199					I	
A PROPERTY AND A PROP	ERWINIA CAROTOVORA	284-311						
	LACTOBACILLUS DELBRUECKII	20.47					\downarrow	
CARCA CARCA SECTION	LACTOBACILLUS HELVÉTICUS							Ī
MINION ACTION ACTION	LACTOCOCCUS LACTIS		233-369 288-319	_	1			
THE CALL AND THE CALL BOTTON	METHYLOMONAS CLARA	106-303						T
TRECA METAL ACCAPAGE	INE THYLOBACILLUS FLAGELLATUM	176-303						
PRECA METRE MECA PROTEIN	MYCOPLASMA PULMONIS	30.50	_	-				
	ANYCORACTS BRIDG TUBERCULOSIS	749-776		L				
	A SIGNATURE CONTRACTOR AND THE	361.110	-					
PRECA NEIGO MECA PROTEIN	REINGRA CONCORDING	017.186						
	PROTEUS MIKABILIS				-			
	PSEUDOMONAS ALRUGINOSA	1	100					
	PHIZOSIUM LECUMINOSARUM	7	П			1		I
Т	MHIZOBIUM LEGUMINOSARUM	٦	368-295				$\frac{1}{4}$	
+	NIIZOBIUM MELILOTI		268-295					
+	RHODOBACTER SPHAEROIDES	991-611						
-	STREPTOCOCCUS PNEUMONIAE	134-161 293	121-162					
7	SYNFCHOCOCCUS SP	134-151	L	L				
7	VIREIO CHOLFRAE	790-317						
-1	PACE LINE COMPANIE	Τ	178.205	-				
	SACILLOS SOBIELIS	8	767.67					
_	ENTREMICTIA COCI	1						
_	PROTEUS MIKABILIS		1		-			
PRECE PSETU RECF PROTEIN	PSEUDOMONAS PUTIDA	=	1		1	+	1	•
PRECE SALTY RECF PROTEIN	SALMONELLA TYPHINIURIUM	147-174	-				$\frac{1}{4}$	
+	ESCHERICHIA COLI	52.79						
PRECI PECONBINATION PROTEIN	BACILLUS SUMTILIS	31-48	156-184 192-247	47 199.116	344.378			
DNA HEI ICASE REC	ESCHENCIUA COCI	468-495						
т-	ESCHENCHIA COLI	107						
PRELA BACSU REPLICATION AND MAINTENANCE PROTEIN	BACILLUS SUBTILIS	П	101-10					
REPLICATION AND	STAPHYLOCOCCUS AUREUS	7-36 91.	101-10			_]	
						ļ.		

					2					
FILE MANGE	PROTEIN	STANDOCOCTIS PRIDE BANDIS	- -	Г					-	4
LENIA STAEP	REPLICATION AND MAI	BACKERICHA COLI	25.52	90-117				1	-	+
EPS ECOLI		5	142-373				1	1	1	+
PREPA BACSU			91.118	228-255			+	+	+	+
MEPA ECOL	META TROICIN	NEISSERJA GONORAJIOEAE	П	28.12	1			+	+	+
PRETA PERO	DEM ICATION PROTEIN REFO	LACTOBACILLUS MANTARUMI	<u>=</u>		1	\dagger	+	+	+	+
PERSONAL CTART	ILEM ICATION DAITIAT	STAPHYLOCOCCUS AUREUS	×		†		1	1	$\frac{1}{1}$	+
PREBU CTAALL	AFPI ICATION INITIATI	STAPHYLOCOCCUS AUREUS	28.28			+		1	+	+
PAEDA CTRACT	NULL BEAUTION	Ę.	430-467	1	1	+		+	+	╀
OREN CYNDY	TEPS PROTEIN		7		1			+	1	ł
	BESTEIN	STAPHYLOCOCCUS AUREUS	╗	173:210		1		+		+
PIEZZ SIAMU	_	ESCHENICHIA COLI		П		1		+	1	+
TOTAL PROPERTY.	PER ICA BION INTER	CLOSTRUDIUM PENTRINGENS			343.375			1	$\frac{1}{1}$	+
101	-	ESCHEDICHIA COLI	991-611	205-243		-				+
MEP ECOL	KET PELICASE	1 ACTORACITEDS PLANTARUM	Т	260-287						+
PAEP LACH.	MEP PROJEIN	C. OCTRIDITION PERFRINCENS	66-102	151-185		_				4
PLESP CLOPE	MESOLVASE	DACAL HE CHATTI IS	36-68							
PREZ BACSU		SACING SOUTH COLI		5.30	l		-	Ŀ		Н
PRT ECOLI		FALL MAKELLA TORINAMENTAL	Γ	163.204			ŀ	L		Ц
PREZ SALTY		SALMONCEAN TOTAL	Į,	443.473			-		-	_
PRES ECOLI	PEPTIDE CHAIN RELEASE FACTOR)	ESCHENCIAL COL	109.226		l	-	ŀ	L	_	L
PILY B ECOLI		ESCHENCIA COLI	105.212				-	L		
PICAG ECOLI	BIOSYNTIG SIS PROTEIN ILAU	ESCHEDINA COLI	99.60	233-266			-	L		
PRIV ECOLI	1,2-GLUCOSYLTRANSFERASE	CALINOVER I A TOMINAMINA	\$6.60	Т	236-263				L	L
PIU SALTY	_	SALMORELLA TOTALISMENTA	115.160	Т		\mid		L		-
PUFAK SALTY	_	ESCHEDINA COLI	166-393					H	L	
WAL ECOLI	•	CALLADARI LA TYPHINGRIDA	3,6-360				-			
PIUM SALTY	O.ANTIGEM LIGASE	ESCHERICKIA COLI	1:3				-			4
TO SECOND	BIOST PITE SIS PROTE	ESCIIENCIIIA COLI	62.89	184-340				1	1	+
MAN ECOL	_		11-45			1	+	1	+	+
UAZ ECOLI			2	~	1	1	$\frac{1}{1}$	\dagger	1	\dagger
PAUBB SALTY			320-339		1	1	$\frac{1}{1}$	$\frac{1}{1}$		+
LEBN SALTY					1	\dagger	$\frac{1}{2}$	+	1	+
RFBS_SALTI	PAINTOSE SYMINASE	SALMONELLA TYPHI	140.134		\dagger	+		+	\perp	ł
PRUEA VIBAN	PRECURSOR FOR FEM	VIBRO ANCOILLANON	11:0				-	-		H
AFH ECOLI		DACE THE THIRD WATER	15.68	90.262	310.313	T	-	-	-	L
PRG13 BACTU	PUTATIVE GIZ SHE-SF	ESCHERICHIA COLI	175.203	Ī		l	-			H
PEANS ECOLI	-	CALMONELLA TYPHRAMALUNI	175.202					ŀ		Ц
ALTYS EVILLA	_	ESCHENCHIA COLI	-					H		Н
THE COL	I BHANNOSE OPERO	ESCHENCHIA COLI	152-179							\dashv
VILLE STORY	BHIR REGILATORY P	RHIZOBIUNI LEGUNINOSARUNI	306-233							+
PRIOR FCOL	RNA HELICASE RULE	ESCHENCHIA COLI	136-169						+	+
PRHO RORBU	╈	BORAELIA BURGDON ERI	215-242	327.369				$\frac{1}{1}$	1	+
PRITOR NACSU	PROTEASE PRODICEG	BACILLUS SUBTILIS	82-100					1	1	+
THEY ECOL	RHSA PROTEIN PRECL	ESCHERUCHIA COLI	149.68			1		+		\dagger
AHSB ECOLI	RHSB PROTEIN PREC	ESCICENCIIIA COLI	3			1	1	$\frac{1}{1}$	+	+
PHSC ECOLI	-	ESCIRENCIIIA COLI	380-414	967-094	1036-1013	1	1	+	1	\dagger
MISD ECOL	RHSD PROTEIN PRECURSOR	ESCHEMCHIA COLI	27.72	1071-1098		1	+	1		\dagger
PRIMSE ECOLI	•	ESCHEMICHIA COLI	2		-		+	+	1	+
PRING ECOLI	ACETYL TRANSFERA:	ESCHELUCHIA COLI	6			1	\dagger	+		+
PIUM ECOLS	_	BLOCKOL MIN LOLI				1	\dagger	$\frac{1}{1}$		+
PUSA PHOLE	MIBORLAVIN SYNTHANE ALPHA LITAIN	BACO LIS SIDER IS	3					-		+
PRISB BAGSO	Т	PHOTOBACTERUM LEIOGNATIII	2.5				\mid		L	\vdash
PRING STRAT	Т	STREPTONIYCES ANTIDIOTICUS	14-72	106-133				H	L	┞

1102,178,4		AREA! AR	AREA! AREA!	AREA	ARTA AR	AREA AREA!	AT AREA E	7
CROTEIN	THE POTOGA MARUTUKA	ΙI	9	+		1	1	\downarrow
SOS RIBOSOMAL PROTE	IOPHILUS	11-45	-		1	1		
SOS RUBOSOMAL PROT		18-43		+		-		\mid
PRESE MICHE SOS REBOSOMAL PROTEIN LIA	N.	21.93			1	+		
PALIS MYCCA SOS MBOSONAL PROJECTALIS		21.48		1	+	-	-	-
MAN THEORY INC.	Hin.C.S	93:134	1		_		 	
SOS MBOSONIAL PRO		27.133		-		-		
TOP INDICATED TOP	10NIATIS	10.15	<u> </u>	+				L
el.		79.113	\ 	-	-		-	-
NOS RIBOSOMAL PRO	114	1.15	+		+		-	L
PALLIS LACLA NOS RIBOSOMIAL PROPERTIES	CND-LH	68.103	1	-	+			
SOS KIROSIMIAL PRO		\$		-		-	-	-
Nes MBOSONAL PRO	RACKLUS STEAROTHII RNOFHILLS	=	1		+	-		
SOS RIBOSONIAL PRO	CHI ANYDIA TRACHONIATIS	8 2			+	+		-
SOS MINOSONIAL PRO	HALOARCULA MARISMORTI'I	10.107	<u> </u>		†			-
PALIS HALMA SOS MBOSONIAL PROTESTA	ANCOM ASNIA CAPRICOLINI	61.88			†			+
MYCCA 168 RIBOSONIAL PROTICIO	ESCHEDICION COLI	23:43			+	1		\downarrow
	THE COUNTY OF THE PARTY OF THE	101.128						$\frac{1}{1}$
	TIALCANCOLA SIGNATURE CONTROLL	1						1
PRI 19 METVA PROBABLE SOS RIBOSONIAL PROTEIN	METHANG OCCUS VANSHELLI	19.19						
	PROTEUS VIJ. GARIS	†	311					
Τ	SULFOLORUS SOLFATARICES							
TAK BIMOSOMIAL PRO	ESCHERICHIA COLI		I	1			-	_
THE STATE OF PROPERTY TO	NIYCOPLASMIA FERMENTANS	-	1			-	L	
OH THE PROPERTY OF THE PARTY OF	BACILLUS SUBTILIS	-				-		-
FELT BACSO NO NO NO SOCIETA PROTECULAR	ESCHENCHIA COLI	35.55						
SOS PUBOSONIA	METHANOCOCCUS VANNIELII	10.57						-
SOS MINOSOMIAL PRO	INIYCOPLASNIA CAPRICOLUNI	32.59						-
SOS RUBOSONIAL PRO	HALOARCULA MARISMORTUI	48.75			†		1	+
SOS MBOSOMIAL TRO	METHANOCOCCUS VANNIELII	8.5				$\frac{1}{1}$		-
SOS MBOSOWA	INICROCOCCUS LUTEUS	16-63	1		1	+		-
THE A MILE OF THE PROPERTY PROTECTION 139	CHLAMYDIA TRACHOMATIS	8			†	1		
SOC PERCENTAL PROTEIN LTD	ESCHERICHIA COLI	9-92	1	+	+			
PRILZY ELOCI 100 MIDOSONIA PROTEIN LY9	MYCOPLASMA CAPRICOLUM	19.85		 		+		-
	BACILLUS STEAROTHERAIOPHILUS	3		\ 				-
TALL BALSI NOS BURDOCOMAN PROTEIN LA	MYCOPLASMA CAPRICOLUM	44-198	1	1	1			<u> </u>
Т	THERMUS AQUATICUS	26.05		1		+		-
TO THE PROCESS OF THE PROPERTY OF	BACILLUS STEAROTHERMOPHILUS	30.10g	1					+
SOS RIBOSOMAL PROTEIN LA	ESCHERICHIA COLI	19.40	+		+			
L	AIETHANOCOCCUS VANNIELII	1	1	1				
TOTAL PROTEIN LO	BACILLUS STEAROTHERMOPHILUS		1	+	1	-		
SOC RINGSOMAL PRO	FSCHERICHIA COLI	2	i	1	1	1	<u> </u>	-
ΙΞ	HALODACTERIUM CUIRURAUM			+			-	-
ACTION BIROSOMAL	HALOBACTERUM HALOBIUM	_						-
ACTION NEOSOMAL	HALDARCULA MAJUSHORTUI	7	53-184	1	1	1		+
	METHANOCOCCUS VANNIELII	194-221			1			+
PENCHAL PROTE	HALOPHILIC EUBACTERIUM MACC 41237	29.E6		1	1			
	HALONACTERIUM HALOHIUM	2-29	-			1	1	1
SOS BINDSOMAL PIEC	IIAI, DARCULA MARISHUR I'UI	3.79	-	1		+		+
THE A DAME OF THE PROPERTY.	METHANOCOCCUS VANNIELII	٦	-			1	1	t
THE BEST OF A PROPERTY OF	MICROCOCCUS LUTEUS	ᄀ	8-13	-		+	1	+
PRIA MICHO INTERNATION PROTEIN	SALMONELLA TYPHINDRIDA	8	┪	╗				+
A PROTEIN	STAPHYLOCOCCUS AUREUS		102-132 177-218	S 266-300		†	1	1
THE AT A PART OF A VATION PROTEIN	SALMONELLA TYPHINIURIUM		7			1		1
RL K PROTEIN	STAPHYLOCOCCUS AUREUS	Ī	103-133 261-293	£		1	1	l
SELVI CTAAL BLX PROTEIN	STAPHYLOCOCCUS AUREUS	7	166-216	+	1		+	+
PRI K CLIN SOS RUBOSOMAL PROTEIN LX	SULFOLOBUS SOLFATARICUS	2						

PCGENE	1107617864	Sequences	Т	•	1000	ADTAA	7	1 7 7 8 7	ARFA 7	ARFAR	AREA!
FILE MANE	PROJECT		0.10	_	т	_	_	_		Г	
PRINC ECOLI	RIBONUCLEASE III	ENTERCRIS COLI	٥	628-662							
PRINE ECOLI	RIBONUCI EASE E	COLA	Т			Ī					
PRNPA BUCAP	RIBONUCLEASE P PRO		159-186								
FRNPH BACSU	NUBONUCLEASE PRI	CCHEMICHIA COLI	116-160								
TRINS ECOCI	ALCOLATOR PROTESTA	BACILLUS CIRCULANS	63-109								
NA BACC	AUDUNOLLEASE DEFCURSOR	BACILLUS INTERACEDIUS	18-72					1			
TEN BACIN	BNA POLYMERASE SIGMA-38 FACTOR PRECURSOR	S	13-107								
TING PLAN		CITROBACTER FREUNDII	30-57		1			1	1		
ALUN BACTE		BACILLUS THURUNGIENSIS	П	63.90						1	
ביים מארוא	ACT DE SOUR A CE CICIA SA FACTOR		339.266		_						
PICTO ALCEU	ANA POLITICA SECTION SECTION	AZORHIZOBIUM CAULINODAMS	174.208								
PRPS AZOLA	IUNA POL I MENASE SIGNA - A PACION	BACTILLIS CIMPILIS	16.43	97.134	274-308 3	196-423					
PRESS BACSU		APONICIA	97.124								
PROST BRUA			148-182								
PROS KLEPN		PUODOS ATTER CAPCIN ATUS	155-185								
200C	ANA POLYNIERASE SIGNIA:34 PACION	MICHOGACIES CAS SOCIATION	145.172	T							
PRUSS BRAJA	RNA POLYNŒKASE SI			T	T						
PRESM ALCEU		NOTICE OF THE PROPERTY OF THE		t	T	Ī					
PRIM ECOLI	PROBABLE SIGMA(54)			t		Ī				Ī	
PRPSN SALTY	PROBABLE SIGMA(54)	SALMONELLA TYPHINIONIUM	T	71.00		336.366	101.119	T		Ī	Ī
PRP 70 BUCA	ANA POLYMERASE SI	BUCHNERA APRIDICULA	T	Т	Т				Ī		
PRP TO CHETR		CHE AMYDIA TRACHOMIATIS	77.4	1			1	Ì	Ī	I	
PRP 10 FCOLL		ESCHENCHIA COLI	327-361					1	1	Ī	
PRP 30 PSEAF		PSEUDONIONAS AERUGINOSA	┪	1							
PRP10 RICPR	IRNA POLYNERASE SIGMA-70 FACTOR	NCKETTSIA PROWAZEKII	╗	٦					1		
AXXXX OIGH	+-	MYXOCOCCUS XANTHUS	╗	118-347	359-316		1				
PRIPCE SYNPY	BILIN BIOSYNTHESIS	SYNECHOCOCCUS SP	180-207	1							
PRPOA BACSU	DNA-DIRECTED RNA	BACILLUS SUBTILIS	\$5-109	1							
PRPOA ECOLI	A.DIRECTED RNA POL	ESCHENCHIA COL! A	33.105		1		1				
		SALAIONELLA TYPHIMURIUMI		1	1			1	T		
PAPOA HALHA	DNA-DIRECTED RNA	HALOBACTERJUM HALOBIUM	100.00		1			\uparrow	Ī		
PRPOA HALMO	A.DIRECTED RNA POL	HAL OCOCCUS MORNINAE	279.770	Т	977 (77			1			
PRFOA METTH	DNA-DIRECTED RNA	METHAMOBACTERUM THERAMONOLOL ROTHILL		616-005	60.79			1	Ī		
PRPOA_SULAC	DNA.DIRECTED RNA	SULFOLDBUS ACIDOCAL DARIOS	Т	Т			T	1			
PRPOA THECE	DNA-DIRECTED RNA POLYMERASE SUBUNIT A	THEIMIOCOCCUS CELER	T	1101.1101	1					Ī	
PROB ECOL!	DNA.DIRECTED RNA	ESCHEMUNIA COLI	Ť		T			T		Ī	
PRFOG MYCL!	E DWA.DIRECTED RNA POLYNIERASE DETACIONIN	MYCOBAC TERIOM LEFTANE	Ť	-	1101.1101	Ī					
PRPOS SALTY	A-DIRECTED ANA POLYMERASE BETA CHAIN	SALMONELLA I TITIINIONIONI	Т	╈	-	627-861					
PRPOB SULAC	A-DIRECTED IUMA POLYMERASE SUBURIT B	THE MOTOR MARITIMA	Τ	Т	Т						
PRIVOR THEMA	A - DIRECTED INA POLYMERASE BE LA CHAIN	ANABABNA CP	152.194					T			
PROC ANAS	UNA-UIRECTED MA		T	948.994	133.133						
PRIPOC ECOCI	ONA-DIRECTED RIVA	IVAL ORACTERIUM IIAL OHIIM	Т	Ť							
PARTY IIAUIA	DAY DIRECTED BALL	HAL OCOCCUS MORRHUAE	T	13.144	201.234						
	NA PIPE TEN BNA	RATOAUTOTROPHICU	ž.	177.302	337.354						
S DATE OF SERVICE	A DIRECTED RNA PO	MYCOBACTERUM LEPRAE	333.300	180-090	916-116	1131-1158					
PROC NOSCO	DNA-DIRECTED RNA POLYNGRASE GALDA CHAIN	NOSTOC CONDAINE	130-192								
PRPOC SULAC	DNA-DIRECTED RWA	SULFOLOBUS ACIDOCALDANUS	Ī	172-214	124-251						
PRPOC THECE	DNA-DIRECTED KNA	THERMOCOCCUS CELER	21-58								
OUTUN UDANA	DNA-DIRECTED RNA	HOSTOC COMMUNE	91	655-500	995.665						-
PROF ECOLI	INA POLYMERASE S	ESCHENCHIA COLI	8:39		-						
PROS ECOL	NA POLYNGRASE S	ESCHENICHTA COLI	281-308								
PROOF HULLIN	DNA-DIRECTED RNA	HALOBACTERIUM HALOBIUNI	П								
PROSA ACKTU	I RNA POLYMERASE SIGMA.A FACTOR	AGAOBACTERUM TUNEFACIENS	\Box	397-427							
PRPSA ANASP	RNA POLYMERASE S	ANABAENA SP	50-12								
PRFSA CLOAB	INA POLYMERASE S	CLOSTADRIMA ACETOBUTY LICUM		1						T	
PRESA STRAU	J RNA POLYMERASE SIGMA FACTOR RPOD	STREPTOMYCES AUREOFACIENS	278-305 I	1]	

		Proharyoit Sequences	17	דו			1	7 7 7 8 8 9	6 7.8.7	ABTA 6	AREA!
FILT NAME	PROTEIN			d d	3	т			1		
PRPSB ANASP	RNA POLYNIERASE SIGNIA-B FACTOR	ANABALNA SP		169.196	300.230						
PRPSB_BACSU	ANA POLYMERASE SIGNIA-B FACTOR	Marieta	21.10								
FRESB MYXXA	RNA POLYNIERASE SIGNIA-BITAL JOH	TICMATELLA AURANTIACA	181.90				1		1	1	
PRPSB STIAU	RNA POLYNIERASE SIGNIA-G FACTOR	INABAENA SP	31-83			1		1	†	1	
TO A PAGE	ANA POL VACERASE SIGNIA-DI ACTOR	SACILLUS SUBTILIS	192-249		1	1	T	+	T		
A 354	ANA POLYMERASE SIGNIA E FACTOR PRECURSOR	SACILLUS SUBTILIS	8	971 911		1	T		T		
PROSE CLOAR	RNA POLYNIERASE SIGMA E FACTOR	LOSTMONUM ACETOBUTY LICUM		300	T	T					
PROCE BACLI	RNA POLYMERASE SIGNIA F FACTOR	SACILLUS LICHENIFORATIS			T		T	-			
PRPSF BACAGE	RNA POLYNERASE SIGNA-F FACTOR	SACILLUS MEGATENUM		100	Ī	T	T		T		
	RNA POLYMERASE SIGMA-F FACTOR				T		Ī	-			
	ANA POLYMERASE SIGMA-H FACTOR	ORNIS				T			T		
PRPSH BACSU	RNA POLYMERASE SIGNIA-H FACTOR	BACILLUS SUBTILIS	2	180.714			T				
PRPSK BACSU	RNA POLYMERASE SIGMA-K FACTOR	BACILLUS SUBTILIS	Ţ			Ī	Ì		T		
PLES STAN	RNA POLYNGRASE SIGNIA FACTOR PLAC		9			T		T	T		
PRUSW STRCO	RNA POLYNŒRASE SI	5			Ī		T				
PLUSX BACTK	POSSIBLE RUA POLY	BACILLUS THURNIGENSIS	3 5								
	SOS RUBOSCOMAL PROT							-			
PASII BACSU	10S RIBOSOMAL PROTEIN SII							-			
PRS13 BACSU	305 RIBOSOMAL PROTEIN \$13	BACILLUS SUBTILLIS						-			
PRS17 METVA	JOS NUBOSONAL PROTEIN SI?	METHANCECCOS VARAILEII	761.00	144.171		Ī					
PRSI ECOLI	TOS RIBOSOMAL PROTEIN ST	ESCREMINATION	3	365.292	149.176						
1 !	JOS NIBOSOMAL PROTEIN SI	PROVIDENCIA SP	15	11.2.17							
	105 NIBOSOMAL PROTEIN SI	MAICOSTINA MELLICON	-								
11	10S RIBOSOMAL PROTEIN \$21	BACILLUS SIEANOITHEANOITHEAN	91.175								
PRS1 SPICE	30S NIBOSOMAL PROTEIN S2	STROTTAND CINE	91.6								
PRS3 ACHEA	SOS PUBOSOMAL PROTEIN SS	MANCON ASMA CAPRICOLUM	77.106	136-163							
PRS3 MYCCA	JOS KIBUSCHALL PROTEIN 33	FICHERICHIA COLL	ŝ								
PRS4 ECOLI	105 KIBUSONAL PROTEIN ST	HALOARCULA MARISMORTUI	160-187								
TAL MAN	THE PROCESS OF THE PROTECT ST	MYCOPLASMA CAPRICOLUM	35-62	183-216					1		
PRICE THE TH	TOS RIBOSONIAL PROTEIN S4	THERMUS AQUATICUS	16-63						1		
PRS7 METVA	NOS PUBOSOMAL PROTEIN S?	METHANOCOCCUS VANNIELII	8.69						T		
PRS7 MYCLE	JOS ILIBOSOMAL PROTEIN \$1	MYCOBACTERIUM LEPRAE	477						T		
PRSE MICLU	JOS PLIBOSOMAL PROTEIN SE	MICROCOCCUS LUTEUS	0								
PRSS MYCCA	105 RUBOSOMAL PROTEIN SE	MYCONLASMA CAPIUCULUM							Ī		
PRSCA ECOLI		ESCHENCHIA COLI	335.36								
PRT67 ECOU		BACH THE ALVIN OF TOTAL FACIENS	175.202	254-281							
PSACB BACAM	LEVANSUCAASE PRE	PACILLIS SUBTILIS	175.202	254-288							
PSACB BACSU	LEVANSIKAASE PRE	STREPTOCOCCUS MUTANS	<u> </u>	155.119	314.369						
DACE STATE	CACO BECAR ATORY	BACILLUS LICHENIFORMIS	3.46								
מינים מינים		BACILLUS SUBTILIS	102-129	169-216							
Aduly 60 Pad	STREPTOCOCCAL ACID GLYCOPROTEIN	STREPTOCOCCUS PYOGENES	394-331	362.319					1		
PSAOX BACSN	SARCOSINE OXIDASE	BACILLUS SP	156.17								
PSAS2 CLOBI		CLOSTNDIUM BIFERMENTANS	7								
PSASG BACCE		BACILLUS CENEUS	<u>=</u>								
PSASG BACST		BACILLUS STEAROTHERAIOFHILUS	200					Т			
PCRCC FCOLL		ESCHENICHIA COLI	SE-360	33.78	<u> </u>	8929	778-812	601-179	78.67		1
PSBCD ECOLI	_	ESCHERICHIA COLI	3.6	34.387					T		1
PSBM ECOLI	_	ESCHENCHIA COLI	<u>?</u>	436-470	531-580				T		1
PSB BACS	_	BACILLUS SUBTILIS	<u>~</u>								
PSCPA STEVY	CSA PEPTIDASE PREC	STREPTOCOCCUS PYOGENES	29-160 126-160	<u>=</u>	2						
PSCRB KLEPN		KLEBSIELLA PNEUAIONIAE	2.20								↓
PSCRB_LACLA	SUCROSE 4-PHOSPIL	LACTOCOCCUS LACTIS		2							
PSCRD STRUMU	SUCROSE + PHOSPHATE HYDROLASE	STREPTOCOCCUS MUTANS	20.46						T		
PSCRK SALTI	FRUCTOKINASE	SALMONELLA THOMITSON	27								

PECENT	1103217844	Proharyotic Sequences	П	П	п				П	т	
FILEMANE	_		Y	3	7	1	1	1	4		1
PSCRK SALTY	FRUCTOKINASE	SALMONELLA ITTRIMUNIONI	Ī	240.267	Ī		T	Ī	T		T
PSCRY KLEPN	SUCROSE PORIN PREC	2	Τ	Т	240.267			T	l	t	Ī
PSCRY SALTY	SUCROSE PORTY PRE		Ī	Ī,				Ī	Ī		Ī
PSECA BACSU		BACILLOS SUBTICIS	2	75			T	T		İ	T
PSECA ECOLI			Τ							T	
PSECB ECOLU			Ι	178-412	•						
PSECU ECOL	PROJECT STATES AND PROJECT SECTION OF THE PRO		٦								
PLECY FOR	PREPROTEIN TRANSLOCASE SECY SUBUNIT		121-101								
PER LACITA	PREPROTEIN TRANSLOCASE SECY SUBUNIT	CTIS	403.430								
PKECY AGETVA	PREPARATERY TRANSLOCASE SECY SUBUNIT		131-161	106-423							
PERION CTATA	PREPROTEIN TRANSCOCASE SECY SUBUNIT	25	П								
PREFC SALEN	SEFC PROTEIN PRECL		137.164	\$65-840							
PSERA BACSU			16:43	147.374							
PSFAA ECOLI	S.FIMBRIAL PROTEIN		===								
PSFSA ECOL	SUGAR FERMENTATI		\$11:11								
PEFUA SERMA	INON-TRANSPORT SFUA PROTEIN PRECURSOR	CENS	19.91								
PSIGH FCOLL	SHILTER ON PROTEIN		314.362								i
1000	SINGLED PROTEIN A		296.362								
PSGUI FCOL	SINJECTON PROTEIN B		234-262								
PSHIM ECOL	SILIFICON PROTEIN B		234-262								
PSHUS ECOLI	SPILIFIELDN PROTEIN C		234-362	402-429							
PEIN ECOLI	SUBSTITUTE OF PROTEIN C		294-362								
	SHABILON PROTEIN D		134.162								
	SINE PROTEIN	ORNIIS	9. 10	43.80							
ı.	SINA PROTEIN		9.36	43.30							
PSLAP ACEKI	CELL SURFACE PROTEIN PRECUASOR	5	Ţ	183-300	(5)-(1)	481-419	\$17.544	563-593	589-199	126-75)	
PSLPA ECOLI	PROPINGE CP4.57 INTEGRASE		911.6								
PSVØ CCOLI	Shir Protein		I								
PSVIPB FCOLL	SMALL PROTFIND		Ţ	=				Ī		1	
PSVIP ECOLI	SALP PROTEIN PRECURSOR			1	Ī		1	1	1		
PSNITE SYND?	TRANSCRIPTIONAL REPRESSOR SMTB		97.70	1				1			
PSOOF COXBU	SUPEROXIDE DISKIU		2						1	1	1
PSOOF ECOL!	SUPEROXIDE DISMUTASE	_						1	1	1	
PSODE AIR TTH	SUPEROXIDE DISKU	METHANGRACIERION THERMOADIOINOR					1	T	1		Ī
PSCO PIOLE	SUPERUATOR DISMUTASE	N. W. III	20.10	T				Ī		Ì	
POUR FOOT	SOME PROTEIN PRECI		T	16.01	273.300			T			
PSOPB ECOL!			182.179								
PSOXA ECOL!	SOXI PROTEIN		3								
PSPOJ BACSU	STAGE 0 SPORULATION PROTEIN 1		11:15						Ī		
PSPIA BACKE	STAGE II SPORULATION PROTEIN AA	HUM	19:53								
PSP1A BACSU	STAGE II SPORULATI		= ==								
PSP2B BACLI	STAGE II SPORULATI		\$						1	1	
PSP2B BACME	STAGE II SPORULATI	KIUM	2.3				İ				
PSP1D_BACSU	STAGE II SPORULATI		5		Ì						
PSP1G BACTK	POSSIBLE ASPARTY	IENSIS	T	-							
PSP12 DACSU	STAGE II SPORULATI		_	9							
PSP1D BACSU	STAGE III SPORULAT		1	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		1		Ì			
PSP11 BACOU	STAGE III SPORULAT		24.73		7				1		-
PSF4A BACSU	STAGE IV SPORULAT		139.180	1			1	1		1	-
PSP4D BACSU	STAGE IV SPORULAT		39.66					1			
PSP4G BALSU	STAGE IV SPORULAT		21.2								
PSP1A BACSU	STACE V SPORULATION PROTEIN AF	GTACELTOS SUBTILIS GTACELTOCOCÓLIS POUNTEI	9.30					1			
SAAA SIIGO			802-181		T		1	T		1	
PSAND BACSO	_		207-101	T	T		T	T	T	1	T
FSFAL DALSO				1				1	1	1]

	Sequences	AREAL	AREAL	48542	AREAs	AREAS	AREA AREA!	_	7	7
PROTEIN	MACILLUS SUBTILIS	П		7						
TO THE PROPERTY OF	STREPTOCOCCUS ARUTANS	123-276	╗	29.363	2,6-6,10	107	1133-1167	2	1	
The Control of the Co			23.198					Ì	1	
		Г	226-267					1	1	
CHECK STATE	OCENES	13.39						1		
- Caron			155-112					1		}
	IFERUNI	195-322						1	1	
A IOSUATION SERVICE A		99-119						1		
ADILLION TO THE PROPERTY OF TH		276.305						1		
	TYNOMONA CHORILIC	19.06								
VCLASE		159.166	244.271							
A PARTIES AND TELM	FCMERICHIA COL.	301-328						1	1	
PARTICLE PROTEIN	LIVERSI ASMA MYCOIDES	21-65	107-141	354-428						
PACIFICE PROJEIN	PACTORIA A MARMOL VIICA	21:33	351-315	115.598	929-970	100.091				۱
TIGEN I PRECURSOR	TASTECHTICATION OF THE PARACENTS	Т								
	STREET OF COLOS PARASITIONS	8:12	101-128							
		61.93								
		63.19A								
GFROIEIM	273	200								
CPROTEIN	SCREALIN PLANCESCENS	20.13	178-287	795.483	\$65-895	676-710	1011-1101			
CURSOR	STARTICUCCOS SANCOIS	135.152								
	METUDATUS ANIMAS	(6.99								
W.SE	ESCHENCAIA COLI	80.10	172.199	110.08						
	IAMATUCCICUS AGREUS	1	364.30							
	STARRECOCCUS AUREUS	17.74								
NSC CONTROL PROTEIN	CLUST MUTUAL BELIEVINGEN	16.61								
-	ESCHENCIA COCI	111.210								
TE AMIDINO I MANSFERANCE	STREET CONTINUES FOUNDS AND STREET CONTINUES AND ST	209-236	211-306							
STREET UKINASE C PRECUNSOR	STREPTOCOCCUS PYOGENES	209.236								
- acception	STREPTOCOCCUS SP	209.236	281.308							
AN PROTEASE EPR PREC	BACILLUS SUBTILIS	435-462	\$32-563	603-639						
PRECURSOR	BACILLUS SUBTILIS	40-67	9:19	2	524.583			Ì		l
OTEIN	SALMONEL LA TYPHINIURIUNI	2.2								
OTEIN PRECURSOR	WECHOCOCCUS SP	2								
OTEM PRECURSOR	SYNECHOCYSTIS SP	20.00								
AG PRECURSOR	BACILLUS LICIENIFORNIIS	E .								
•	BACILLUS MESENTERICUS	- I								
PRECURSOR	BACELUS SP	9	20.5							
CCHARTICUS PRECURSOR	BACELUS SUBTELIS	22.25								
•	BACILLUS SUBTILIS									
SUBTILISM I PRECURSOR	BACILLUS STEAROTHERAIOPHILUS	197.224								
SUBTH ISON E PRICHESOR	DACILLIS SUNTILIS	2		 - -						
MINUR EXTRACELLULAR PROTEASE VPRTRECUR	BACILLUS SUBTILIS		200							
	ESCHERICKIA COLI	767.077								
SUCROSE PHOSPHORY LASE	ENTERONAL TER AFROCENES	60.21		L	L					
CELL DIVISION INRIBITION	ESCHENCHIA COLI	157.711	125-752	70.621						
ACOUNTY! JOHN CONTINUEDS!	ESCHERICHIA COLI	130-359								
CLATANCE THAT CONTINUES	BACILLUS STEAROTHERAIOPHILUS	49.76								
CLUIMANT TEMA SYNTHETASE	BACILLUS SUBTILIS	49.76	151.316							-
GLUTANYL TRNA SYNTHETASE	THEAMUS AQUATICUS	405-432								
PIENTLALANYL-TRNA SYNTHETASE A CHAIN	BACILLUS SUBTILIS	7.14								
MENYLALANYL. TRNA SYNTHETASE BETA CHAIN	BACILLUS SUBTILIS	140-367	403	_						
PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN	ESCHENCINA COLI	246-523	607.634	24-73						
CYL-TRNA SYNTIETASE BETA CIIAIN	ESCHENCHIA COLI	2	2							
HISTIDYL-TRNA SYNTHETASE	STREPTOCOCCUS EQUISIMILIS 176-403	6 2 2 2								
	Control of the state of the sta									

FILE NAME PSYK1 ECOLI PSYK1 ECOLI PSYK1 ECOLI	LAOTLIN									ľ	
PSYK! ECOLI PSYL ECOLI		ESCHEDICULA FOR 1	Г							1	
PSYK2 ECOLI	LYSYL-TRAA STRITLE		Т	283-310	П	Ħ			+	1	
PSYL ECOU	LYSYL-IKMA STRINE		120-247				1	+	1		
10000	┰	THERMOTHLUS	69.69		1	1	1	1	+	1	
1000	ARETHONYL. TRNA SY		ž.	1		1	1	1		\dagger	
L COL	PROLYL-TRUA SYNTH		2	1		1	T	T		\dagger	
PSYO ECOLI	T						T	T	-	†	
PSYRD PSESY	Г	RINGAE.		†	1			†	 	\dagger	
PSYR ECOLI	ARGINYL-TRNA SYNTHETASE		T	100	1		1	T			
PSYTI BACSU	THREONYL-TRNA SYNTHETASE		7	200	1	T	I		1	\dagger	١
PSYV BACST	VALYL-TRNA SYNTIETASE	THERMOPHILUS	Ī	Т	10,10	T	1	T	+	†	١
PSYV ECOL	VALYL-TRUA SYNTHE		T	T	16.0	1	1	1	+	\dagger	
PSYW BACST	TRYPTOPHANYL-TRN	HERNOPHILUS	_	274.700			T	1		Ì	١
PSYYI BACSU	TYROSTL-TRNA SYNT			33:408			1			1	
PSYY3 BACSU	TYROSYL-TRUM SYNT		1		1			1	+	T	l
PSYY BACCA	TYROSYL-TRUM SYNT		┑	917		1		1	+	T	
PSYY BACST	TYROSYL-TRNA SYNTHETASE	THERMOPHILUS	Т	Т		1			+	T	
PTIMI ECOU	ENZYME ECORIZATIN PROTEIN		٦	T	Ť			1000		\dagger	1
PTIRE ECOL	ENZYME ECOALDUI A PROTEIN		٦	160.5	97.72	Т	╈	301-004	1	T	
PTIR ECOLI			138-363	1			1	1	\dagger	1	l
PTIST ECOL	ENZYME ECORISMI I SPECIFICITY PROTEIN		124-11	1				1	\dagger	T	l
PTISA ECOLI	ENZYNIE ECOA I SPECIFICITY PROTEIN		279.306	1					1	T	
PTICE ECOL	Т		230-312						1	1	
PTISO ECOLI	Т	ESCHENICHIA COLI	249-283							1	
1000	Т		279-306							1	
143	ENZYNE SPECIFICITY PROTEIN D	SALMONELLA POTSDAM		╗						1	
2 3 3 1 4	ENZYNE SPECIFICITY PROTEIN	חושו			П	╗	٦			1	
PT337 FCOLI			·	267.33	96.440	639-682	667.726	926-934		1	
PTAL ACICA	TYPE II NESTINCTION	L'COACETICUS		П					1		
PIZE BACSU	TYPE II RESTRUCTION			Т	7				+	1	
PT2BR BACSU	TYPE II RESTRICTION		1	N. C.	DE 9-100	66.27			1	Ť	
PTZCI CITTR	TYPE II RESTRICTION		7	1					+	1	
PTICI HERAU	TYPE II RESTRUCTION		176-215	1					\dagger	Ť	
PTICI HERAU	TYPE II RESTRUCTION	HERPETOSIPHON AURANTIACUS	12.00	1					1	Ť	
PT1D1 DESDN	TYPE II RESTRICTION	ş	771-6	1					+	Ť	١
PIZDI STRPN	TYPE II RESTRICTION	PREUNIONIAE					Ī		+	T	
PT2E1 ECOLI	TYPE II RESTRICTION	ESCHENCHIA COL.	27.5						\dagger	T	l
PT2E2 ECOLI	TYPE II RESTRICTION ENZYME ECORUI	ESCHENCIA COLI	7	17, 71,					\mid	T	
PTZES ECOU	TYPE II RESTRICTION	ESCHENCIA COLI	T							Ī	
PT2F1 FLAOK	TYPE IIS RESTRICTIO	PLAVOBAC JEMOM OREAMONOILES	T	40.04						T	
PT3HI HAEIN	TYPE II RESTRICTION	INCREMENTAL OF THE ARM STREET AT	١		-					Ť	
PEZIE HAFFA		INCHEST OF THE PRESENCE OF THE PARTY OF THE	9							Ī	
PIZID HAENA	TYPE II RESIDING TO THE	HAFMONITHS INTITIES AF	87.138							Ī	
PIZEL HAELN	THE II RESTRICTION	KLEBSIELLA PNEUMONIAE	ŝ	178-205					L		
FIZKI KLEFF	TYPE II AESTRICTION	MORAXELLA BOVIS	19.5	\$12.711	115-252				L		
OBSOL STATE	TAPE HE BESTALLTIN	MORAXELLA BOVIS	3:30	Г	337-364						
TIME MOVE	POSSIBLE TYPE II RE	METHANOBACTERIUM THERMOFORMICICUM	105-151								
ONE ONE	TYPE II RESTRICTION	NEISSENIA GONORAHOEAE	117-144	331-338							
PTIC CIETA	TYPE II RESTRICTION	STREPTOCOCCUS SANGUIS	5-33	19-11	395-446						,
SH252 SH050		SHIGELLA SONNE!	1	256-288	•						
TACL STAKE	TYPE II RESTRICTION	STAPHYLOCOCCUS AUREUS	70-102							1	
NISS SALLY	1	SALMONELLA INFANTIS	144-181								
PT2SM SELMA	TYPE II RESTRICTION	SERRATIA MARCESCENS	П							1	I
PIZTA THEAQ	Q TYPE II RESTRUCTION ENZYNG TAQI	THERMUS AQUATICUS	_	Т		197			1	1	
PTIMO ECOL	LI SYSTEM ECOPIS ENZYNE MOD	ESCHENIONA COLI	T	Т	230-230	378-403			+	1	
PTIRE BACCE	E SYSTEM ENZYNG RES	BACILLUS CENEUS	67-Z0						1	1	

INTERPRETATION OF ACCOUNTS 1999	PCGFME	107417814		AREAL	ABLAL	AREAL	AREAS	AREAS	AREAL	AREA!	AREA !	7777
10 D DATE OF VALUE	П			П			1	1	1		T	
AUTO INTERCACE AUTO INTERCACE AUTO INTERPRETATION AUTO INTERCACE AUTO INTERPRETATION AUTO INTERPRE	_			٦	98.329	1	1		T	\dagger		
THE STATE OF STATE	ASI TREDE	S) KD MEMBIKANE ANI			3		1		t		T	
	ACY BACAL	ALVEOLYSIN PRECURSOR	NEMNGENS		┪		1		1		T	
INTEGRACIAN INTEGRACION PROPERTY PROPERTY PROPERTY	ACY CLOPE	PERFRINCOLYSIN O PRECURSOR			╗	┑		1	1	ļ	T	
Interface of the property of		IVANOLYSIN PRECURSOR			╗	Т	27		1		T	
STATEMONTONIAL STREET TEMONTONIAL STATEMONTONIA		LISTEMOLYSIN O PRECURSOR			٦	╗	3		Ì		T	l
		SEELIGERIOLYSIN PRECUASUR		П	П				Ť		T	١
TECHNOCACID BIOSTONIASIS PROTEIN TECHNOCACID BIOSTONIA BIOSTONIA BIOSTONIA BIOSTONIA BIOSTONIA BIOSTONIA BIOSTONIA BI		PHEUMOL YSIN			П	40-470			1	1		
Interfedence Activity Stignth, Stig		STREPTOLYSIN O PRECURSOR		63-69					1	1	Ī	
		TECHOIC ACID BIOSTM TRUITIN B TREE			7	П	П			1		
Interviol.CACID BROTATHESTS PROTEIN DIGITAL STRINGS DIGITAL		TECHOIC ACID BIOSYNIMESIS PROTEIN C		Г			╗	29.00	1			
Transferour Comments Transferour Comments	TAGE BACSU	TECHOIC ACID BIOSYNTHESIS MOTEIN E		182-209								
	TAGE BACSU	TECHOIC ACID BIOSYNTHESIS PROTEIN F	1	Τ	Т	Г	10-010					
Transcriptional Ecological Control C	OFFICE	THANSFERMIN-BINDING PROTEIN I PRECURSOR		Τ	Т	135.402						
NEWSCOPPIDIONAL COLOR ENAMERALY VIRTHOMANIAN	TOTAL BEEFE	BUTENCH 2.MONOOXYGENASE		٦.	T							
VERNO FORTER VERN	A4 140	THANKERIPTIONAL REGULATORY PROTEIN TCDT				100.311	341.780	344.375	459-486			
CF PLLUS BIOSTWITESIS PROTEIN TOTAL CF PLUS BIOSTWITESIS PROTEIN TOTAL CF PLUS BIOSTWITESIS PROTEIN TOTAL CF PLUS BIOSTWITESIS PROTEIN TOTAL CF PLUS BIOSTWITESIS PROTEIN TOTAL CF PLUS BIOSTWITESIS PROTEIN TOTAL		ANGUANG PROTEIN TOPC PRECURSOR		į						-		
CF PALLOS SCOREION ROTEN TOPE VIRBLO CHOLERAE 511-218 511-	201	TOTAL THE BLOCKSTONE CIC PROTEIN TOPE		T						İ		
CF PLUIS BIOSTWINESIS PROTEIN TOH VIRBID CHOLEME 19-17 174-106 19-17	CYE VIBOR	TOTAL SECRETION PROTEIN TOP		٦								
	ובני אופרט	TOTAL SECTION AND		221.56		70.	94. 77.					
	CPH VIBCH	TOTAL TOTAL STATE OF THE PROPERTY IN THE PROPE		23-52	734-261	801-617						
TCP PILLS WANDERSON TO THE PROPERTY 199.31	CM VIBCH	ICF FILLS BIOST FILE		48.75								
TETALCYCLINE RESISTANCE PROTEIN VIBRIO CHOLENAE 131-141 131-141 14	CPN VIBCH	TCP PILUS VIRULEACE		230-257								
TCP PLUS BIOSYNTHESIS PACIENT (72) VIBRIO CHOLEAGE	CPO VIBCH	TCP PILUS BIOSYNING		121-14								
TETRACYCLINE RESISTANCE PROTEIN SCHILLUS SUBTILLS	ICPY VIBCH	-		44.85								
IETACYCLINE RESISTANCE PROTEIN SACILLUS STEAKOTHENIONIAL 423-431 IETACYCLINE RESISTANCE PROTEIN STAFFTOCOCCUS AURUS 423-431 IETACYCLINE RESISTANCE PROTEIN STAFFTOCOCCUS FAURUS 423-431 IETACYCLINE RESISTANCE PROTEIN STAFFTOCOCCUS FAURUS 423-431 IETACYCLINE RESISTANCE PROTEIN STAFFTOCOCCUS FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN STAFFTOCOCCUS FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN STAFFTOCOCCUS FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS IETAC FAURUS 133-36 IETACYCLINE RESISTANCE PROTEIN IETAC FAURUS IETAC	ICPZ VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN TOTAL		404.434								
	CR2 BACSU	TETRACYCLINE RESISTANCE PROTEIN	PACILLUS STEAROTHERMOPHILUS	422-453								
FETALYCLINE RESISTANCE PROTEIN STREPTOCOCCUS MELANONIAL 172,413 173,713 173,	TCR BACST	TETRACYCLINE AESIS I ANGE 900TEDA		404.431								
FETALCYCLINE RESISTANCE PROTEIN STREPTOSCOCUS PNEUMONIAE, 10.319 10.3	TCR STAND	TELECONOMINATION OF THE PROPERTY		422-453								
TOCAGO PERON TANNERAPTIONAL ACTIVATOR ESCHERACINA COLI 110-154	TCR STRAC	TETTA CYCI NE RESISTANCE PROTEIN		422.453								
TETACYCLINE REPRESSOR PROTEIN PLACE FEGURALISA COLI 197-164 161-359 400-439 197-164 161-359 400-439 197-164 161-359 400-439 197-164 161-359 400-439 161-362 197-164 161-362 197-164 161-362 197-164 161-362 197-164 161-362 197-164 161-362 197-164 161-362 197-364	TOUR STORY	TIPCARC OPERON TRANSCRIPTIONAL ACTIVATOR	ESCHENCIUA COLI	10.27								Ŀ
	1003	TOCC PROTECN	ESCHERICIUA COLI	20.00								L
	TEES STROY	TAYPSIN. RESIST SUR	STREPTOCOCCUS PYOCHEMIS									
	TEN ECOLI	TETRACYCLINE REPR	ESCHERICHIA COLI	96.15				L				
	TERS ECOL		ESCHERICHIA COLI									
ECTENCYCLINE RESISTANCE PROTEIN TETAL ENTEROCOCCUS FAECALIS 136 136-139 170-306 137-344 136-139 170-306 137-344 136-139 170-306 137-344 136-139 170-306 137-344 136-139 137-344 136-13	TELY ALCSP	TELLURIUM RESISTANCE PROTEIN TERA	ALCALIGENES SF						L			
	TESP ECOLI	ACTL-COA THOESTERASE II	ESCHENCIA COLI	9	130-130	13.20	217.244					
ILLANGYCLINE BLSSTANCE PROTEIN EAGLEMOCING COLUMN 17.106 116-134 1	TETS ENTER		ENTEROCOCCUS PAICALIS	2	130-139	117.244	260-287					
ILLANSPOSON THO TECH TO ROLEN 15.000 11.10	TE TO ENTEA		COCUMINITAL OF THE COLUMN TO T	25.106	16-138							4
FETALCYCLINE RESISTANCE PROTEIN THE NOTICE ALTO ALTO ALTO ALTO ALTO ALTO ALTO ALTO	TETC ECOLI	TRANSPOSON THIS TETC PROTEIN	ENCHERCIAL COL	13.100								
FETALCYCLINE AESISTANCE PROTEIN 15 IN UNEATOCOCCUS NUTANIS FETALCYCLINE RESISTANCE PROTEIN 12 IN UNEATOCOCCUS NUTANIS FETALCYCLINE RESISTANCE PROTEIN 12 IN 12	TETA STILL	TETILACYCLINE RESI	STREET LONGES ELECTRICAL	2	130.159	217.244	260.287					
Interaction resistance froten tell	TETM UREUR	TETRACYCLINE RES	CANGES OF THE COM	2		L						
IETAACYCLINE RESISTANCE RODIENTED STREPTOCOCCUS NUTANIS 2.19	TETO CAMC	TETRACYCLINE RES	CAMPATIONAL TERMINA	97.2	L	L						4
ETRACY CLURE ASSISTANCE FROTEIN SACTEROIDES FACILLS 13-43 13-4	TETO CAMIE	TETTACYCLINE RENSIANCE PROTEIN TETO	STREPTOCOCCUS NIUTANS	3:39								
ET MANT CHILD RECURSOR	TETO STRACE	TETTACYCLINE RESISTANCE PROTEIN	NACTEROIDES FRACILIS	13-62					_			1
TRANS VALUE TRANS TRAN	PTETX BACK	TEIRACTCLING MES	CLOSTRIDUM TETANI	274.304	540-567	615-642	602.319	2012	240-127			1
CHILDROTRICHED TO TO THE PROTRIED TO THE PROTR	PTETX CLOTE	TELANUS LOAIN TA	PYROCOCCUS WOESE!	216-251								1
QUEUNE THAN AUBOSYL TRANSFERASE ECCREDICHIA COLI 11) 200 FIGEOWINE DERIYDRATASE BIOSYNTHETIC LACTOCOCCUS LACTIS 181-301 FIGEOWINE DERIYDRATASE BIOSYNTHETIC LACTOCOCCUS LACTIS 181-301 FURAN OXIDATION PROTEIN THOF ESCHERICHIA COLI 183-180 193-226 FURAN OXIDATION PROTEIN THOF ESCHERICHIA COLI 226-240 4-31 FIRAN OXIDATION PROTEIN THOF BACHLILIS SUBTUDA 226-240 4-31	PIPZIB PTRWC	CH CROCATECHOR	ALCALIGENES EUTROPHUS	33				1				1
THREGNINE DEHYDRATASE BIOSYNTHETIC		OF FILME TRNA-RIBO	ESCHENICHIA COLI	2		_		1	\downarrow			ļ
TRUE GOINTE DE INTOLATASE CATABOLIC ESCHENCHIA COLI 19-320 19-320 FURAN OXIDATION PROTEIN THDF BACILLUS SUBTILIS 133-180 192-336 104-31 FURAN OXIDATION PROTEIN THDF ESCHENCHIA COLI 228-260 404-31 FURAN OXIDATION PROTEIN THDF RECHOMONAS PUTIDA 228-260 FURAN OXIDATION PROTEIN THDF RACTILLIS CEREUS 4-31	101	THE FOUNDE DENTY	LACTOCOCCUS LACTIS	22.20			\downarrow					\downarrow
FURAN OXIDATION PROTEIN THOF BACILLUS SUBTILIS 135-100 193-120 193-120 193-120 193-120 193-120 193-120 193-120 193-120 193-120 193-130		THEONINE DENYDI	ESCHERICHIA COLI	2 2 2								
FURAN OXIDATION PROTEIN THUF ESCUENCIAL COLI 228-260 FURAN OXIDATION PROTEIN THUF PROTEIN THUF PARENS RACHITIS CEREUS 138-260 RACHITIS CEREUS 13	IS TY JULIA	FURANOXIDATION	BACILLUS SUBTILIS	23	22.28							ļ
FURAN OXIDATION PROTEIN TYDF PSEUDOMONAS PUTUA 4-38	PTIDE ECOL	FURAN OXIDATION	ESCHERICHIA COLI	20.00	1				1			
RACHING CAREON	PTIEST PSEPU	FURAN OXIDATION	PSEUDOMONAS PUTIDA	7	345.347	1			ļ	L		L
DATE OF THE PARTY	PTHER BACC	THE LUMOL Y SIN	BACILLUS CENEUS									L
THE EMILE THE PACE UNDON	PTHER BALS	I DERMOCTSIN PRECUASOR						1				

	PCCCONE 1103	0031784	Praharyotic Sequences	Т		1000	Abras	ARFA 9 //	AREA 6 A	AREAT	AREAS	AREA?
Interpretation	FILE MAME ZB			Т	Т	_	Т		j	1		
Interport	PINER BACTH TH			191:161								
THE PORTON	PTHET THE VU TH			Т	975-10							
INTERPRETATION STATEMENT	Philic ECOLI								1	1	1	
	Printe ECOLI	SOR		┪	86.23	1		Ì	1	1	1	
THE PROPRIATE WINDS NAME AND THE PRECORDS INTO THE PRECORDS INTERFORMED STATES AND THE PROPORTION OF THE PRECORDS INTERFORMED STATES AND	PHILE BREIA	Г	Z	2	T				\dagger	1	T	
THEOREMA, MEDITAL PROTIEN A PRECUSOR ESCREMICIAL COLD PROTIEN A PRECUSOR THEOREMA PROTIEN A PROTIEN A PRECUSOR THEOREMA PROTIEN A PROTIEN A PRECUSOR THEOREMA PROTIEN A PROTIEN A PRECUSOR THEOREMA PROTIEN A PROTIENCA A PROTIENCA A PROTIENCA A PROTIENCA A PROTIENCA A PROTIE	PTHIR SACER PU	П		9.60	Ì			Ī		T		
TEPOPEAL HEBINATE NOTION IN TEPOPEAN FALLIDON 11.100	PTIG ECOLU TR	П			Ť	T		T		T		
The Docklay Registry Color Front Reforement 19.18 19.19	-	ABRANE PROTEIN A PRECURSOR		907-917	1	T		Ī	T			
THE SPORGANE TAKE AND AND TREPORTED HANDERSHIS THE SHOP		ANE PROTEIN B PRECURSOR		- 1		1		T	\dagger			
TAMESTORY INTO TRANSCRIPTOR FOLIA TO THE TOTAL	AT HERM TR	ANE PROTEIN B PRECURSOR		3	1		1		\dagger	T	Ī	
Interprotate Interprocession Interprocession Interprocession Interprotate Interprotate Interprocession Interprotate Interprotate Interprocession Interprotate Interprocession Interprotate Interprotate Interprotate Interprocession Interprotate	PTVAN FCOLL	OPHAN PERMEASE		Ť		1	1		1		Ī	ĺ
Intervience Intervience	TOTAL STANI			1		1	1	T	t	Ť	1	
	т	KESOLVASE		╗	=	1			İ	1		
	-			<u>=</u>		1			†			Ī
The state of the	+-			_				Ī	1	\uparrow	T	
TANASTOSSEN PITT TRANSPOSTING PROTEIN TWO ESCRENGIAL COLI	7			٦	26.50	14-20			1	1		
TANKINGSON TOTAL STATEMENT TANKINGSON TOT	7	TRANSPOSITION PROTEIN THISB		П	56.537				1		1	
TAMENDOSCIA TRANSPOSITION PROTEIN TYSE ESCREMENTA COLI SUBJAT TOLLINER 1. SHORT CREATER EFF. SUBJAT TOLLINE 1. SHORT CREATER EFF. SUBJAT TOLLINE 1. SHORT CREATER EFF. SUBJAT TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER TOLLINE 1. SHORT CREATER		CHSPOSITION PROTEIN THSC			<u> </u>					1	T	
TOURSE TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR FOR EACH STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR CRANGE ALTHA STORING TOUR STORING ALTHA STOR	_	UNSPOSITION PROTEIN THISD		36.56	1		Ī				T	
	_	NSE		97.69			Ţ		1		T	
TOTAL FROM TOTAL STATEM 1911 19	_	LITENE 1 2-DIOXYGENASE ALPHA SUBURIT		200					1			
19.119 1		I IENE I 2-DIOXYGENASE BETA SUBUNIT		2							T	
TOTAL PROPECT HYDALASE PSEUDOMONA PUTIDA 101-119	1.	A THEM I 2 DIOXYGENASE SYSTEM		136.71								
TOTAL FROTEIN 10-11 10-21 10-24 14-17 11-21 10-24 14-17 11-21 10-24 14-17 11-21 10-24 14-17 11-21 10-24 14-17 11-21 10-24 14-17 11-21 10-24 14-17 11-21 10-24 14-17 11-24 11-2	Т	IN PRODUCT HYDRATASE		2 13					1	T		
OUTER MCMORANE PROTED 1942-15 1942-15 1942-15 1942-15	_	I A PEOTEIN		┪	٦	┑						
The common com	_	THE MEMBRANE PROTEIN TOLC PRECURSOR	ESCHENICHIA COLI	┪	┪	Т	345.373					
THE CONTRACTOR RECURSOR 191-104	_	A TOPOISOMERASE!	SYNECHOCOCCUS SP	203-230						T	1	
FERTISSISTONN SIRBUNT 1 (51) PECUASOR BOADEFELLA PERTUSSIS 11-740 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-141 10-140 10-140 10-141 10-140 1	7	DATE THY LAMINE. N. OXIDE REDUCTASE	ESCHERICHIA COLI	70.024								
FEATUSSIS TOXIN SUBUNIT 2 (51) PRECLIATOR DOLORIO	_	RTUSSIS TOXIN SUBUNIT I (SI) MECURSOR		82.2								
TOWN A PEEUDOMONA DEFICILE 19-10 19-24 131-469 131-569		ATUSSIS TOXIN SUBUNIT 2 (\$3) PRECURSOR		Τ	Т	304.311	147.169	373-414	847.962	866-994	997.1024	1341-1402
TAMSFORM A PLECUROR 10.05 FEB. 13.163 199-241 13.169 131-169 1	PTOXA CLODI TI		DEA	Т	Т							
TAMASHER BRANE REGILATORY PROTEIN TOXS VIBBIO CHOLERE 11-40 10-41 10	PTOXA PSEAE E.			Т	133-163	Г	175-869	923-950	1334-1388	1403-1433	1306-1565	1716-1747
TANSPER PROPERTY TREFONEMA PALLIDDM 106-161	FIOXO CLODI	SXON B		Γ								
TRUGSEMOSPHATE ISONERASE 15.00 10.110 11.101 11	PIOXS VIBCH	CASSICALITY OF THE PROPERTY OF	TREPOWENA PALLIDUM	106-143								
TRIOSEPHOSPHATE ISONEAASE	Ť	ATE		83-110								
FRIDGE PROTEASE PRECIRISOR FORMHYROMOUNT SINGULALS 17-144	Τ.		MORAXELLA SP	39-166								
TYPPTOPIALN'S 1-MONOOXYGERASE AGROBACTERUUM TUMERACIENS 139-246 501-329 170-746 170-	1	HOL PROTEASE PRECURSOR	PORPHYROMONAS GINGIVALIS	T								
THYSTOPHAN 1-MONODYTGENASE		TYPTOPHAN 1-MONDOXYGENASE		╗	625-102							
TAMSFOGASE TAMONOCYCERASE CYCERASE TAMONOCYCERACIAC COLI TAMONOCYCERASE TAMONOC		TYPTOPHAN 1-MONOOXYGENASE ;		907-677	201.00					Ī		
TANISTOSASE TANISTOCOCCUS AUREUS TANISTOCOSASE TANISTOCOCCUS AUREUS TANISTOCOCCUS		KYPTOPHAN 2-MONOOXYGENASE	PSEUDOMONAS SYLINGAL	1								
TAMENOSASE ESCREACHA COLI 711-755 711-		IANSPOSASE	STAPHYLOCOCUS AUREUS	-	35-13							
TAMENOSASE		KANSTOSASE	ESCHERICHIA COLI	121.755								
TANSPOSIAE 11-20 11-40	_	TANCOCASE	NGZOBRJM MELILOTI	179.206								
TANNSPOSASE ESCREDICHA COLI 111-200 109-340 11-200 11-		TANCPOSASE	STAPHYLOCOCCUS AUREUS	13-60	\$6-99							
TLANSFOSASE ESCHELICHIA COLI 11-18 TLANSFOSASE SHOELLA SONNEI 13-18 100-1217 TLANSFOSASE SHOELLA SONNEI 13-18 130-1217 139-136 139		PANSPOSASE	ESCHENICHIA COLI	181-208	101-140	720-754						
TAMISTOS ASE SINGELLA SONNEE 11.78 200.127 TAMISTOS ASE ECCHENCHA COLI 729-164 TAMISTOS ASE ECCHENCHA COLI 729-164 TAMISTOS ASE BACILLUS THURNOCIENSIS 211-301 TAMISTOS ASE BACILLUS THURNOCIENSIS 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASE STAPPTLOCOCCUS ASTREED 211-301 TAMISTOS ASTREED		PANIPOSASE	ESCHEDICHIA COLI	11.11								
TACANSPOSASE ESCHEDICIA, COLI 129-156 159-156	_	RANSPOSASE	SHIGELLA SONNE!	51.78	200-227	131-258						
UTATIVE TRANSFOSASE MYCOBACTELUDA TUBERCULOSIS 119-186 \$5310 PROBABLE TRANSFOSASE BACILLUS TRUBRIGENSIS 211-304 \$2310 PROBABLE TRANSFOSASE BACILLUS TRUBRIGENSIS 211-304 TRANSFOSASE STAPITOCCCUS AUREUS 4.31 \$321 PROBABLE TRANSFOSASE BACILLUS TRUBRIGENSIS 211-304 \$12 PROBABLE TRANSFOSASE BACILLUS TRUBRIGENSIS \$11-304	-	KANSPOSASE	ESCHENICHIA COLI	729-756		<u>-</u>						
\$2110 PROBABLE TRANSPOSASE BACQLUS THURDAGENSIS 211-304 \$2311C PROBABLE TRANSPOSASE BACQLUS THURDAGENSIS 211-304 TANSPOSASE STAPPT LOCOCCUS AUREUS 21-304 \$2311 PROBABLE TRANSPOSASE BACQUUS THURDAGENSIS 11-304 BACQUUS THURDAGENSIS 19-127 TRANSPOSASE 90-127	PTEAS MYCTU	3	MYCOBACTELUM TUBERCULOSIS	159-126								
STANTO PROBABLE TAANSPOSASE	PTAR BATTE		BACOLUS TRURINGENSIS	201.304	419446							
TANSFOSSASE	PTRAC BACTB		BACILLUS THURINGIENSIS	281-308	419-446							
S331 PROBABLE TRANSPOSASE BACILLUS THURNGIENSIS 91-137 TRANSPOSASE 91-137	PTIME STANU		STAPHYLOCOCCUS AUREUS	-								
TRANSPOSASE STATE BACILLOS THURMOTENSIS	PTILAX BACTB	ETIV	BACILLUS THUMINGIENSIS	M - 12	91.00							
	PTIA BACTU	TANSPOSASE	BACILLUS THURMGIENSIS	721-127	309-339							

		Probaryatic Sequences	П	1			,,,,,,		,	ABFA
CCI.NL			1		TOTAL PRINCE		4	Т	Т	
PTA PCEAE	SASE		Т						ı	
100	751000 0100	ESCHERICHIA COLI			1	1	1		Ì	
1000	TI DE LOS	ESCHERUCHIA COLI	٠ ٠						1	
ונותו לנותו	JANIP TROIEIN		70.07							
- 1	I KBI PROIEIN		1006-1058							
_1	TRAC-I PROTEIN		1102-1149						1	
_1	TRAC. PROTEIN		114-931	-	_					
PTRC) ECOLI	TRAC.) PROTEIN		397.148	<u> </u> 		_				
FIRDI COLI			Т	107 (67	1	-				
	PERIN ASMIC TREILALASE PRECURSOR		7	2	1					
1			240-307							
PTREC ECOLI			5.12	105-132						.
TRFA ECOLI	TAFA TRANSCRIPTIONAL REPRESSOR PROTEIN			Г	897-898	Sé				
The Groun	TRAGPROTER		Ī	Τ	Г					
	MICHORAL TO A		╗	-			1			
			195-223	211.565					1	
PIRGS ECOLI	TRAG PROTEIN		155.209	197-624 687	111.06(1 110.18)	1111				
PINI ECOU	TAIPROIEN		Т	Γ	447.014 1150.1177	1111				
10.5	TRAIPROTEIN		Ţ	Т	1					
	753.000 1 400	ESCHENICHIA COLI	47.74	176-171		1			1	
		E CLIFERICIIIA COLI	96-63							
TIDA ECOLI	IND FROIDS		5.32		_					
PTRAIL ECOL!	IN AND PROTEIN		107.137	-			_			
PIRMA ECOLI	TRNA (URACIL-3-)-NE		Τ							
TOUR GOLD	RAY (CUANINE NI)		Ť							
	HAVE TOWNED AND CONTE		170-747		1					
ALINA BALSO		SCENTUS	241-275	_		-				
PINA CAUCK			176-203			_				
PINA PSEAE	TRYPTOPHAN SYNTHASE ALPHA CHAIN		2			-	-			
PTRPB ACICA	TRYPTOPHAN SYNTE	LCOACETICOS	Ť				+			
TO BE BACK	THY SWAHOLD		7	(6,14)	1					
מוצים מארים		ACTOFERMENTUM	<u></u>		-					
PTIVE BALLA	IN THE PART OF THE PARTY		111.0							
PIRE LACCA	I KYP I OF HAN STRIN		20.7	164-191		_				
PINE LACLA	TAYPTOPHAN STAIN	71/115	5	-		-				
PTRPO VIBPA	TRYPTOPIIAN SYNTHASE BETALMAIN	A SCHALMA	20000		-					
PIRE DRELA	INDOLE J. GLYCEROL				1					
PIEC ECOLI	INDOLE-3-GLYCEROL	ESCHEMICHIA COLI		1			-			
PTUPE LACLA	INDOLE-J-GLYCEROL		2		1	1			T	
PTRIN VILLE	INDOLE- J-GLYCEROL		+				+			
70,00	ANTHRANII ATE PHOS	rcus	Ï	160-294						
2000	NTITE AMILATE FILES		105-232							
THE CAPAC	AND THE WATER OF THE PARTY OF T	PERITOMONAL PUTIDA	205-232				_			
FIRFU PSEFU	ANTHURANILATE PIO	SECTION OF THE PARTY OF THE	1.70				-			
PTRED VIBPA	ANTIGRANILATE PHO	VIBRO FACORACIONE	8			-				
PTRPE BACPU	ANTHORANILATE SYN	DACILLOS PUMILOS			1					
PTRIPE CLOTM	ANTHRAMILATE SYNTHASE COMPONENT IS	CLOSTRIDGIOM THERMOCELLUNI	077:601							
PIRPE LACLA	ANTHRANILATE SYN	LACTOCOCCUS LACTIS		!		-			İ	
1	ALTITUDENI ALE CYNTHANE COMPONENT	LIPTOSPIRA DIFLEXA	145:178	_		_	1			
	The second secon	REIZONIUM MELILOTI	139.166				_			
FIRTE AIIME	AN HIMMING AND AN AND AND AND AND AND AND AND AND	CAT MONET LA TYPHING IRLINA	161-218		L		-			
TIME SALTY	-+	CHE ICH COLEATABICHE	T	298-328	-		_			
PTRIPE SULSO		Wine to execute Carlotte	9.16	14.81	-	_	-			
FIRPE VIDPA	_	VIERIO PARAILA: MOLT INCO		<u> </u>	1	<u> </u>				
PURINI ACION	ANTHRANILAH: SYNHASH COMPUNINT IN	ACIMITORACTI: A CALCOACI: HC US	-] [$\frac{1}{1}$			
PIRES AZONIA	ANTHRAMILAH: SYNTHASI: COMPONINT II	AZOSFIKILLUM IIKASILENSE	<u>-</u>							
1000	AMTHRANIL ATE SYNTHASE COMPONENT II	ESCHENICHIA COLI	5.33							1
	AND AND A TE SY	LACTOCOCCUS LACTIS	÷	-	16					-
	A LATE A MILL A TE SYN	PSEUDOMONAS AERUGINOSA	12.39							
יייייייייייייייייייייייייייייייייייייי		SALMONELLA TYPIIIMURIUM		-	_	L				
LINE SAL		SERRATIA MARCESCENS	3		_		L			
LINE SERVE		SHIGELLA DYSENTEALAE	<u>::</u>							
200		PSEUDOMONAS AERUGINOSA	103-136		_	_				
TIES PARA	Ť	ESCHENICHEN COLI	1111		_					
יונטני	7	FUCHERICHIA COL!	184-221				-			
PTRT3 ECUL	KESIS I AMUE PROTE									

PCGENE	1107117014	Proharyotic Sequences	П	П		-	П	П	П	П	
FILE RAME	PROTEIN		3	ANEAL	AREA	ANGALA	AREAS	A A A A A A	ANTA A	ARTAI	AREAS
≥	TRAY PROTEIN		200	T			\dagger	\dagger	\dagger	1	
PTRYP STRGR	TRYPSIN PRECURSO			1	Ī	\dagger	Ť		†	1	
PTSR STRAZ	RENA METHYLTRAN		7		Ī	1	Ì	1	1	1	
PISST STAND	_	STATE COCCOS AUREOS	٦,		T	\dagger	T	1	\dagger	T	
TOTAL STORY	CHARREL-FURMING		221				T	\dagger		\dagger	
PTIK ECOL	CITE BRANCH PROTEIN		Τ	107-134				İ	\dagger	T	
PTYCA BACBR	PLYCA BACBA TYROCIDINE SYNTHETASE		117.167	134.361	1019-1031		l			Ī	
PIYTI TREPE	ANTIGEN TYF!	TREPONEALA PERTENUE	106-143					_			
PTYTA BACSU	POSSIBLE PREPIENATE DEHYDROGENASE		244-271	112-342			Ī				
PIYMA ECOLI	CHONISMATE MUTASE		329-376								
PIYAR ECOLI	TRANSCRIPTIONAL REGULATORY PROTEIN TYRA	ESCHENICHIA COLI	413-510								
PTYSY LACCA	THYMIDYLATE SYNTHASE		139-173							_	
PTYSY LACLA	THYMIDYLATE SYNTHASE		15-109								
PTYSY STAAU	THYMIDYLATE SYNTHASE	AUREUS									
PUIPE ECOLI	SENSOR PROTEIN UICHB			316-343		_					
PUDDS SALTY	SENSOR PROTEIN UMPB		174-303	116.343							
PURICE SALTY	UNCUC PROTEIN		204-331								
PUPP ECOLI	URACIL PHOSPHORIBOSYL TRANSFERASE		30-53								
PURA ECOLI	UTACIL PERMEASE		150-184								
PUREI MELPY	UREASE ALPHA SUB	DIO.	18-42								
PUREI PROMI	UNEASE ALPHA SUBLINIT		73.99								
PURE! PROVU	•		3.99								
PURE! UREUR	UNEASE ALPHA SUB	ICUM		43.517							
PUREZ HELPY	UREASE BETA SUBL		62.9								
PURED HELPY	UNEASE OPERON UNED PROTEIN	HELICOBACTER PYLORI	2				1	1		1	
PUREE PROMI	UNEASE ACCESSORY PROTEIN UREE 16		2.5				1	1	1	1	
PUREF KLEAE	UREASE ACCESSORY PROTEIN UREF PRECURSOR	ES					1	1	1	1	1
PUSAS LACLA		LACIUCUCCUS LACINS	T	Т	101-0/7		1	Ī	1	1	Ī
PUSHA ECUL		SIX SIMILARY					Ť		1	Ī	I
TOUR YEAR			Т	171.000	Ī	Ì	T	T	t	T	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	EXCIPACLEASE AND	reus	309.01	T	614.711	973.049		\dagger	t	T	Ī
PUVRA PARDE	EXCINICLEASE ABO	KANS	Т	Т	Т		T			Ī	I
PUVRC BACSU	EXCIPACLEASE ABC	8	242-372	\$11-518							
PUVRC_ECOLI				333-362							
PUVRD ECOLI	HELICASEH		100-301								
PVANA ENTEC	VANCOMYCIN RESISTANCE PROTEIN VAM	ENTEROCOCCUS FAECIUM	187-300								
PVANC ENTGA	VANCOMYCIN RESIS					1	1	1			
PVIDA ACRTS			2 2 2			†	1	1	1	1	Ī
ACE ACE ACE	VISION PROTEIN		16.00	1		1	T	1	1	T	Ī
PVIRA AGRITO			130.227			1	T	\dagger	\dagger	Ť	
PVIBX AGRTS	VIRBIO PROTEIN		Т	212-239		T	T	T	T	Ī	
PVIBX AGRT6	_			211-238							
PVIBX AGRT9	1	AGROBACTERUM TUNEFACIENS	33-59	212-239							
PVICI AGRICA		UNIFFACIENS	91-10E								
PVICI_AGRTS	VIRCI PROTEIN		101-101								
PVICI AGRT6		2									
PVID) AGRIA	VIRD) PROTEIN		٠	П							
PVIKA AGNE	WIDE HOST PANGE		T	7	53.084						
PVIRA AGRT6		ACROBACTERUM TUMEFACIENS	T	1	653.660		1	1	1	1	
200	WIDE TO A MICE WATER ACTIVATOR		40.7.		030-660			1	1	1	
PVIRE YEREN	VIRTIENCE REGULON TRANSACTIVATOR	KITICA	T	Т		1000	1	1	†	1	T
PVIRG AGREA	VIRG REGULATORY		1461	Ī		\dagger	T	T	t	T	Ī
PVIRE AGRT6	LIMITED HOST RANG	AGRODACTERUM TUMEFACIENS	106-157	Ī	Ī	T	T	T	t	T	T
									1	1	

	Probaryolie Sequences	ABFAI	AREAL	AREAS	AREA	AREAS	AREAS	AREA! A	AREAI	AREA?
THE PANE PROTEIN	FSCHERICHIA COLI	1								
PVISC ECOLI VISC PROTEIN	MYCOPLASMA HYORHIMIS	211.56								
	BORREL!A (ERAISII	18-95						1		
DUTER NEMBRANE LI	BORRELIA (ERMISII	333-359						1		
DUTER MENBANK LI	T	110-157						1		
DOTE A VERGO ANT	Т	47.143			1					
PARTY BORNE OUTER MEMBANE LINORATERY 25 PRECURSOR	Ť							1		
WITHOUTH FIXATION	Т	_	31.36							
MITEOCENACE VANAC	AZOTOBACTER CHROOCOCCUM MCD I							1		
WITHOUSENAKE VANA	AZOTOBACTER VINELANDII	П	373-403					1		
A KIN VIRIA PACE PR	SALMONELLA CHOLERAE-SUIS	309-536		1				1		
SUBSTITUTE ACED VIBILE FACE PROTEIN	SALMONELLA DUBLIN	\$11.538						1		
COR CALDIT VARIA ENCE PROTEIN VSDE	SALMONELLA DUBLIN	3.36						1		
ACCOUNT AND TOTAL VERY CECESTION PROTEIN	VIBRIO VILMFICUS	30-38						Ì		
WALL AREACIATED P	STREPTOCOCCUS MUTANS	170	113-386							
MUNICIPAL STATE OF THE PROPERTY OF THE PROPERT	ESCHENICHIA COLI	911-68								
V BANK VECETIBE	ESCHENICHTA COL!	161-101						1		
ì	ESCHENICHIA COLI	104-131								
TAIN ECOLI A POLITICATION	ESCHENCHIA COL!	104-131								
١.	ANABAENA SP		19.116	135.162						
7	ESCHENICHIA COLI	268-295								
CYLOSE ISOMERASE	STAPHYLOCOCCUS XYLOSUS	41.43						Ì		
PYYLK KI FAE XYLLD OSE KINASE	KLEBSIELLA AEROGENES	٦	┪							
TK LACPE IXTLUIOSE KINASE	LACTOBACILLUS PENTOSUS		┑	7				1		
PXYLK STAXY XYLULOSE KINASE	STAPHTLOCOCCUS XYLOSUS	٦	7	38.23	246-273			1		
AR BACSU XYLOSE REPRESSOR	BACILLUS SUBTILIS	T	700.787							
PXYLR LACPE XYLOSE REPRESSOR	LACTOBACILLUS PENTOSUS	A 77 05	101	317.181	221.255	274.301	1	T		
ALK STAXY XYLOSE REPRESSOR	BEELINGACONA & BITTIDA	T	Т	Т						
PXYLZ PSEPU ELECTRON INMARER CONCORES	CALDOCELLUM SACCHAROLYTICUM	Ē	Ī							
SYNA BACCI D. 1-BETA-XYLANASE PRECURSOR	BACILLUS CIRCULANS	47.74								
PXYNA BACSS ENDO-1 4-BETA-XYLANASE PRECURSOR ;	BACILLUS SP	13.200						1		
NDO-1,4-BETA-XYLA	BACILLUS SUBTILIS	7						1		
PXYNA CALSA ENDO-1,4-BETA-XYLANASE A PRECURSOR	CALDOCELLUM SACCHAROLYTICUM	<u>^^</u>	200	1				Ī		
THA PSEFL ENDO-1.4-BETA-XYLANASE PRECURSOR	MACHINE PINGLING	459-416	Ī					Ī		
PXYMB BACPU BETA-XTLOSIDASE	CAL DOCELL IDA SACCITAROLYTICUM	40-474	Ī							
SYNN CALSA MILIA-A LEGISLANIC	PSEUDOMONAS FLUORESCENS	П	351.378	117.144	475-502					
AL PHA L. ARABINOFU	✝⁻		141-176							
LNIXO-I 4-DI:TA-XYLA	ī	103-210								
HYPOTHETICAL 1491	HALOCOCCUS MORRHUAE	\$6.03								
HYPOTHETICAL 23.1	STREPTOCOCCUS GRALIS	7						1		
HYPOTHETICAL 36 7	METHANOBRE VIDACTER SAIITIII	T	20.5							
HYPOTHETICAL 346	ESCHENCAIA COLI							T		
PYAAC PSEFL HYPOTHETICAL 31 9 KD PROTEIN	ESCUEDICHIA COLI									
HAPOTHETICAL ST	F SCHERICHIA COLI	917.53								
	ESCHENCHIA COLI	201.55								
HYPOTHETICAL 149	ESCHENCINA COLI	131.134								
	ESCIENCHIA COLI		627.654							
HYPOTHETICAL 63 9	ESCHENICHIA COLI	431-455								
PAYOTHETICAL 33 9	PSEUDOMONAS AERUGINOSA		150-137						ا	_
PYAD2 CLOSS HYPOTHETICAL 21 6 KD PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	╗	114.144							
ADS CLOAD HYPOTHETICAL IS S KD PROTEIN	CLOSTRIDIUM ACETORUTY LICUM	2	8 - 38	20.21				1		
FYADS CLOAD IIYPOTIETICAL PROTEIN	CLOSTILDIUM ACETORUTY LICUM	10.53	Ŧ				1	T		
PYADA YEREM INVASIN PRECURSOR	VERSINIA EN EROCOCITICA	-1								
PYADA YERPS INVASIN PRECURSOR	TENSINIA ESEULATIONEMENTATION	1	21.]				1		

199-256 199-	PCGENE	107117814	=			П			т	Т	П	
	EILE MAME	LROILIN		A SEC	A SEC	V V	_	Т	_	Т	4	4
100 100	PYADC ECOLI	HYPOTHETICAL PROTE		2		1		1	Ì	Ī		
	PYAEA RICRI	17 KD PROTEIN		10:10								
	PYALL ECOLI	HYPOTHETICAL 29 4 K		231:34								
	PYAFD ECOLI	HYPOTHETICAL 29 1 3		-			Ī		1			
STATE STAT	PYAFE ECOLI	HYPOTHETICAL 23 0 1		2				1				
A	PYAIB ESCFE	HYPOTHETICAL PROT		2								
NYCOLIGE HOLES NYCOLIGE TRAINER NYCOLIGE TRAI	PYAMI SALTY	PUTATIVE AMIDASE	HINCURITIN	B				1				
MACIONE MACCOLATESPICIÓN 13-13 11-131	LYAEL SYNY)	HYMPHHEHEAL BOK	-				7	1				
NYCOLASAN GALIERICAN 111-238 1	PYATP MYCLE	LIYPO PROTEIN PUTATIVE ATP OFERON	LEFRAE	Ţ	91.151	311.538	1					
MALENCE MOTERN AND CALLESTICIAN 19-14 (4-15)	PYATE BACFI	HYPOL ATP-BINDING TRANSPORT PROTEIN		211-238								
NATIONER SCIENCIAMA CALFERRICM 19-18 19-13 1	PYATS MYCGA	HYPOTHE TICAL PROTEIN		7.41								
	PVATE MVCGA	HYPOTHETICAL PROTEIN		29.56	60.83							
	NOTE OF THE PARTY	ACCOUNT OF TO A VISIO ENCE DECIENT		68.98	199.126							
STATE SCIENCIA COL 11-15	TAN AAM	ATTOMICS OF THE PROPERTY.		40.70								
NATION RESTRICTION COLUMN CO	MAN ECOL	HYPOTHETICAL 24 I NO PROTEIN					Ī					
WATCHERGE ALL NO PORTER WATCHERGE ALL NO PORTER WATCHERGE ALL NO PORTER WATCHERGE ALL NO PORTER WATCHERGE ALL NO PORTER WATCHERGE ALL NO PORTER WATCHERG ALL NO PORTER	PYBBA ECOLI	HYPOTHETICAL ABC TRANSPORTER							1			
TOTALISTICAL PROPERTY SCRENGING COLUMN 19-14 19-15 1	PYBED ECOLI	HYPOTICETICAL 9 B KD PROTEIN		71			1		1			
TYPOINTER, LALL SERVING STATE 14-41 14-4	PYBID ECOLI	HYPOTHETICAL IN I KD PROTEIN		97.174	\int							
Tropiestical in the Pattern Section of the Pattern	PYCAE ECOL!	HYPOTHETICAL 24 S K		2.0								
WOOD IN COLUMN WATER WAT	PYCBA ECOLI	HYPOTIETICAL PROTEIN		31-65								
The Properties at Document 19,19	PYCBL BACUN	HYPOTHETICAL 17 3 KD PROTEIN		66-100								
Propriet California California Colifornia Colifornia California Colifor	PYCEA BACLA	HYPOTHETICAL PROTEIN	S	111-138								
1-4 1-4	PYCEC ECOLI			87-79								
14-10 ROD RODERN ESCREUCHIA COL 14-10	PYCHO ALCEU			31-48								
Proprietal Propriet Proprietation Prop	PYCIN ECOL	HYPOTHETICAL 20 BK		3								
Thronie Through Through Through Thronie Thro	NCIE ECOL	SA PROPERTY.		7.68	134.166							
VERTIFIESTED, 19 KD FROTEH VERTIFIESTED,	יייייייייייייייייייייייייייייייייייייי			3								
INVOINTERICAL 19 I KD PROTEIN STYREGISCOCKUS 37 136-34 136		AVECTOR AT A 1 P PROTEIN		24.6								
1970/10E 1744 17 17 17 17 17 17	AGIAS GAA	MANDETICAL 20 3 KD PROTEIN		194-221								
INTEGRIEGAL 19 1 LO PROTEIN STREECHOCY 2115 SP 13-104	ACE STAN	HYDOTHETICAL 28 0 KD PROTEIN		2.54	120-154							
Varyone field, brotein MASTIGGOLADUL LANIMOSUS 13-99	VCPS SYNY)	HYPOTHETICAL 19 5 KD PROTEIN (277.306								
VAPOTIETICAL PLOTEIN PROTEIN PAGELLAN ADAREM SP 10-40	PYCPG MASLA	HYPOTHETICAL PROTEIN	AMINOSUS	62.2								
17-10-11 17-10-11	PYCPY PSEAS	HYPO PHYCOCYANIN OPERON PROTEIN Y		310.407								
17-107 1	PYCILL BACTK	HYPOTHETICAL 29 I KD PROTEIN	GIENSIS	47.74	133-150							
INTEGRIFER MACFILLUS SUDTI	PYCSS ECOLI	HYPOTHETICAL PROTEIN PRECURSOR		12-59								
INFOINERICAL NOTERN ESCHENCIAL COLI 10-10 13-10 131-10	PYCWS BACSU	HYPOTHETICAL PROFEIN		1.30	99-69							
13-66 113-161 1	PYDIM HERAU	HYPOTHETICAL 68 4 KD PROTEIN		12-19	131-171				П			
VAPOTHETICAL B 0 TO PROTEIN ESCHENCIAL COLI 00-107	PYDBA ECOLI	HYPOTIETICAL PROTEIN		12.66	113.144		13.267			676-717	1136-1163	1499.1530
	PYDDD ECOLI	HYPOTHETICAL PROTEIN		1								
INTOTRETICAL 10 1 KD PROTEIN ESCHENCINA COLI 131-104 131-1	PYDOB ECOLI	HYPOTHETICAL 86 7 KD PROTEIN		7	П	26.73			Ì			
	PYDDC ECOLI	HYPOTHETICAL TO I KD PROTEIN		7	╗	521.648						
INVOITE ICAL 19 KD PROTEIN	PYDOD ECOLI			133-174								
VYPOTRETICAL 15 15 DPROTEIN ESCRENACIIA COLI 1313-160 131-150 131-151	PYDEH ECOLI	HYPOTHETICAL 20 S KD PROTEIN		96-130								
THOOR RELICAL IS STATEMENT SECRETARIAN STATEMENT	PYDEJ ECOLI	HYPOTHETICAL II J KD PROTEIN		16.3			Ī					
TYPOTHE FICAL IN TAD PROTEIN SULFOLOBUS SOLFATANCUS 11-38	PYDEK ECOLI	MITOTAL 63 3 AUTROLEIM		201:101		746-696						
TATOFICETICAL 16 F KD PROTEIN SULFOLOBUS SOUFATANCOS 11-38	PYDNN BOXED	HYPOTHETICAL IT A MUTROLEIN		2								
TATOPHETICAL 10 TAD FROTEIN TOTAL COLI 19-170 19-	PYDOI SULSO	HYPOTHETICAL 14 7 KD PROTEIN			101		Ī	T				
VECTOR LECAL TO KD PROTEIN SECRETICHIA COLI 19-77	מכוחג נסטר	MINDING IN THE PROPERTY OF										
INTOTICE ILCAL 10 KD PROTEIN ESCRELCHIA COLI 10-174	PYEBA ECOLI	HTPOINE II. AL PROIEIN		71-170								
HYPOTHETICAL IN CONTRICTOR HS.170	TESO ECUT	HITCHIA IV NOTATION										-
INFOTHETICAL IN TO PROTEIN 15-170 11-170	LATER ECOLO	ATTO I RELICAL JEST		2				Ī				1
HTYPOTHETICAL 19 FLO PROTEIN ESCHENCHIA COLI 19-178	TATE ECON	NAME OF TAXABLE PARTY.					T					ľ
19-17 19-1	Y 2			7/1-69	915		Ī					
HYPOTHETICAL 19 1 KD PROTEIN ESCHELICHIA COLI 96-133 HYPOTHETICAL 19 1 KD PROTEIN ESCHELICHIA COLI 191-30 HYPOTHETICAL 19 1 KD PROTEIN ESCHERICHIA COLI 191-30	1			181.13	100		T	Ī				
HYPOTHETICAL 141 0 KD PROTEIN ' ESCHENCHIA COLI 191-370	PVEID ECOL			86.133			T	T		ļ		
HYPOTHETICAL 131 1 KD PROTEIN 2 ESCHERICHIA COLI	PYEHE ECOLI	HYPOTHETICAL 141 0 KD PROTEIN		045-(14								
	PYFELL PCOLI	ILYPOTHETICAL 131 1 KD PROTEIN		35.70	102.179		Ī					

	The state of the s	ADTAI	2 4 2 4 4	ARTAS	AREAL	AREAS	ARCAG	ARCA?	7	3
PROTEIN	ORCAUSS		Т		Т		_	Т	Г	
	ESCIE MCHIA COLI	46.80			T	Ī	T		Ī	
HYPOTHETICAL 33 6 K	ESCREMENTA COLI	41.00			Ī	l	T		Ī	
HYPOTHETICAL PRO	ESCHERICHIA COLI				Ì	T	İ			
PVEIL SCOLL HYPOTHETICAL 43 4 KD PROTEIN	ESCHENCINA COLI	77.			1	t	Ì	Ì	T	
т	ESCHENCHIA COLI	9		1	1	1	1	1	T	
HYPOTHE TICAL PRO	ESCHENCHIA COLI	433-480					1	1	Ī	
ACCOUNT TO THE PROPERTY OF A KIN PROPERTY.	ESCHENCIHA COLI	199-411						1		
Ť	ESCHERICHIA COLI	175-202								
201 101 101 101	BACILLUS STEAROTHERAIOPHILUS	133-160								
TYPUZ HACSI HITTOHICHCAC WORD COLL	BRADYRHIZOBILM JAPONICUM	109-150								
LAJA MYPOTHETICAL PROTEIN	BACH FIRE MCCATCHINA	40.67								
PYGAP BACME HYPOTIETICAL 37 7 KD PROJEIN	SCHOOL MICH CO. 1	214.241								
COLI HYPOTHETICAL 39 4 KD PROTEIN	ESCRENCE COL	56.36			Ī					
PYCCB ECOLI HYPOTHETICAL 109 KD PROTEIN	ESCHEDUINA COLI				Ī		İ	Ī		
PYCIC ECOLI HYPOTHETICAL 31 8 KD PROTEIN	ESCHERICHIA COLI	200.230			Ť	Ì		Ì	Ī	
PYCIL MACTU HYPOTHETICAL 12 8 KD PROTEIN	BACILLUS THUMUNGIENSIS	20.0				1	1	1		
PVG11 PSEP11 HYPOTHETICAL 32 4 KD PROTEIN	PSEUDOMONAS PUTIDA	10:12				1	1	1	Ī	
PACIF ECOLI NAPOTHETICAL 41 4 KD PROTEIN	ESCHENCINA COLI	223.264						1		
ACCT INVESTIGATION 15 1 KD PROTEIN	BACELUS STEAROTHERMOFHILUS	£33								
ACT THE PROPERTY OF SECURITY O	(BACILLUS STEAROTHERMOPHILUS	182-209								
TYCL BACSI MITCHERICAL MAD PROTEIN	IBACILLUS CEREUS	19.124								
ALLE HYTOTHER ALL 13 AUTROLES	BACH LING GIRSTILLG	20-47								
PYCHO BACSU HYPUINEINAL PROIEIN	BACH LINE CIRCLE	1								
PYGRE BACSU HYPOTIETICAL IT I NO PROTEIN	DACE LIE CONTROL	98.125								
ACSU HIYPOTHETICAL 19 0 KU PRUIEIN		91.								
LOAD HIYPOTHETICAL 31 8 KD PROTEIN	CLOSINDIUM ACETOBOT TELEUM			116 363	Ī	T	T			١
PYGT1 STRAND HYPOTHETICAL PROTEIN 2	STREPTOCOCCUS MULANS			,,,,			T	Ī	Ī	
COLI HYPOTHETICAL 20 6 KD PROTEIN	ESCHENCHIA COLI	807					Ī	Ī		
PYNAC ECOLI HYPOTHETICAL 43 3 KD PROTEIN F	ESCHENCHIA COLI	96.09					1	1		
COLI HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	-	3							
PYING ECOLI PROBABLE ABC TRANSPORTER .	ESCHERICHIA COLI	176.203					1			
SEPU PROBABLE ABCTRANSPORTER	PSEUDOMONAS PUTIDA	74-101	8	271-10			1			
PYIMG THIFE PROBABLE ABC TRANSPORTER	THIOBACILLUS FERROOXIDANS	13:140					1		Ī	
HYPOTHETICAL 55 &	ESCHENCHIA COLI	267-297								
PYHEM DACSU HYPOTHETICAL 12 0 KD PROTEIN	BACILLUS SUBTILIS	355.53				1	1	1		
ILYPOTHETICAL PRO	ANABAENA SP	2.50					1	1		
PYILLIA ECOLI INVPOTHETICAL 16 6 KD PROTEIN	ESCHERICHIA COLI	26-84						1		
INTOTHETICAL 15 1	ESCHERICHIA COLI	43.77								
HYPOTHETICAL 14 5	ESCHENCHIA COLI	43.73								
HYPOTHETICAL PRO	LACTOCOCCUS LACTIS	167-194								
IIYPOTIETICAL 38 0	LACTOCOCCUS LACTIS	90.134	132-159					1		
т	LACTOCOCCUS LACTIS	85.148								
HYPOTHETICAL 30 7	LACTOCOCCUS LACTIS	11.104	156-183							
TOTAL STAAL HYMITHTHE AL PROPER	STAMINI OCCICOS AUMIEUS	19-11								
IVENTINE RECAL IS 3	VIDIO CIOLERAE	96-136								
HYPOTHETICAL 12.2	METHANOTHERMUS FERVIDUS	106-133								
	CLOSTNDRAM ACETOBUTYLICUM	41-83								
HYPOTHETICAL 20 (CLOSTADIUM ACETOBUTYLICUM	98-125								
IIVMITIE: TECAL 42	MITHER ACITION YILKIN	23:52	30x-253	276-310						
IIVELLIII: 11CAL PRO	LACTONACILLUS III:I. VE TICUS	93:130	137.151	 						
	PSEUDOMONAS SP	217.266								
SVIII HATTA HYPOTHETICAL 38 0 KD PROTEIN	HALOBACTERUM HALOBIUM	245-272	L							
15926 HYPOTHETICA	MYCOBACTERUM TUBERCULOSIS	19-46	L							
	PSEUDOMONAS AMYLODERAMOSA	96.9	L							
PYISE ME THE ISMI HYPOTHETICAL 48.3 KD PROTEIN	METHANOBREVIBACTER SMITHII	73.100	134-184	138.365						
-	HALODACTERIUM HALODIUM	86-113								
_	ESCHENCHIA COLI	201-119								
ऻ	ESCHERICHIA COLI	676								
Ì										

Ī.		rroughtene orquence	T.		A B R A B A B B A A	,,,,,,,				
Т	PROTEIN	ORGANISM ESCHESICH A COLL	10.00	Т				т	Т	
PYBO ECOL	HYPOTHETICAL IN I KD PROJECT	ESCUENCIA COL	143.170		l					
╗	HYPOTHETICAL JI 2 KD FROIEIN	ESCHENCIA COLI	137.139						Ī	
PYICD ECOLI	HYPOTHETICAL 31 I KD PROJEIN	ESCHEMICAL COL	217107							
YICH ECOLI	HYPOTHETICAL 62 3 KD PROTEIN	ESCREMUNIA COLO	13.1.40							
	HYPOTICTICAL 88 I KD PROTEIN	ESCHENCHIA COLI	141,75	1	 	-				
YICN ECOLI	HYPOTHETICAL 18 2 KD PROTEIN	ESCRENCIA COL	130,363	+	1	-				
YICO ECO! 1	HYPOTHETICAL 49 9 KD PROTEIN	ESCIENCHIA COLI		$\frac{1}{1}$	 -	+				
	HYPOTHETICAL I) & KD PROTEIN	ESCREDICHIA COLI	Т	103 300	2					
PYIDE ECOLI	HYPOTHETICAL SO 9 KD PROTEIN	ESCHERICHIA COLI	Ţ	7	5	+				
	INFOTIETICAL 15 1 KD PROTEIN	ESCHENCHIA COLI	26.83							
	HYPOTHETICAL 63 I KD PROTEIN	ESCHENICHIA COLI	2.10							
PYIDE ECOLI	HYPOTHETICAL 27 3 KD PROTEIN	ESCHENICHIA COLI	63.97		-					
Т	KYPOTHETICAL 49 2 KD PROTEIN	ESCHENCHIA COLI	221-248	H	_					
1	niroine in the profession	Contraction Co. 1	T	330,307		-				
	HTPOINE IICAL BU B KU PROIEIR	COCHE COMPANIES	T							
_7	HYPOTHETICAL PROFEIN	ERWINIA CHATSAN ITENI	10.77	+	<u> </u>					
	HYPOTHETICAL 34 & KD PROTEIN	ESCHEWCHIA COLI	071-00	1	1	1				
PYIEG ECOLI	HYPOTHETICAL 46 9 KD PROTEIN	ESCHERICHIA COLI	/27:32/	$\frac{1}{1}$	1					
Г	HYPOTHETICAL 24 7 KD PROTEIN	ESCHERICHIA COLI	51-38							
YIEM ECOLI	HYPOTHETICAL 13 0 KD PROTEIN	ESCHENICHIA COLI	73-105							
VIEO ECOLI	HYPOTHETICAL SI'S KD PROTEIN	ESCIERICHIA COLI	201-242 380	100-401						
evise scott	HYPOTHETICAL 19 6 KD PROTEIN	ESCHERICHIA COLI	175-202			_				
1000	DVPOTUETICAL 14 0 KD PROTEIN	ESCHENICHIA COLI	21:03	L	_					
	AND PROPERTY AND AND PROPERTY	F CHERICKIA COLI	120-154	\mid	L					
ברסרו	THE CONTRACTOR OF THE CONTRACT	ESCUEDICINA COLO	207.314							
	HTOINE ILOU SA S AND TROITEIN	ESCUENCIA COCI	70.17	1		1	-			
	HYPOTHETICAL 18 I KD PROTEIN	TOO THOUSANDER	90.161	+	 	 	ļ			
	HYPOTHERICAL 22 J KD PROTEIN	ESCRENCIAL COLI	30.00		1		-			
	HYPOTHETICAL 27.5 KD PROTEIN	ESCHEMICHIA COLI		+		-				
	HYPOTHETICAL 21.2 KD PROTEIN	ESCHENCIA COLI	2 3	$\frac{1}{1}$	1					
TYPE ECOLI	HYPOTHETICAL 10 3 KD PROTEIN	ESCIENCRIA COLI	200	+	+	+				
	HYPOTHETICAL SAIKD PROTEIN (ESCHENCIA COCI	90(-7/7	$\frac{1}{1}$	+	1	1			
THE ECOC	HATOIRE I ALL IN I AD PROTEIN	SCOREDUCT CO.		+		-	ļ			
THE ECULI	HTTOTHE IN AL 83 4 NO PROTEIN	Escurations con	١	30.00	307.134	-				
יוסא ברחרו	MATCHER MAL 18 VAC PROTEIN	Establish Col.	t	Т		+				
MINO ECOL	HATOURE IKAL BIOKE TAUTEN	Escuencia con	711.53	+			-			
PYING ECOLI	INCOME THE PARTY OF THE PROPERTY	ECCHERICATA CO. 1	77.00	$\frac{1}{1}$	1					
	THE PROPERTY OF A PROPERTY OF THE PROPERTY OF	ESCIGNICITA COLI	19.6	+	-	+	\downarrow			
LINY ECOL	INVOLUENCE IN THE REPORTED	ESCIGNICHIA COLI	11.3	+	-					
TO STATE OF THE PARTY OF THE PA	INVESTIGATION 13 9 KD PROTEIN	ESCHERICHIA COLI	13.63		-					
ייייי בנסני	NAPOTHETICAL SA KID PROTEIN	ESCHERICHIA COLI	28.71	-		-				
	LANDTHETICAL 36 KD PROTEIN	ESCHERICHIA COLI	136-163		-	+	-			
1023 213	NAME OF THE PROPERTY AND ADDRESS AS A SECOND OF THE PROPERTY O	ESCHERICHIA COLI	135.363	+		-	-			
	IIVPOTHETICAL 11 2 KD PROTEIN	ESCHERICHIA COLI	16-51	-		L				
	HYPOTHETICAL 12 I KD PROTEIN	ESCHERICIIIA COLI	214-241	l	-					
1	HYPOTHETICAL 66 6 KD PROTEIN	ESCHENICHIA COLI	Т	419-446		_	_			
PYINL LISMO	HYPOTHETICAL 16.8 KD PROTEIN	LISTEMA MONOCYTOGENES	7.7	ŀ		_				
PYISI SHISO	INSERTION ELEMENT 15600	SHIGELLA SONNE!	63.19	-	-					
PYISI STACO	ISTIO HYPOTHETICAL 43 6 KD PROTEIN	STREPTOMYCES COELICOLOR	125-152	-		-				
PYTS3 SANSO	INSERTION ELEMENT 15639	SHIGELLA SONNE!	86.180	L	L	_				
VISP BACK	SIYPOTHETICAL 43.1 KD PROTEIN	BACILLUS SP	312-339		1		L			_
PYIAG ECOLI	HYPOTHETICAL 22 6 KD PROTEIN	ESCHERICHIA COLI	11.18	_	-					
YIAI ECOLI		ESCHENCHIA COLI	18-122							
YIBH ECOL		ESCHENICHIA COLI	93.120							
YIBL ECOLU	INTOTHETICAL 9.7 K	ESCIENCIUA COLI	30-57							
РУЛЯМ ЕСОП		ESCHENICHIA COLI	112-149							
YIBO ECOLI	HYPOTHETICAL 15.7	ESCHERICHIA COLI	٦	Т	-	-				
VICC ECOLI	HYPOTHETICAL 60 I KD PROTEIN	ESCHENCHIA COCI	38-65 414	414-441 451	451.492	4				

107417814		VACA	ARFA 1	AREA 3	AREA 4	AREAS 1	AREA 6	AREA? IA	AREAL	AREAS
PROTEIN	ORGANISM		Γ		т	П	1	1		
ETICAL 60 5 KD PROTEIN	ESCRETATION COL	194-421								
HYPOTHETICAL SO 2 KD PROTEIN	Estrement Coll	911116								
MYPOTHETICAL 25 I KD PROTEIN	ESCREPAINT COLI	243.240		Ī						
HYPOTHETICAL 53 4 KD PROTEIN	ESCRENCHIA COLI	366-396	Ī							
HYPOTHETICAL 73.7 KD PROTEIN	ESCRENCIAL COL	3								
ETICAL ABC TRANSPORTER	ESCRENCHIA COL	T	\$81-159	Ī						
HYPOTHETICAL N4 2 KD PROTEIN	ESCIENCEIA COL	2		Ī				T		
ETICAL PROTEIN	ESCREMENTAL COL	T	22.3							
HYPOTHETICAL 17.5 KD PROTEIN PRECURSOR	Synerical Cold				Ī					
HYPOTHETICAL 48.8 KD PROTEIN	BACILLOS FORMOS	47.74	Ī	T				-		
HYPOTHETICAL PROTEIN	LACTURACILLUS ACIDORITI IIC	3					Ī			
HYPOTHETICAL 145 KD PROTEIN	LACTUBACILLUS ACIDOTATIOS	47.74								
ETICAL 14.4 KD PROTEIN	LACTOBACILLOS ACIONATUROS	5		Ī						
ETICAL 24 4 KD PROTEIN	SULFOCOROS SOCIA I ACCOS	١,	14.14					İ	Γ	
ETICAL 44.7 KD PROTEIN	PSEUDOMONAS PUTIDA	T			Ī			1		
OPROTEIN PRECURSOR	YERSIMA ENTEROCOLITICA		1					1		
PYLTS ANAVA HYPOTHETICAL 23 6 KD PROTEIN	ANABAENA VAMABILIS	***			Ī			Ì		
PYLUD LACLA HYPOTHETICAL 29.3 KD PROTEIN	LACTOCOCCUS LACTIS	2			T		Ī			
HYPOTHETICAL 35 3 KD PROTEIN	BACILLUS SUBTILIS	22:3	Т	Т			Ī	1		
HYPOTHETICAL 114 4 KD PROTEIN PRECURSOR	MYCOFLASMA GENITALIUM	\$6.83	29.193		201-100					
ETICAL PROTEIN	CLOSTRIDIUM PERFRINCENS	9								
HYPOTHETICAL 31 2 KD PROTEIN	CLOSTRUDING PERFUNCENS		6:6							
ETICAL PROTEIN	METHANOCOCCUS THENAIOLITHOTROPHICUS	55-10								
HYPOTHETICAL 9 3 KD PROTEIN	PARACOCCUS DENITRIFICANS	52.86						1		
ETICAL 28 1 KD PROTEIN	ANABAENA SP	171-198								
ETICAL MOTEIN	ANABAENA SP	17-165								
ETICAL 21 4 KD PROTEIN	ESCHENCHIA COLI	\$-11								
ETICAL 41 3 KD PROTEIN	ESCHENCHIA COLI	104-17	200.316							
ETICAL 15 0 KD PROTEIN	ESCHERICHIA COLI	3.5								
HYPOTHETICAL 91.5 KD PROTEIN (ESCHENCHIA COLI	17.17.								
HYPOTHETICAL 9.5 KD PROTEIN	ESCHELICHIA COLI									
HYPOTHETICAL S4.3 KD PROTEIN	ESCHENCIA COLI							1		
ETICAL 36 1 KD PROTEIN	ESCHENCIAL COLI						T			
	PHOLOGACI ENOMS ST	100								
PROTEIN: TYROSINE PHOSPHAIASE TUPH	VERSIONA BEST TOTAL BEST IN ORIG	41.100		T						
	TERSINIA PSEUDOI DEFACULOSIS	2 6	10.33	314.363						
OUTER MEMBRANE PROTEIN YOPN	TERSINIA EN LEGUCULITA	25.55	Ī	196.76						
OUTER MEMBRANE PROTEIN TOPN	CERSINA CACONOLOGENCOLOSIS		T					İ		
YORO PROTEIN PRECURSOR	HAPMOPHILUS ONE LENZAE	147.174								
TOTAL STATE	LISTERIA MONOCYTOGENES	11-11								
	PYROCOCCUS WOESE!	111.210								L
	ILAEMOPHILUS INFLUENZAE	39.66								
HYPOTHETICAL 19 9 KD PROTEIN	HAEMOPHILUS INFLUENZAE	40.79								
PYONE LIAGIN I ND PROTEIN	IIIAEMOPIILUS INFLUENZAE	47.74	100							
z	HAEMOPHILUS INFLUENZAE	199.239								
HYPOTHETICAL 13 7 KD PROTEIN	IIAEMOPIIILUS INFLUENZAE	7.34								
	HAEMOPHILUS INFLUENZAE	416-450	641-722							
	BACILLUS SUBTILIS	140-175								ŀ
HYPOTHETICAL PROTEIN	PYROCOCCUS WOESE!	66-93		1	-					1
	LISTERIA MONOCYTOGENES	¥.:								
	STAPHYLOCOCCUS AUTEUS	3	613							
	BACILLOS SUBTILIS	- A								
HYPOTIETICAL 21.2 ALD PROTEIN	STANDON OCOCOLS AURENG	14.10								
HYPOTHETICAL 23 0 KD PROTEIN	ISTAPHYLOCOCCUS AUREUS	31.60	63.60	20.05						L
			40.70	25.50				•		

Г	1074178.4	Punhamada Cananaga			ľ		1	İ			
FILENAME	ROIEIN		AREAL	AREA 3	AREAJ	AREA	AREAS /	AREAG	AREA 9	ABFAI	ARYA 6
П		AGROBACTERIUM TUMEFACIENS	П		1	т-	т-	Т	Т		
PYPAJ LEGPN IN	HYPOTHETICAL PROTEIN		861.36								
PYPAS ENTFA H	HYPOTHETICAL 13 KD PROTEIN	ENTEROCOCCUS FAECALIS	39.106								
PYPA BACAN	IYPOTHETICAL 21 6 KD PROTEIN	BACILLUS ANTHUACIS	17-11	115-162							
PYPCI ECOLI IN	HYPOTIETICAL 27 6 KD PROTEIN		1.11								
	HYPOTILETICAL 27 3 KD PROTEIN	BACILLUS SUBTILIS	114-232								
	IYPOTHETICAL 12 6 KD PROTEIN		16-43				Γ				
			19-0(
П	HYPOTIETICAL 19.7 KD PROTEIN			43.77	13-149						
	HYPOTHETICAL 14 5 KD PROTEIN		1-59								
	YPOTIETICAL 18 4 KD PROTEIN		110-137	263-290	303-340						
	HYPOTHETICAL 38 S KD PROTEIN	UGINOSA	13.53					Ī			
	YPOTHETICAL PROCESSING PROTEASE		329.356					l			
	HYPOTHETICAL PROTEIN		243.270								Ī
-	HYPOTHETICAL 13.1 KD PROTEIN		27.54				Ī				
PYPVI METTE H	HYPOTHETICAL 40.7 KD PROTEIN	Т	£ 5	301.335				T			
PYPV3 METTE H	YPOTHETICAL 22.5 KD PROTEIN	Г	š			Ī	T	İ	Ī	Ī	
PYPV7 METTE H	HYPOTHETICAL 17.3 KD PROTEIN	Т	\$8.11.9				T			Ī	Ī
PYPVB METTE H	YPOTIETICAL 49 6 KD PROTEIN	Т	333.360	389-430			T	T	Ī		Ī
PYPYB BACSU H	HYPOTHETICAL 72 4 KD PROTEIN	Т	T				T	T		Ī	
PYPZI METTF H	HYPOTIGETICAL 40 6 KD PROTEIN	JM THERMOFORMICICUM	۲	306.335	T	T	T	T	1		
PYP23 METTF H	YPOTHETICAL 33.1 KD PROTEIN	T		34-188			T	T	Ī	Ī	
PYP2S METTE H	HYPOTHETICAL 54.1 KD PROTEIN	Т	2	236-253	391.408		T	T	T	T	Ī
PYP27 ACETTE III	YPOTIETICAL 9.7 KD PROTEIN	Г	Т	Т			İ	T	T	Ī	Ī
PYRIB THEPE H	HYPOTHETICAL 18 7 KD PROTEIN	Г	63-109			T	T	T	T	T	Ī
PYTEI HALCU H	YPOTHETICAL 40 KD GTP-BINDING PROTEIN	HALOBACTERUM CUTIRUBRUM	20.51	Ī		T	Ì	T		Ī	T
PYREC SYNDS H	HYPOTHETICAL 28.7 KD PROTEIN 14		9.76				T	T	Ī	Ī	Ī
	HYPOTIETICAL 40 6 KD PROTEIN		061-091							Ī	T
╗	YPOTHETICAL SI O KD PROTEIN		428-455								
_	HYPOTHETICAL 20 6 KD PROTEIN		36.62								
PYRS6 SALTY H	HYPOTHETICAL 16 6 KD PROTEIN	UNUM	130-157								
PYRG2 LACLA H	YPOTHETICAL PROTEIN		140-167								
PTRUI METVA H	HYPOTHE IICAL PROTEIN		7	29-156							
TANA MEN VA	CHOINE HICKE HEAD PROJEIN		9								
BYEET CITY	DVBOTHETICAL ILANDINGEN	SULFOLOBUS ACIDOCALDAJUUS	<u>.</u>								
PVE TO BACKET	VPOTURE 1 21 IN PROTEIN		- 1				1	1			
	HAPOTHETICAL 11 4 KD PROTEIN 1.							1			
PYSCB YEREN H	HYPOTHETICAL YSC OPERON PROTEIN BY	DETTICA	Ţ				1	1	1	Ì	
PYSCC YEREN Y	YSC OPERON PROTEIN C PRECURSOR		T	363.390	T		1	Ì	Ī	1	
PYSCD YEARN Y.	SC OPERON PROTEIN D		5		Ī	T	\dagger	T	Ť		
PYSCH YEREN Y	YSC OPERON PROTEIN H					T	T	T		T	
PYSCH YEARS Y	YSC OPERON PROTEIN H	TOSIS	200				T		T	Ì	
PYSCI YEREN Y	YSC OPERON PROTEIN I		49.76						Ī	Ī	
_	YSC OPERON PROTEIN I	LOSIS	49.76					İ			
PYSO YEAR	YSC OPERON LIPOPROTEIN J PRECURSOR		93.136							Ī	
٦.	VAC AREA ON BEATHER !	LOSIS	90.136								
	TAC OPERON PROTEIN L		3								
	St. Of EACH PROJECT L	CULOSIS	41.68					_			
NEW SCHOOL STATE	SYSTEM SERVICE INCOME INCOME.		2								_
NEO DEST	MYNOTICAL MALENA		66-109	1	=						
	INTO THE FIGURE TANKS IN THE PROPERTY OF THE P	PENCIL DIROLOBUS ANGIVALENS	<u>.</u>								
A SUPERIOR	POTICAL PROTEIN		٦	Т					H		
PYSY3 BACSU H	PYSYS BACGU HYPOTHETICAL 19 6 KD PROTEIN		2.4	1274	706-327		1				
PYSYN METER H	HYPOTHETICAL PROTEIN	FERVIOUS	78-105	Ī	1	1	1	†	1		
PYT37 STRUR H	HYPOTHETICAL 37 I KD PROTEIN		246.771	T	\dagger	1	1	1	1	1	
					1	1	1	1	1	1	7

						ļ	}			Γ
		Parkamente Connendes								Ī
	103-178-6	I TORON ON THE PARTY OF THE PAR	Г	ATGA PAPEA	ABEAN TABEAN TAREAS TAREAN TAREAN TAREAN TAREAN	AREA S	<u> </u>	RAY ARE	717	_
	7000	ORGANISM	1	1					-	Γ
TOOL TO	CONTENT	PACTILIS SUBTOLIS	244-271	279-308			1			Ī
PYTOK BACSU	n i	Traches A BICLEYA	(11-71)		_					1
PYTHE LEPRI	HYPOTHETICAL 23 KD PROTEIN	LEFTUSTING BITTERN			-					
100		LACTOCOCCUS LACTIS					Ì			Ī
2	. 12	BACILLUS SUBTILIS	37.64				1	1	+	1
51		CORDOLASMA CITRI	103-149				1	1	$\frac{1}{1}$	T
PYTSF SPICE	- 1	A CH 115 CI B 11 15	17-64	16:69			1			
PYXON BACSU	YXXX BACSU HYPOTHETICAL ITTENDIBLIN		147.160				-	_	_	
DAY BACKL	OVER BACKLI HYPOTHETICAL 21 0 KD PROTEIN	BACILLUS SUBTILLIS								Γ
200	7131000 64 64 64 64	AACILLUS SUBTILIS	-							Ī
PYX13 BACSU III	VPOINE IN AL 28 V	DACTI LIS CIBITI IS	165-207	161-189					1	1
PYXIS BACSU	YPOTHETICAL 61 P	מענוירס פספורים	97.1	14.41				_	-,-	
DAVIG BAFEII	INVESTIGATION OF THE PROTEIN	BACILLUS SUBIRLIS	Ī	T			Ī			Ī
	CHO STREET, VI DI D	BACILLUS SUMTILIS	36.13	211.51				1	1	Ī
PYXIV BALSO	ויייייייייייייייייייייייייייייייייייייי	MACHILLIS SUBJILLIS	34.58							1
PYX20 BACSU		42 47 47 47	17.104			_			_	Ī
PYXIX ANASP	HYPOTHETICAL IN PROTEIN	ARABAEITA SI	١				ľ		_	
200	A MINDOTHERICAL 10 7 KD PROTEIN	CALDOCELLUNI SACCITAROLY IICUM					İ		l	Ī
	CALLES CALLS LANGUIGHT A PROTEIN	CALDOCELLUM SACCHAROLYTICUM	3-1-				1		1	T
777		CCCUEBICHIA COLI	¥.						$\frac{1}{2}$	1
-		ESCHOOL SOL								

WO 96/19495 PCT/US95/16733

TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

75.5	Pletif Kerch on AU Homen Protein Septentes	Т	AREA 2 AREA 2	ANIA	ARIAS	ARIA	24110		3
FILENAME			1		T				
PIAJE HUMAN	(AGALEMT)				-				
PIASS HOMAN		77.		 	-			Ī	
MANA LA MANA		26-19							
		28-55							
	Г	17.114		_					
NAME OF THE PARTY	PLACEASS I MISTOCOMPATIBLE TO SECURITY AND CHAIN	11:114							
PIA24 HUMAN	Т								
PIBOS HUMAN	OCCUPATIBILITY ANTICEM BY BUILD ALTON CONTRA		10.10	-					
PIBOS HUMAN	٦								
PIRIO HIMAN	HAIN	84-113		-					
	THE ACT ACC ALM TO THE HATTER THE TAN THE TOWN TO BE 1501 ALPHA	#: E2						1	
NOW THE	THE CONTRACTOR OF STREET	76-107						_	
	ILA CLASS I RISTOCOMPATIBLE ACTIONS TO THE CHAIN	111.48		-					
PIBIS HUMAN				+					
		2						Ī	
	-	24-115				1		1	
NACE ACCRECA	~	84.115							
PIB23 HUMAN	IN A CLASS I HIS IOCURA HIBITITI ANTIDER, B. J. B. J. C.	į						-	
PART FURAN		2016		+					
PIRT MINAN	IN A CLASS I HISTOCOLO A TIBILITY ANTIGEM, B-35 B-3509 ALPHA CHAIN	14.115		1					
	+	#: E						-	
NESS PROMON	THE CLASS THIS TO COMPANIES TO A MITCEN BUT OF 100 AL PRIA CHAIN	84:15		_					
FIB27 HUNCAN	ILA CLASS HUSIOCOMO HIBITI I CONTOCI DE CONTO	211.78							
PIB28 HUMAN	_			-	ļ				
PIBIS HUMAN	MLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-37 B-3701 ALPHA CILAIN	2	1						
PIRIZ MIMAN	FILA CLASS I HISTOCOMPATIBILITY ANTIGEN. B-19 B-1902 ALPHA CHAIN	17.114							
NV NV	IN A CT ACCT HISTOCOMO TIBILITY ANTIGEN, BW-60(B-40) B"-4001 ALPHA CHAIN	2.3							
101	TEN STATES THE CHAIN	84-115							
PIBM HUMAN	MACACLASS INISTICUTATION CONTRACTOR AND AND AND AND AND AND AND AND AND AND	14.115		 -	_			•	
PIB35 HUMAN				-					
PIBJ6 HUMAN	III A CLASS I HISTOCOMOATIBILITY ANTICEN, B-40 B *4004 ALMIA CHAIN			1					
PIRTS HIDAAN		14-115		1				1	
PIB10 MANA	-	11.114							
	7	111.98							
FIB40 HUMAN	TA CLASS I INSTITUTE OF THE TAY ANTICEN BU AAM 19 B 4402 AL PILA CHAIN	17-114		_	L	L			
PIECE HOMAN	Τ	13.114		-				7	
P1842 HUMAN	Ť	14:115							
PIB43 HUMAN	7			+		-			
PIBH HUMAN	_				-				
PIBAS HUMAN	l	2			+	-			
NACK AGIT	-	2-12		+					
PIR47 HIDAAN	т	17-114							
NALATIN ELECT	۲	84-115							
NAME OF STREET	1	87-114							
	+	87.114		_					
FIBSS HUMAN	-	13:14				_			
VIBSO HUMAN	-	87.114							
PIBST HUMAN	-1								
PIBSE HOME	_			<u> </u>					
PIBSO HUMAN	_	•							
PICE REMAN	F	17:114	1	1					
PICOS HEDAAN	Т	17-114							
MANUEL PROPERTY	۳	13:114		_	_				
7	+	87-114		_					
	Ť	11:10							
	7	9.114		<u> </u> -	_				
	✝	17:114							
	Т	17-114			_				
ALC IS RUMAN	7	+=							
	┪	-		<u> </u>	-				
73A6 HUMAN	_	97.			-	L			Ĺ
TAKA HOMAN		¥	79.106		 -	ļ			
PZAAB HUMAN		177.218	T	_		ļ			
PARA HUMAN		1		+	-				
TAIL MUNAN	7				-				

	1971/7814 Mail Search on All Haman Protein Sequences		Н							
EULHAME	CROTCH		4 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7 7 7 7 7 7	1	4	4		3	1
PAS HUMAN	FOUNTAINED TRUITING TO THE PROTEIN BAND 4.2	8	216.545	T						
P4F2 HUBAN	FINC) (LYMPHOCYTE ACTIVATION	311.333		H					-	
PSHIE HUMAN	•	300-110								
PSHIF HUMAN	S-HYDROXYTRYPTALGNE IF RECEPTOR (S-HT-1F) (SEROTOMIN RECEPTOR)	132-353		1		1				
PSH2A HUMAN	S-HYDROXYTRYPTAAMME 2A NECEPTOR (3-HT-2A) (SEROTONIN NECEPTOR)	*		1	1					
PSH7 HENCE	SHYDROXYTAYPTAMINE PRECEPTOR (S.HT.) (S.HT.X) (SEROIONIN NEC PROR)			\dagger						
PAIAC HUMAN	ALTHA-I-ANIICHTRO INTESIN PROCESSON (ACT)	T		†						Ī
TAING HURAN	ALTHAS I ANTITE VIEW BEING TO THE UNIT PROTECT ON MINITORIAL PHA. I.	164.202		\dagger						
NAME AND ASSESSED.		161.197		T	Ī					
PATAR MINAN		Ť	165-395	T	T					
PANT HIMAN		T								
NAME OF TAXABLE	ALPHA-3-ALACEDCE CORIL IN PRECINSOR (ALPHA-3-M)	1	119.349	1003-1112	1407-1479				•	
PA4 MINAN	ALZHEIDGERS DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II)	SF12								
PAACT HIBMAN	ALPHA-ACTIVITY OF CROSS LINKING PROTEIN)	93.119	120-747						-	
PAATM HEBAN		96-136								
PABRY HUMAN	DEDOTHELIAL ACTINABINDING PROTEIN (ABP. 380) (NONMUSCLE FILANIN)	81-19	119-147	1604-2633						
PACI3 HUMAN	-	106-333							1	
PACIS HUMAN	-	15-71	$\overline{}$	968-700						
PACDE HUMAN		П	\Box	113.340						
PACET HUMAN	_	٦	Ť	676-710						
PACE MUMAN		2	200-23	282					ŀ	
PACHA MUMAN		2							-	
PACHE HUMAN	ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON CHAIN PRECIRSOR	7								
PACHO HUBAN	ACETYLCHOLDIE NECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR			1		1			-	Ī
ACIO MUNAN	VELTICIAL ACETACAMONING MECETICA PROJEIN, BELANCHONNI (PROMINE)	Ī,		T						
1	ACK DESCRIPTION OF THE STATE OF	18.30							Ī	
PADTI HIBAAN	-	162-189								
PADTI HULLAN	ADP ATP CANALEA PROTEIN, LIVER ISOFORM T2 (ADPIATP TRANSLOCASE 1)	061-(91							•	
PAKTO HUMAN	A-KINASE ANCHOR PROTEIN 19 (AKAP 19) (CAMP-DEPENDENT PROTEIN KINASE	_	31718							
PALLY HUBAN		36-63					Ì			
PALFO MUMAN	FRUCTOSE BISPHOSPHATE ALDOLASE (EC 4.1.2.13) B (LIVER)	3:13	1							
PANDI MUNTAN	AND DEAMINASE I (EC 1.1.4 6) (MYOADENYLATE DEAMINASE) (ANP DEANINASE	9		1						
PAND HUMAN		49.76	7	170			Ī			
A HOW	ALGROPET IDASE N (EC.1.4.11.3) (MILKOSUMAL AMINOTER I DASE) (URISO)	1	200	04.07						
PALCE MINA	ALE PALA JA A CROCK ORIGINA RECEPTOR ASSOCIATED PROTEIN PRECURSOR	Т	263.290		T					
PANCE HEMAN		Т								
PANK! HUMAN		613:11	1004-1031 1617-1644	617.1644						
PANKE HEMAN		1844-1831								
PANKC HUMAN	N AKKYUN, BRAIN VARIANT 2 (AKKYUN B) (ANKYUN, NOKRAYTHROID)	=1								
PANDA HUMAN	4 ATRIAL MATAUMETIC PEPTIDE RECEPTOR A PRECURSOR (ANP.A) (AMPRA) (GC-A)	┪	23-652	1	1					
PANTE MEDIAN	I ATRIAL NATRUMETIC PETENDE RECEPTOR B PRECURSOR (ANY-B) (ANPRB) (GC.B)	10.037	+	†						
PARTI HUMAN		2 4	111,701	1	T					Ī
TAPAC HUMAN	ANNEALY II (LACCONTIN II) (CALA ACTIN THEAT I COLIN AND PROTEIN III)	215.262		T	T					
PANTA HIBAN	ANGENDA VI CHOCOLITO VI) (PA) (PROTEIN III) (CHOCOMOBINDIN 20)	۲	626-653							
PANTI MINAN	_	Ī	37.5				Ī			
PAOPA HUMAN	_	T	26.10							
PAOFE HERAN	-	64.03	П							
PAPAI HUMAN		33.64								
PAPB HUMAN	APOLIPOPROTEIN B-100 PRECURSOR (APO B-100/APO B-41)		1073-1100 1353-1360 1524-1584 2074-2113	333-1360	324-1384			3132-2159 2181-2215 2240-2231 2360-2369	1240-1211	2360-2369
		1464-1507	2529-2559 2150-3000	100.3000		3480-3570	1620-3654	4040-4074 4090-4120	4090-4120	1354167
		4274-4701	4774-4301 4397-4438 4453-4492 4477-4344	17600-600	10,000]]]

PCGENE 1103-178-4 Ma	197a 178a 6 Maid Search on All Iluman Pratein Sequences	П		•		1 1		\Box	\mathbf{r}	
7		7	74.17	Z V S	A SEA	S PRIOR	1	4	1	N W
ŧΤ	APOLIPOPROTEIN CILI PRECURSOR (APO-CIL)	45.172	417.651	134.161	1795-1822	3172-2212 2572-2609	1972.2609	T	+	
CHACK MANAGE WAS THE STATE OF T	APPLICATION OF THE PARTIES AND FILE.	Т	Т							
77	APOLITOPA UTERNAT PRECUISOR (EC 3 4 21) (APO(A)) (LP(A))	6448-4475				П				
	LS AND KIDNEY	19.73								
_	BETA. ADRENGIC RECEPTOR KONASE I (EC 2.71 126) (BETA-ARK-I)	133-553								
PALLY HUMAN ARGINENOSU	CCINATE LYASE (EC 43.21) (ARGINOSUCCINASE).	69-103								
	SOFFICEPTOR MUCLEAR TRANSLOCATOR (AUNT PROTEIN) (DIO	223-250								
PAIRC HIMAN BETA ARRESTIN 2	T.W.1.	215-243	33.33			1				
Į	ALLESTIN (RETINAL S.ANTIGEN) (48 KD PROTEIN) (S.AG).	£	Ì						+	
	ATYLAMME N-ACETYLTIANSFERASE, MONDMONPHIC (EC 2.3.1.5) (MMAT)	2							1	
PARYZ HIMAN ARYLAMINE	ARYLAMINE N.ACETYLTRANSFERASE, POLYMORPIUC (EC 2.3 i s) (PMAT)	╗			İ				Ì	
PASNS_HUMAN ASPARAGINE	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.54) (TSH CELL	1	147.374						Ť	
PATCD HUMAN CALCIUM-TR	Ansporting atpase sakcoplasmic reticulum type (EC) 6 i 38).	20-19			Ì				1	
PATCE MIMAN CALCIUM-TR	ANSPORTING ATPASE ENDOPLASMIC RETICULUM TYPE (EC 3 6 1 38).	2.58							İ	
PATEL HUMAN TRANSCRIPTI	TRANSCRIPTION FACTOR ATF-1 (FRAGMENT)	0 0							-	
PATES HUMAN TRANSCRIPT	TRANSCRIPTION FACTOR ATF.) (FRAGMENT)	3	Ì		-	İ		:	•;	_
	TRANSCRIPTION FACTOR ATF-5 (FRAGMENT)	2	i				-	-	-	:
	TRANSCRIPTION FACTOR ATF 4 (FRAGMENT).	14.68							†	Ī
PATFA HUMAN TRANSCRIPT	TRANSCRIPTION FACTOR ATF-A AND ATF-A-DELTA	31.34			1		Ì			T
_1	ATP SYNTHASE B CHAIN, MITOCHORONIAL PRECURSOR (EL.) B.1.34)	6			T	1	1		Ť	
_	NUCLECTAL PROSTRUCTOR BLACK COLLECTROSMAN (NUMA 1927)	303.110	145.333			T		Ī	T	
PEAK RUMAN BEIN-E-ALM	BETANGALENCE MELETING TO VERBOND BAND AT 100 BEOTERN BAND I							Ī		Ī
_T	CARE PROJECT (PROFEST INVOICEMENT CARE PROJECT) (STORY)	5717	35.50	409.616					-	Ī
PRINT HIMAN ERYTHROCY	SAYTHAN OF VIEW BAND & DATE CRAIL MEMBRANE PROTEIN	9	┰		T	Ī				
		100	110.117	733.807					-	Ì
	NO PROTEIN BCL-2-BETA	178.205								Ī
	(MCGF.13 KD)	3	Ī						ŀ	
	AREA MODIT CLISTER REGION PROTEIN	784-825								Γ
72	BETA-GLUCTACHIDASE PRECURSOR (EC 3.2.1.31)	344-280	<u> </u>						-	
	BONE MORPHOGENETIC PROTEDY 2 PRECIDISOR (BMP-3) (BMP-2A)	216-250							•	
	BONE MONTHOGENETIC PROTEIN 3 PRECURSOR (BMP-3)	102-329								
	HOGENETIC PROTEIN 6 PRECURSOR (BAD-4)	174-301								
	HOGENETIC PROTEIN ? PRECURSOR (BMP-?) (OSTEOGENIC PROTEIN I)	192-219								
Ţ	×	74.31							1	
-+	BACTELICIDAL PERMEABILITY INCREASING PROTEIN PRECURSOR (BPI) (CAP 51)	20.00	Ī				Ì			
PBKS) HUMAN BOMBESIN R.	BOWGESTA RECENTOR SUBTITIES (BASS)	100	711.151							
_	A CO PROTEIN PACE I TRANSPORTED CENE I PROTEIN	3						Ī	T	
-	C.I. TETRAHYDROFOLATE SYNTHASE, CYTOPLASHOC (ACTIVILENETETRAHYDROFQ)30-363	130-363						T	Ī	
-	MAIC CLASS II THAMSACTIVATOR CITA	931.948								
•	COLLAGEN ALPHA I(DD) CHAIN PRECURSOR	120-150								
PCAIR HUMAN COLLAGEN	COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.	341.364								
	LCRIM-BINDING PROTEIN (CABP), AVIAN-	¥:2								
	7	23.750								
	JP) (UVOMORULIN) (CAM 12010)	136.865						1	1	
	NEURAL CADHEADN PRECURSOR (N-CADHEUM)	77	86.5			1			1	
	- 1	1) Second					1		1
	ACTUR-KELATED PROTEIN 8) (MUC-8)	2					1		1	T
	CALCITORIN RECEITOR PRECURSOR (C.1-R.)	2 2	707 577	Ī	1			1	1	
PCAMA HUMA CANTILACE	CALTELAGE MATRIX PROTEIN PAECUASOR.	161.188	K - 10							
_	CALPAIN 2 LANGE (CATALYTIC) SUBUNIT (EC.) 4.23 17) (CALCIUM-ACTIVATED	257.284	\$02.579		Ī		T		T	Ī
-	CALPAIN P94, LARGE (CATALYTIC) SUBUNIT (EC 3.4 22 17) (CALCIUM-	674.701				Ī	T		İ	
	PLACENTAL CALCIUM-BODDNO PROTEDI									
PCAP HUMAN ADENYLYL	ADENYLYL CYCLASE ASSOCIATED PROTEIN (CAP)	111.136	163-197	331-355						

PCGENE	107117816 Medi Search on All Ituman Practa Sequences			1		-23.004		- 6 4 4 6 4	-91.30	
PCART HEMAN	CALESTINIA 29 KD CALENDINI	1 × ×		}		1			Ţ.	
PCASE HIBRAN	BETA CASEN PRECINSOR	1	T							
PCATA HEMAN		422-456							-	
PCATO HIBAAN		23:32								
PCATH HUMAN	CATHERSIN H PRECURSOR (EC 3 4.22 16)	89-14								
PCATT. HUMAN	CATHEPSIN LIPRECURSOR (EC 3.4 22 15) (MAJOR EXCRETED PROTEIN) (MEP.)	278-309								
	CATHEPSIN S PRECURSOR (EC 3.4.22.27)	10-37	43-169							
	CCAAT-BINDENG PRANSCRIPTION FACTOR SUBUNIT B (CBF-B) (NF-Y PROTEIN	15-52	138-165							
	CORTICOSTEROID-BONDING GLOBULIN PRECURSOR (CBG) (TRANSCORTIN)	771-98	П							
	Г	66-139	178-305	319.346						
	CALBOXYPEPTIDASE H PRECURSOR (EC) 4.17 (0) (CALBOXYPEPTIDASE E) (CPE)	355-382							_	
	CDC21 HOMOLOG (PI-CDC21) (FRAGMENT)	33-63								
	PROTEIN CDC17HS.	109-240								
	TRANSCALPTION DITTATION FACTOR TFILD 350 KD SUBUNIT (TBP-ASSOCIATED	1298-1342							İ	
NAME OF	MONOCYTE DIFFERENTIATION ANTIGEN CDIA PRECURSOR IMPELOID CELL-SPECIF	142-169							ŀ	
PCDIA HUMAN	T-CELL SURFACE GLYCOPROTEIN CDIA PRECURSOR (CDIA ANTIGEN) (T-CIII.	135	101.101						j -	!
POIL HUMAN	CDIE KIDIAN IT-CELL SUNFACE GLYCOPROTEIN CDIE PRECURSOR (CDIE ANTIGEN) (R2G1)	33.104	İ		1			Ī	ļ.	
PCD26 HIMAN	BLYNGHOCYTE ANTIGEN COXO (B.L.YNOHOCYTE SURFACE ANTIGEN BI) (LEU. 16)	226-255								
_	CONDITION PRECIETOR	236-255					Ī			
	TOTAL SURFACE ANTIGEN COS PRECURSOR (T.CELL. SURFACE ANTIGEN	100	T		Ī		i		-	!
PCD14 HIDAAN	NEMORGIETIC PROCENITOR CELL ANTIGEN COM PRECURSOR	74-108	İ							
PCD17 MIMAN	LEGICOCYTE ANTICEN (D)?	121	T				Ī	T		
_	DTEIN COLGAMMA CHAIN PRECURSOR (T-CELL RECEPT	3.34		Ī						
		Ì,	111.313	Ī	-		Ī	Ì	-	
NAME OF STREET	COM ANTIGEN EDITIES IN FORM PRECISOR (COMPRISON PRACOCYTIC	1			T		T	T	-	
PLA HIDAAN	THE LANGE ACTION OF PROPERTY OF PRECINGOR OF CRITICAL SINGRACE ANTIGEN	۴	26.267			T	Ì	Ī		
MINAN	PERMOCYTE SURFACE ANTICEN CDS)	Ī.					Ì	Ì	ŀ	
PCD72 HUMAN	B-CELL DIFFERENTIATION ANTICEN CD72 (LYB-2)	111.17	T					Ī		
PCDKS KIRAAN	CELL DIVISION PROTEIN KINASE 1 (EC 2.7 L.)	5.32							ļ.	
PCDKU HIGKAN	CELL DIVISION PROTEIN KINASE 3 (EC 2.7 I) (KIMASE PSALRE)	27.5					Ī	Ī		
PCEBB HUMAN	CCAATIENHANCER BINDING PROTEIN BETA (CEBP BETA) (NUCLEAR FACTOR	396-330							-	
		\$65-898							-	
	CENTRONGRE PROTEIN C (CENP-C) (CENTRONGRE AUTÖANTIGEN C).	П		П						
	CENTROMENIC PROTEIN E (CENP-E PROTEIN)	172-399		209-055	115-752	521-192	850-884		963-995	1040-1107
				1250-1277 1340-1367		1440-1481	1486-1556	1646-1660	1684-1724	1808-1846
		ੜੀ	1890-1917	1940-1988	1021-1048	216.2316	1440-2478	2498-2563		
PCERU HUMAN		93.940	1	Ì						
PCETP HUMAN		7	Т	7						
NO THE HUMAN		7	W. 204	22.66	0.21					
P.C.C. HUMON		67017								
PULL HUMAN	CTSTATHUMINE UNMANATARE (EL 4.4.1.1)		1	1						
	CHLOROBEUME MEDULI (ASE (EU. 1.1.1.22) (LUA)							1		
	CHONOLOGIA AND AND THE PROTEIN	Ī,	Т				Ì			
PCDIA HIMAN	SODITING CHANGEL PROTEIN CARDIAC AND SKELETAL MUSCLE ALPHA-SUBUNIT	1	041.970	Ī			Ī	T		
PCI CA HIBAAN	_	т					T			
MOLCO HIBAAN		3:13	T				T			
PCLCY HUMAN	CALCYCLEN (PROLACTEN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH	9.30 6.30								
PCLUS HUMAN	CLUSTERIN PRECURSOR (COMPLEMENT-ASSOCIATED PROTEIN SP-40,40)		87:50	367.384			ľ			
PCMON HUMA	CHROMOGRANDI A PRECUISOR (CGA) (CONTAINS: PANCREASTATIN AND WE-14)	93.120	130-657	Γ					Γ	
PCYTT HUMAN	-	П				Γ				
PCORT, HUMAN	_	95.62	101-56							
PCOS HUMAN	COMPLEMENT CI PRECURSOR.	П	193-630	137.867						
PCO HUMAN	COMPLEMENT OF PRECURSOR	-	7	T						
NO HIGH		Т	3	8,026	200.00	1				
200	CONFIDENTIAL CONTECTIONS	200	†	T	Ī		1	1	T	1
P.O. nomer.		147.45.	1	1		1	1	1	1	

PROJECT		346-373							
ESTEGNATION TO THE TATAL T		6.173							
1, it it is is is so such that is it is it is is it is is it									
14 i 1) [(436-1) [ETILANOL INDUCIBLE] WITAJE (ANDIOVIL TALANSTEALER IP PECURSOR 11 FALMITOYT ITAJASTEALER IP PECURSOR 11 FALMITOYT ITAJASTEALER IP PECURSOR 14 ROMATASEL (CC 1.14 to 1) (ESTROGEN 14 FR PRECURSOR (CM.) (COMPLEMENT CLD RECEPTOR) 91 FR PROTEIN GHC PAOLER 19 FR PROTEIN GHC PAOLER 19 FR PROTEIN GHC PAOLER 19 FR PACH SON (CR. 8P1 FR PACH SON (CR. 8P1 FR PACH SON (CR. 9P1 F									Ī
MTASE (ALDACONIA) NOTOCHONDRIAL PRECURSOR PALAUTOYT.TIA.YSEBASE II PRECURSOR ANACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 94 9) (STERROD 11-ALPA-1 TO MACACIP (EC. 114 94 94 94 94 94 94 94 94 94 94 94 94 94									
TALMITOYL TIKANSFEKASE II PRECURSOR, 440-CIT) (EC. 11 or 9) (STEROUD TI-ALPHA-1 240-CIT) (EC. 11 or 10) (ESTROUD TI-ALPHA-1 251-FRECURSOR (CRU) (COMPLEMENT CID RECEPTORY) 351-FRECURSOR 351-FRECURSOR (CST) (ARCS) 351-FRECURSOR (CST) (ARCS) 351-FRECURSOR (CST) (ARCS)	36-237	420-447						1	
496CI) (EC 1.14 99) (STEROID 11-ALPMA- 23 ARATASE) (EC 1.14 19) (SESTROGEN 23 BE PRECISSON (CR.) (COMPLEMENT (ID RECEPTOR) 24 ES PROTEINS (MC) (COMPLEMENT (ID RECEPTOR) 24 ES PROTEINS (MC) FROM (CR. 9.7) 24 ES PROTEINS (MC) (COMPLEMENT (MC) 24 ES PROTEINS ES PROTEINS (MC) 25 ES PROTE	34-239	-							
ROMATASE (ECT.14 14 1) (ESTROGEN PET PRECURSOR (CU.) (COMPLEMENT CID RECEPTOR) 99 THE PROTEIN GRAPE BOTTOR OF THE BOTTOR AND CREB B) FOUNDED FROTEIN CREB BY BODING PROTEIN CREB BY RECA. RECA. RECA. RECA. RECA. RECA. RECAR OF SUBUNIT (CSTF 50 KO SUBUNIT) (CF-1 CTTOR. 10 RECURSOR (CSF-1) (AVCSF) RECATOR TO SUBUNIT (CSTF 50 KO SUBUNIT) (CF-1 CTTOR. 10 RECURSOR (CSF-1) (AVCSF) RECATOR TO SUBUNIT (CSTF 50 KO SUBUNIT) (CF-1 CTTOR. 10 RECURSOR (CSF-1) (AVCSF)	34.271								
FE T PLECURSOR (CRU) (COMPLEMENT CID RECEPTOR) 91 FINDING PROTEIN OF CREB-A AND CREB-B) FINDING PROTEIN CRE-BP1 FINDING PROTEIN CRE-BP1 FINGE-BP1	101-1013	_							
ER PROTEIN (ACC PROTEIN). SIGNAL PROTEIN CRE. BF1 RSGR. N.(S.1) N.(S.1) N.(S.1) LTON, 10 KD SUBUNIT (CSTF 90 ROUNLY) (CF-1) CTON, 10 KD SUBUNIT (CSTF 90 ROUNLY) (CF-1) CTON, 10 KD SUBUNIT (CSTF 90 ROUNLY) (CF-1)				<u> </u>					
CREB-A AND CREB-B) SOR (CSF-1) (MCSF) 9 KD SUBUNIT) (CF-1	-	379-420 6	13.471	124.754	163.790				
	84.135		ľ					`	
	310-414	T							
	f	12.00							
\prod	٥		Ī	:	į	: :	:		
Т	9	T							
		Ť						-	
1		İ	Ī					-	
	60,313	Ì							
	01.10					Ī		-	
Ť		İ						T.	
		İ	T						
T		Ť				Ī			
	T	Ť	30.5			T			
	T	T				Ī			
		T	T					-	
		1	Ī	T					
		T	1					1	
	7	Ť	7	171				1	Ī
ONTAINS MCF2)	+	7	T					ŀ	
	4	Т	✝		Т	177, 117	Т	Т	410.474
	7	Ť	T	100.000	Т		Т	Т	
	Ţ	7							
	1	7	Т	Т	100.		1901 1998	1744.1364	1414.1474
				9	1104 1001	1013-1019	170, 7101	1170071	
	ê	2		N . 7 . 7 . 7		10.57	5	****	
	1	7	91						
	Ĵ	T.						T	
7)	+	i i							
	Ť								Ī
	T	•							
T	T	101							
I	Τ	Т	107.691						
Ī	Ī.	T	T						
Ī	t								
	523-550								
ED RECEPTOR 2 (EB12)	2.4								
	105-132								
	===								
	Ť	40-467							
	47.74								
_	=								
		146-273							
POLYPROTEIN	387-730								
		Т							1
	1	1	(117-67						Ī
TED PROTEIN PRECUASOR (EAC 71)	ļ	Т							T
	2/2-5								
[2] [2] (1년 전 전 1년	8	TENDY ED PROTEIN	ED PROTEIN	TENIN ALPHA-1) 610-119	TENN ALPRA-3 681-311 TENN ALPRA-3 681-312 TENN ALPRA-3 681-313 TENN ALPRA-3 681-314 TENN ALPRA-3 681-314 TENN ALPRA-3 681-314 TENN 3) (CX3) (GAS JUNCTRON 31 KD 11-144 TENN 3) (CX3) (GAS JUNCTRON 31 KD 11-141 TENN 3) (CX3) TENN 3) (TENN 3) (TENN 4)	Third All Protein Third	THE PROTEIN THE PROTEIN THE PROTEIN	ENGLAND COSTENS Control Cont	TENTALE AND TENTALE TE

П		П						_		
FILE NAME PROTEIN		7	3	OREAL ORIGINAL	7	ARIA!	4	All All All	SEA.	ABIA'
		Т			Ì	T	T	-	†	
-		99:					\dagger		†	T
T		182.309					l		†	Ī
12		29.56			Ī		-		l	
PEZRI HUMAN (EZRIN (PRI) (GYTOVILLIN) (VILLIN-3)		119-146	351.392	402.429 5	512.539		-	-		
		2103-2137								
		171.908	1007-1034	1194-1230		-	-			
-		271.758								
-		П	249-301	106-111					L	
_	Г	\$11:18								
PFCEA, HRMAN HIGH AFFINITY BOANNOCLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (FCEN)	PECEPTOR ALPHA-SUBUNIT (FCERU)	140-174				-	\mid		T	
-		310-337				t				
_		131-165	151-120						†	
PFIBB HIDNAN FIBRINGEN BETA CHAIN PRECURSOR		149-116							-	
+=		T	125-160			ļ	\mid		-	
+=		T	25.160		T			+	1	Ī
+		8612							+	
+-		72.209				1	\dagger	+	+	
PINDS HUMAN DESCRIPTIONE MONOOXYGENASE (N.OXIDE FORMING) 3 (EC 1.14.13.8)	XIDE FORMING) 3 (EC 1.14.13.8)	184.218	356.203	301-326	Ī		t		İ	
-		Г			Ī			-	İ	
ݗ		133-160			Ì		T	+	+	Ī
+=		49-180			Ī	\dagger	\dagger	\dagger	t	Ī
-		2			T	T	+	\dagger	+	T
-		1			T		\dagger	\dagger	1	
PFSHIR, HUMAN FOLL ICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R		364.395			T			\dagger	†	
PFUCO MUMAN TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (EC 12 i SI) (ALPHA-L-FUCOSIDASE	UCOSIDASE	304-335						l	1	
PPUMPH HUMAN FUNARATE HYDRATASE, MITOCHONDRIAL (EC 4 2 1 3) (FUNARASE)		15772			T		r	-	<u> </u>	
-	2	3.5				-				
		146-173			ļ			+	+	
Ť		16.50						-	-	
	П	111.315						-	l	
		154-201					-			Ī
	LPHA-I SUBUNIT PRECURSOR (GADA(A)	110-111							 -	
	RSOR (GABA(A)	311-355				-	-			
_		39.103				-		-	t	
_		22-49					-	\mid		
		13-49					-		r	
PGBAK HIDAAN GUANDRE MUCLEOTIDE-BINDING PROTEIN C(R), ALPHA SUBUNIT (C(I) ALPHA-1)		13-49				-	-	-		Γ
PCBAS MUMAN GUANDNE MUCLEOTIDE BINDING PROTEIN G(S), ALPHA SUBUNIT (ADENYLATE							-			
PGBAT HUMAN GUANTRE RUCLEOTIDE BINDING PROTEIN G(Y), ALPRA SUBURIT (ALPRA-11)		<u>~</u>						_	-	ĺ
PLABO HUMAN GUAVINE NUCLEO ILIZ-BINDING PROTEIN ((I)X(S)X(T) BETA SUBUNIT)		┪							H	
		7	32.55 23.55	289-316						
-	.1	9,411			1					
COST, NOTON COLONIA CO	Ť	╗	7	7	╗					
٦,		Т	29)-120	367.394	36-423	647-674				
		24.50	7	+	1	1				
		¥1.0	1	+	†	1	+	-	1	Ī
		¥ .	1	1	1	1	+	-		
-		9	1	1	1	1				П
		97:10	Ī	+	1			Н		П
-		Ť		+	1	1			П	
		97.6	200	110-101						
-		Τ	116776	1	†	+	+	+	+	T
		Τ	144.13	\dagger	\dagger	\dagger	\dagger	+	+	T
		1		1	1	1	1	$\frac{1}{2}$	1	7

PCGENE	1671 1784 Meil Search on All Human Prairin Sequences		1 1 1 1	ABEA 3 AR	ANTAG	AREA 5 A	AREAS	AREA?	AREAL	AREA?
FILENAME	PROTEIN	Т			_					
POLY2 HUMAN	SERING HYDROXYNGTHYN TRANSFERASE, MITOCHONDIAL (EL. A. 1. 4. 1) (SERING	T	\$98-625	-						
PCRTS HUMAN	18 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GIV 18) (IMMIUMULUBULIN	T	341.366							
PORAZ HUMAN	GLYCING RECEPTOR ALPHA-3 CHAIN PRECURSUR	Ţ	91.89		 					
PORAV HUMAN	GRAVIN (FILAGMENT).	١		<u> </u>	f	-				
PORFE HUMAN	GROWTH HORMONE: NELEASING HORMONE RECEPTOR PRECURSOR (UND) RECEPT		t	+	t					
POTHE HUMAN	GLUTATHIONE S-TRANSFERASE HA SUBUNIT 2 (EC 2.3 1.18) (OLIVATA)	ţ	1001							
POTTA HUMAN	GTPASE ACTIVATONG PROTEIN (GAP) (RAS PZI PROTEIN ACTIVATOR)	+	+		T					
MOTE HUMAN	GLUCOSK TRANSFORTER TYPE I, ERYTHROCYTE/BRAIN.			ļ	1		İ			!
POTEL HUMAN	GLUCOSE TRANSPORTER TYPE 3, BRAIN.	111.10		+	\dagger	\dagger	T		T	
POTTER INTELLAN	N.RESPONSIVE.	290-317		1	1		1		-	
		61-10				1	j		1	
THIS HOUSE		33:104								
PHIA HUMAN		10.101	-							
PHIB HUDAN			ł							
PHIC HUMAN	HISTONE HIC (HI 3)	70.	+		-	İ			İ	i
PHILD HUMAN		20-101	1		1	+	Ì			
MANUEL PRINT	TIM BACKSIA	74-109							-	
THE PERSON	-	10-01			<u> </u>	1			-	
THE PARTY OF THE P		20-47				1				
PAUS HUMAN	_	20.47								
PH2B HCBCH	MUSTONE HAB (HAB I A)	142.169	\mid		-	l				
PHA25 KUMAN		10.00					l			
PHONIX HOMAN		11.00	1		t		ľ			
PHEST HERACAN	HEA CLASS II HISTOCOMPATIBILITY ANTICEN. DRIVE) BEIN CHAIN FRECONSON.				t		İ		-	
PHONO HOUSE	HEA CEASS II HISTOCOMPATORILLY ANTIGEN, DRWY) BETA CHAIN FREE UNSUR	2		+	†	T	İ			
MERSS HEDMAN	HELA CLASS IL HISTOCOMO AT IBILITY ANTICEN, SB BETA CHAIN (FTAGMENT)	3	1		1	1	1		-	
MANAGE COLORS	HEPARIMARING GROWTH FACTOR PRECURSOR! (NIBGF-1) (ACIDIC FIBROBLAST	102-129	1		1	1	1			
MAN CONTRACTOR		16-19								
TOTAL STATE		84-15	159.186						1	
THOUSE COMPANY	AND THE PERSON OF THE PROPERTY OF THE PERSON	264-312								
ACE HOME	TO THUI ELY (NOT BUTCHES) THE CONTRACT OF 1 311 A BUNCHMANNING N. III	34-110		-	l					
PHEMA HUDAN	UNOPOURING COMPANY STRINGS (EL C. T. T.) UNOTOWN I MANAGEMENT	8	+		İ					
PHEPS HUMAN	HEPARIN COFACTOR II PRECUISOR (RC-11) (FRU EASE DETABLEON ECOSES 11 1)	2	\dagger	l	T	T			-	
PHERS HUMAN			ł	$\frac{1}{1}$	T					
PIEXA HUMAN	BETA JEXOSALUNDASE ALPHA CHAIN PLECURSOR (EC.).21.33) (P.ACETTL.		1	1	†	1	T			
MEXI HIDAN		200-012	Ì	$\frac{1}{1}$	†	Ì	T			
HOCK! HEMAN		176-2112		1	1	1	1			
POUT KOKY		2	1	1		1	1			
THO HUMAN	7	197-224	1		1	1	1			
MOTO HUBAN		306-333	7							
PICK HOLAN		¥.	914-974	1637-1666 22	2713-2780 2	1289-2310	3317-3344	144		
PHS1 HUMAN	1	4).70			1					
PHYSA MEMAN	HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86).	2772	640-674	1		1				
PHSER HIMAN		3. 3. 3.		1	1					
PHSFI HIBAAN	HEAT SHOCK FACTOR PROTEIN I (RISF 1) (REAT SHOCK TRANSCRIPTION FACTOR	113-140	164-209		1		1			
PHSF1 HIDAAN	HEAT SHOCK FACTOR PROTEIN 2 (HSF 2) (HEAT SHOCK TRANSCALPTION FACTOR	13. 14.		1	1	1				
PHY21 HUMAN		67-108		+	1	1	1			
PHYST HEDRAN		47.74			1	Ì	1			
PHYLL RUMAN		261-289				1				
MANA LANAN		135-162								
NAME OF STREET		53.60								
	-	113-210		_						
No.	+	331-276			Ī					
777.00	-	27.54			r					
STATE STATE	-	474-504	156.00		- 					
PINE HUMAN	7	232-259	323-349	r						
NAME AND ASSESSED.	+	149-176	406-433							
NAME OF	_	308-349								
PUBA HUMAN		10-107	183-210		1		Ì			
PILIA HUMAN		76-110	172-199	1	1	1				

PCCENE	197a 178a Melif Search on All Haman Protein Sequences		П				н	_	1	П
THE MANIE	PROTEIN THE PROPERTY AND THE PROPERTY OF THE P	4	7	3	1	7	10380	7	1	7227
PILIS HUMAN	Υ-	159.186	Ì					Ī	1	
NAME OF EIGH	+		T	Ť		T	Ī		Ī	
TALK AND A	_		1		1	Ì			1	I
7170	+		Ť	Ť		T	Ī			
POWER STREET	INTERPRETATION ALTERNATION DESCRIPTION ALTERNATION AND ALTERNA	2 2	101	111 001	30.98	Ī	1	Ī	Ī	
7.74	-		T	Т			1			
Phill In KAN	INTERESTRACTOR DE LA TRECUESCA (FUNCACIO)		T	1	Ī					
1000	ANTENERS HANDERS IN THE PROPERTY (CONTINUES IN LEGISLOCATION CONTINUES IN LINE AND CONTI	T	1						1	
THE RUMAN	_	7		383-430	Ì					
PUNCH HUMAN		╗	┑	╗		1			-	
PLAVO MUNAN	-	_	238-273	326-363	386-430				1	
PIPIK_HUMAN	_									
POSP HUDAN	1	20-117	306-233							
PIRRP HIDAAN	ONTERPHOTORECEPTOR BETTOOD SHOOTEN PRECLINSOR (1289)	-	İ	İ		Ī		Ī		
PIRES MINAN	INTERFERM REGIS ATORY FACTOR 3 (185.3)	167, 101		T	•		1	-		
NAME OF	190 KD NACHTALL A CTRICOLOGOLATE CONTROLATANE SECTIONS	176 316	Ì	Ī		T		1	1	
A	-	Т						1		
THE PROPERTY	FLATELET MEMBANAS OLYCOPROTEIN IN TRECONDOR (UTA) (COLLADER RELEFT (577-000	1	Ť							
ALLAS MUMAN		7	٦	163-792	1					
PITAS HUMAN	INTEGRIN ALPHA 4 PRECINSOR (VLA-4) (INTEGRIN ALPHA-E) (CD49F)	-							4	
PITAL HUMAN	_		310-341	795-823						
PITAN HORAN	_	1044-1078								
PITAV HUDKAN	•	230-264							ŀ	
WITH HUBAN	ı	216-245	354-399							
PITES HUMAN	-	339-366	105-732				Ī		-	
MANUEL CELLA	BETA-	324-351								
PITE ALEKA	_	342-369								Ī
PITES HENCAN	INTEGRIN BETA-5 SUBUNIT PRECURSOR.	24-751		İ	Ī	T		Ī	1	
PITTE HEBAN	DYTECALD'S BETA & SUBUNIT PRECURSOR.	T	152.393	T	Ì	Ī	T	T	Ī	
NAME AND PARTY	INTEGRIN BETA-4 SUBUNIT PRECURSOR.	Ť	100	İ	Ī			Ī		I
NAME OF THE	+=	۲	T.	772.6110		Ī	Ī	Ī		
PKIC HUKAN	_	Т	Г	Т	428.462	Ī		Ī	T	Ī
KICK KOKAN	KERATOL TYPE I CYTOSKELETAL 13 (CYTOKERATIN 13) (K13)	13:142		Т				Ī	T	Ī
PKICH KUMAN		T	306-335	193-424	Ī	T			T	
PKICO HUMAN	•	t	Т		Ī		T	1	1	
PKICH HUMAN	-	96.39	T	T	Ī	Ī	Ī		1	
PKICO HUMAN		T	Ť	193-431	Ī		T		Ī	Ī
PRICE HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18)	17-114	251-294	337.385		Ī			Ī	
PRICE HUMAN	KERATOL TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19).	Т	Т	130,197	Ī	Ī	T	T	T	T
PRICE HUMAN	ı	196-226	146.384	190-467					Ī	Ī
PKICE HUMAN		215-248		461-418			l		T	
PRICE HUMAN	KENATON, TYPE II CYTOSKELETAL 4 (CYTOKENATON 4) (K4) (FRAGMENT)	42.73	126-153	189-248			İ		Ī	
PRICE HEMAN	_	185-246	112-373							
SEE SON	-		125-366 4	433-449						
NO HENVE	KERATIN, TYPE II CYTOSKELETAL (CYTOKERATIN 1) (K1)	67								
ACC HOLD	KENATIN, TYPE II CYTOSKELETAL 56 KD (KAA KENATIN) (FINGWENT)	┪	130-161	217.244						
TATE HEAVY	PHOSPHOPRUCTORDVASE, MUSCLE TYPE (EC 27.1.11) (PHOSPHOFRUCTORINASE	_								
NEAL HUNCA	6-PHOSPHOFAUCTORLINASE, LIVER 117PE (EC. 2.7.1.11) (PHOSPHOFAUCTOR INASE	┪	2: 2: 2:							
A HOUSE		-525								
ACAC REPORT	IU KAPPA CHAIN C REGION.	2								
THE PERSON	KALLMANN STRUKCHE PROJETY PRECURSON (ALMESKON MOLECULE-LIKE X-LINK	2								
	CAMPULATION FROM ALMANE 11TE I-ALTHA RECULATORY CHAIN	8								
THAT HOME	CAMP-LEVENDENT PROTEIN KINASE ITTE HEETA REGULATORY CHAIN	7								
PERSONAL LANGE	ANY SECTION OF THE PARTY OF THE PARTY OF THE PROPERTY CHAIN	1	286.317	1						
PKCE TOTAL	THE THE CHARGE B CHAIN (FC 2 3 1 2)	200	1	1	1	1		1		
PKECK HIBAN	PAROSONE PROTEDNEDASE ECK PRECINSOR (FC 2.7.1.113) (EPITAE) (A) CE 1.	107.777	t	1		1	1	1	1	
PKFER HIMAN		Т	107 777	T	1	1	1	1		
		٦.		1		1	1	1	1]

			-		F					
FILENAME			□	ANIA AM	AHLA 4	415.42_A	ABEAS_ ABEAL		1	242
PRFES HUDAAN	PROTO-ONCOCENE TYROSINE-PROTEIN KINASE FESFPS (EC 2.7.1.112) (C-FES)	201-162	20.00	+	+	t	T		1	
PKFLT HUMAN	NECEPTOR-NELATED TYROSINE KINASE FLT PRECURSOR (EC. 7.1.112)	Т		+	l		1		Ţ.	
PICHS HIDAN	MACHOPHAGE COLONY STROUGHING FACTOR FREEZFION PRECURSOR (CST. 177)	100					İ			
PER HUMAN	PROTOCOM COLEME I TRUSIME PROTEIN AINANE I IN LEC	2		-	\vdash					
TACK HOUSE	COMPLEMENTAL PROPERTY BENEFIT BEST IN (FC 2 1 112)	£4.50		-	-					
PKICK HUMAN	FRUSTRE LURASE FLANCE TON PERCENCE (1907)	Т	435-452	471-542 633-	633-680 68	619-716 8	172-899			
PER TOTAL	RIT PROTO CHANGE TYROSINE KINASE PRECURSOR (EC 2.7.1.112).	135.263								
PKNOT HIDAAN	HEPATOCYTE GROWTH PACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE	\$26-968			-	1				
NAME AND ASSESSED.	KININOGEN, HOW PRECUISOR (ALPHA-3-THIOL PROTEINASE INHIBITOR)	505-532			1	1	1		-	
WAYN SERVEN	CALACTORY, TRANSFERASE ASSOCIATED PROTEIN KINASE PSUGTA (EC 2.7.1)	801-18			_				-	
PKPG REALNY	DATER EROM INDUCED, DOUBLE STRANDED RNA. ACTIVATED PROTEIN KINASE	П	191-325	285-312	1					
PKP78 HEBAAN	PUTATIVE SEADME/THOSONING-PROTEIN KINASE P71 (EC 17.1)	287.609			1		1	1		
PKPCL HADAAN	PROTEIN KINASE C BTA TYPE (BC 2.7.1) (NPKC-ETA) (PKC-L)	П			1	1			+	
PKPT! HUMAN	SERINE/THRECONNE-PROTEIN KINASE PCTAINE-I (EC 17.1)	П	20.53		1	1	1	1	+	
PKPY1 HUDGAN	PYRUVATE KRIASE, MI (MUSCLE) 1502 YME (EC 2.7.1.40) (CYTOSOLIC THYROID	£			1	†	1		-	
PICPYS HUMAN	YRUVATE KDIASE, MZ ISOZYNŒ (EC 2.7.1.40).	20770			†	1			-	
PKPYR HUMAN	YRUVATE KINASE, ISOZYME Ř (EC 2.7.1.40)	2	1		1	1	ĺ		1	
PICRET HUMAN	ROTO-CONCOCENE TYROSINE-PROTEIN KINASE RET (EC 2.7.1.112)	2			+	1			+	
PKROS HUMAN	ROS PROTO-CHICOGENS TYROSING KINASE (EC 2.7.1.112) (FRACHENT).	20.50	1		+	†	1	T	•	
PKSRC HUMAN	PROTO-CHECCENE TYROSINE-PROTEIN KINASE SAC (EC 2.7.1.112) (P60-SRC)	2		1	\dagger	1	Ť			
PKUT HUMAN	LUPUS KU AUTOANTIGEN PROTEIN P70 (70 KD SUBUNTI OF KU ANTIGEN)		T	-	†	T	T		1	
PKUSE HUMAN	LUPUS KU AUTOANTIGEN PROTEIN POG (16 KD SUBURIT OF KU ANTIGEN)	121-121	1	1		1	Ť		-	
PKYES HIBAAN	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.7.1.112) (POL-TES)	200	17.144	13.101	214.241 39	197.424	480-507	\$10.539	+	
PAN ROAN		T	3	1	Т	т	T			
MAN MONEY	LAMIN A (70 KD LAMIN)	T	59	292.143	t	İ	T		}-	
PLANC MONA	LAMIN C. A BECTEN BECT BOOK OF FIRE ANTIGEN BELATEDI (EC.) 13.48)	935-969				T				
TAN MURKE	CAN TRAILEM TACKGOOM (LECTION TYPE B ANTICEN (S.B.))	191-122	295-342		H				-	
TA RUMAN	PAINS BLATTEN CHAIN THE STEER ACTUITANSS BLACK ROOK (EC. 2.3.) (4)	131-158			H				-	
PART HITTON	1. LACTATE DEHYDROGENASE HICHAIN (EC. 1.1.1.27) (LOH-B).	101-10	926-500						7	
P DIGH HUMA	LACTATE DEMYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A)	255-522		_						
PLDLA HUMAN	OW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR.	483-510								
PLECH HUBAN	(SIALOGLYCOPROTED) RECEPTOR 1 (NEPATIC LECTIN HI) (ASGPR).									
PLEND HIDAN	P-SELECTIN PRECURSON (CHANGLE MEMBRANE PROTEIN 140) (CAG-140) (PADGEM)	٦	87.116		+	1				
PLOUE, HUMAN	LACTOYLOLUTATHOMB LYASE (EC 4.4.1.5) (METHYLOLYOXALASE)				†	1	1			
ME ROMAN	LEUKAEMAA INNUBITORY FACTOR PRECURSOR (LØ) (DØFERENTIATION-	221:56		15		18	1014 1044			
PIN HIMAN	LINE I REVERSE TRANSCULTASE MONOCO.	7		Т	Т	t		Ī		
PLIPO HIDAN	THACT GLYCEROL LIPASE PARL DARSON (EU. 3.1.1.3) (LUCASE, UNSTRUCE)	201.301			†	T				
THE PERSON	TOWNSHING SEVERITY & LAW MARK ASS RECT 1 1 24 M. TALA HYDROLASSI MEUKOTHENE	(1-1)	290-324	-	T					
NAME OF THE PARTY	I ANDRIN A CHAIN PRECIDEOR.	1311-1345	1741-1771	1705-1012 1122	1834-1831	1164-1921	1963-1999	2026-2059	2091-2118	
N MOI MINAN	I LAMONDO BI CHAIN PRECURSOR.		1364-1394	1897-1631 168	1681-1714 17	1723-1781				
YCARO HUMAN		1103-1135	1513-1547							
PLYOT HUMAN	-	135-182								
PLOXI HUMAN	-	341-364			1	1				
PLOXS, HUMAN	ANACHEDONATE S-LIPOXYGENASE (EC 1.13.11.34) (S-LIPOXYGENASE	ş			1					
MEN HUMAN	Н	10			†	1				
PLRIB HUMAN		2010	100		\dagger	T	Ī			
PLUS HOMEN	=+		1307 7001	2000	t	T	Ī			
MAN HUMAN	PROTEDITYROSDIB PROSPRATASE ZETA FRECURSOR (EC. 1.1.) 49 (F.1F-ZETA)	77.77	448.480	AND IN	\dagger	T				
PLSHON HUMAN	TO I AND A CHAIN V. I REGION OFFI	3			\mid	T				
NAMO HOAAN		185-912	ļ							·
PADOM HUMA	L MOTOCHONDRIAL 2 OXOGLUTARATIONAL ATE CARRIER PROTEDY (OCCP)	22	_							
PACE HOLA	1=1	219-246		+	†	1	1	T		
PHANG HUMA	NAMES OF ALTHE MANNEY IN THE STATE			4	1	1	1	brack		

	PCGENE 107117014 Modif Search on All Human Protein Sequences									
ACCOMPANIEST EXCENTED FORTER TO ACCOMPANIEST	_	_		7	P VIIIO	2010	9		-	
	-	-	1147-1182							
		474.78								
11.144 1		408-449								
ACTIONION NEWSTANDS 1973 1974	AN MAX PROTEIN.	117-144								Ī
11.25 11.24 11.2	A MONI PROTEIN (PSS-ASSOCIATED PROTEIN).	235.320								
GENERAL PROGRAM GALGAR CALIN A) FAGGERY GENERAL PROGRAM GALGAR CHAN A) FAGGERY GENERAL PROGRAM GALGAR CHAN A) FAGGERY GENERAL PROGRAM GALGAR GALGAR GALGAR GALGAR GENERAL PROGRAM GALGAR GALGAR GALGAR GALGAR GENERAL PROGRAM GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GALGAR GAL	AN MULTIDAUG RESISTANCE PROTEIN I (P.CLYCOPROTEIN I)	\$61.195								
The control of the	AN MERLEN (SCHWAINGEN)	г	\$32.566							
#### COUNTY REPORTED NOTE OF THE PROPERTY IN TANKERASE (CC. 11.0) (CO. 99.11) ##################################		_	136-173	431-438	791-616					
1970 1970		Г								
ACCORDING EXLINER TO EXTEND NOTE TO EXAMPL	AN MITOTIC KINESIN-LIKE PROTEIN-1.	_	319-346	\$10.337	349.608				_	
### ### ### ### ### ### ### ### ### ##	AN IMELANIN-CONCENTRATING HORMONE PRECURSOR.									
The ADDITION CONTRING ENTROGEN HILL STEEL AND THE PROTECT	AN MIXED LINEAGE KINASE I (EC 2.7.1) (FRAGMENT).	130-137	321-348							
Item Item		393-430								
12.00		119-146	351.403						-	
1.59 ALTINICAL BROUCES ACCUPANTATION 1.59 ALTINICAL BROUCES ACCUPANTATION 1.59 ALTINICAL BROUCES ACCUPANTATION 1.59 ALTINICAL BROUCES ACCUPANTATION 1.50 ALTINICAL BROUCES ACCUPANTATION 1.50 ALTINICAL BROUCES ACCUPANTATION 1.50 ALTINICAL BROUCES ACCUPANTATION 1.50 ACCUBANTATION 1.50 ACCUPANTATION	286-313							-	Ī	
ALTOCATION AND CORPORATE ACTION AND RECURSOR (TAMA) 194-199 191-1911	N IMPRASE DIDUCER PROSPRATASE 3 (BC) 1.1 40)									
ALTIDING RESIDENCE ALROCATED MODERN RECORD (CHANA 1964) 196-158 19		19.50							-	
ALTINICATION SESTITANCE, ATTOCATED PROTECTION 154-21 101-200		AN & 1569-1596	2437-2478							
STATEST TO A TOTAL A TOTAL A TOTAL A TOTAL A TOTAL A CONTRACTOR STATEST AND TOTAL A	•	396.423	\$0.56						1	
ACCOMMANDE SCYUTION TYPES AVECUATION 175.04 175.0		Ì								
International Control	AN MACE OBLACES OF A CONTROL OF SECTION TO SELECT AND 11 ANA CHARLES A CRETA	AVERIST SAL	236.366							Ī
		367.414	W 102						1	
STATE LALL LATTO AND LATE PACTORS OF EACH STATE AND LAT		212/0/	30						1	
The NELL ATED RESISTANCE OF BADDON PROTEIN LACK INTERESTOR. 101-194		717-101								
NEBERION RECOLATED RESISTANCE OF BEINTANCE OF BEINT MACK INTERESTOR 101-64									-	
The Late Action Protection 1985-95 1985-										
17-11/10 17-11/10	IN INTERFERON REGULATED RESISTANCE GTP. BINGING PROTEIN MOBILITIES		670-607						-	
VICTORIO CONCOCEDE ROTEIN	IA MYB-RELATED MOTEIN A (PRAGMENT).	619-646								
The International Concrete and the International Control of the Internat	MAN MI DAGLA I LA TROITEM B.	111111								
19-144 1	M. THE CROLOCALOR ROLLING	207-107	2						1	
13-144 1		227-677							-	
MYELDA AGIGENT) 41-10 AGIGENT) 41-10 41-13 41		31-4-18								
### ### ### ### ### ### ### ### ### ##		127-1948								
MATELIA 10.70 10		70-110								
March Marc		63.70								
46-75 591-961 1971-104 1081-1121 1192-1234 1206-1332 1306-1401		38-75	=======================================	137-178	236-324	198-135	440-485			
141-1342 1640-1641 1641-1710 1801-1813 1641-1810 1641-1810 1641-1810 1641-1810 1641-1810 1641-1810 1641-1810 1707-1714 1827-1840 1821-	_	48-75		997-1044	1048-1122	1192-1234	1266-1332			445-1533
170-174 186-907 931-107 119-1144 1191-1319 1261-1441 170-174 181-184 170-174 181-184 170-174 181-184 170-174 181-184		1541-1582	-	1683-1710	101					
1707-174 1817-183 181-184 213-272 401-483 516-514 481-716 1817-183 181	AN MYOSIN HEAVT CHAIN, PAST SKELETAL MUSCLE, EMBRYONIC.	66-7 3	-	952-1077	19-1146	193-123	1267-1340	1364-1413	1403-1597	641-1673
131-50 191-135 141-188 215-272 403-481 507-752 518-654 481-756 131-50 131-50 191-280 646-817 131-160 191-280 646-817 131-160 191-280 646-817 131-60 646-87 131-60 646-87 131-62 131-	The state of the s	1707-1734	1827-1858			7	7			
13-150 13-207 1	AN IMPOSIN REAVE CHAIR, PERINA I AL CAUDIAL MUSILLE (FRAUMENT)	20-77	95-125			7	7	┑	,	1
13-150 13-150 14-61 14-150 14	AND PACE OF THE PA	123-907		•				┪	╗	
MYELDA TRANKCADTION FACTOR I (ANTII) (FLAGMENT). 640-671 100-773 100	MICE THAT I COM, SALLE THE MOSTER (PANELLY).	201-171	2	Т	2077	68.320	8	7	┪	5
SOUGHACALCINA EXCHANGER FACULATOR SOUGHACE SOUGHACE SOUGHACE SOUGHACALCINA EXCHANGER FACULATION	AN INVESTING THE ANALYSIS THE SACTOR I ASSETT THE ACCUSANT	440.438							1	
REURAL CELL ADRESTON MOLECULE, PHOSPIATIDYLANGISTICLA, LINGED ISGGORM, 315-731 REURACHEL CYTGSOL, RATTOR (1061-477) (401-4	AN COUNTY AT CHILD FYCHANGE PRECIECE IN A LEGAL SECTION OF THE PROTEIN	407.510	167 701	704.714		Ţ			1	
NEUTROPHIL CYTOSOL FACTOR 1 (NCF-ATR) (48 KD AUTOSOLALL CHRONC 324-361 110-317		7								
NEVITACHEL NADPH GXDASS FACTOR (No.)-HIGY. 5-13 10-13 14-13	_	-	211.011	Ī					1	
DNA-BINDING PROTEIN NETA PRECURSOR. 19-77 11-112 141-315			100	T	Ī					
NEWELYSIN RCC 3 4 3 4 11 (NEUTRALL ENDORE) TO 14 5 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					Ī	Ī	7			
NEUROF BROAMN (NEUROF BROAMN OSSA, RELATED PROTEIN NF. 1) (FRAGNENT) 1145/117 1146121 (695-1666) NEUROF BROAMN (NEUROF BROAMN OSSA, REUROF LAMENT PROTEIN) (NF. 4), 11.128 11.1400 NEUROF LAMENT TRUFET I PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4), 10.141 (64-164) NEUROF LAMENT TRUFET I PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4), 10.141 (64-164) NEUROF LAMENT TRUFET I PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET IN PROTEIN (68 KD NEUROF LAMENT PROTEIN) (NF. 4) (64-164) NEUROF LAMENT TRUFET LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN) (68-164) NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN) (68-164) NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN) (68-164) NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN) (68-164) NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN) (68-164) NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (68 KD NEUROF LAMENT PROTEIN (710 011				1				
NEUROE LAKENT TRUE I PROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.) 1131 114-104 115-1100 NEUROE LAKENT TRUE I PROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) 113 114-104 NEUROE LAKENT TRUE I PROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) 101-101 104-104 NEUROE LAKENT TRUE I PROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) 101-101 104-104 NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) 101-101 104-104 NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) 101-101 NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN) (FF.1) NEUROE LAKENT TRUE I MEROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AMENT PROTEIN (100 ID NEUROEL AME	+	T	10000	7777						
NEUROELLAGENT TRUELE PROTEIN (SE ED PREUROELLAGENT PROTEIN) (N°T.) 111.00	7	7	2291-226	93.1800					1	
NEUROFICAGENT TRIPLET IN PROTEIN (146 DO NEURO) IL AGENT PROTEIN) (175-14) 101-141 144-154 115-216	7	7	24							
SUBSTANCE PRECEPTOR (SPR) (AR. I R.C. P. FORM (AR. IR.) MATURAL, KILLER (FILLS PROTEINS PRECEPTOR) (AR. IR.)	-	-	7	200			П			1
NATURAL KILLER (FILS PROTI IN 4 PRICITION		Ť	7		711	37.75	╗	12:913		
		161.491		Ī					1	1

	167217814 Moul Search on All Human Pratein Sequences	V I VARV	, VIEW	AREA 3	AREA		AREAS	AREA?	SEA.	ABEA:
The control of the	PROTEIN	Ť	ı		101.742	_	1000-1133		-	
Many Micro Course Free Land Micro Course	NR. TUNOR RECOGNITION PROTEIN (AA LOISANE PROTEIN)	Ť			:	_				
MAIN FILE COLDS FINTERIAL EQUICATION FILE CONTRIBUTION FILE COLDS		Ť		1792-1319						
The property of the property		189-416								
		131-131								
The property of Control of Cont	SOURS AND CHECKENERY GABA HAMISTORICA I		ŀ							
The posterior programme is a proper part of the posterior programme is a programme in the posterior programme in the posterior programme is a programme in the posterior programme is a programme in the posterior programme in the posterior programme is a programme in the posterior programme in the posterior programme is a programme in the posterior programme in the posterior programme is a programme in the posterior programme in the posterior programme in the posterior programme in the posterior programme is a programme in the posterior progra	NEUROTENSON RECEPTOR (NT-R.)									
MANIE MANNE MINISTER OF CONTROLLED FOR THE MINISTER OF THE M	PYTSE KRACA SODIUM DEPENDENT SEKOTOWIN TRANSPORTER (THE EXPLANATION OF			Ī		ļ		! !	!	
REMAIN INTERFEGINGENER EXCHANGE TARE CHAIN 1 (EC 14.1) 11-14.1	PHITA HIMAN SORUM AND CILOADE-DEPENDENT TAURING INCHASTOR FOR		Ī							L
Halley Holze Group of the Color of the Col	PHIZM HELAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC. I. 6.3.3)	T								
State	PARION MILLANDIAN DATA OCTOOR DATA SECULATION 4 (EC. 1.6.5.1)	٦	44.57						-	ļ
The control of the	SOUTH MANAGE CONTRACTOR CONTRACTO		60-387							
A	ACCOUNTS TAXABLE TO SELECT THE SE	462-508								
MANN WITH REALMENT BE TAKEN THE TA	3	115-162					•			_
Continues and property (Continues Activation (Continues Activation Activation Activation Activation Activation (Continues Activation Activation Activation Activation Activation Activation (Continues Activation Activati	AMAN PUTATIVE NEUROPETIME I MECETION			-	:	i			•	
CONTACTE AND STREAM TO A CONTROL BE (CCT A) 177-17	ORNITHING AMINOTRANSFERASE PRECINGOR (EC. 2.6.1.13) (URBITHING-4131)								Ĺ	
CONTINUE ACTUAL DESIGNATION ACTION IN CICIL BY CONTINUE ACTUAL DESIGNATION ACTION IN CICIL BY CONTINUE ACTUAL DESIGNATION ACTION IN CICIL BY CONTINUE ACTUAL DESIGNATION ACTION ACTION ACTION CONTINUE ACTUAL DESIGNATION ACTION ACTION	Ι.	[]								ļ
100 100	-	17.78								1
University Control C	I AWAY OCH OCH BANDENAL SYNDROWE PROTEIN.								1	1
DINTERSOL LINGUISER ACCEPT (FLAND) 17-10	LOWE S COLUMN TO ANGERA OF COMPONENT (ES) PRECITISON OF SPANCHED CITAL	Г	19.401							
MILESTERIEN CORNER OF HELE CONFEDENCE (MOG) 13-10	UNDAMINE ALTERNACIONES ANTERNA	25.88				_				
ALLEGATING OF SHAPE OF SHAPE OF SHOUNDER NOTES OF SHAPE	DIRYDROLINGAMILE ALEITE I ILANGE CAME CHEST (1-7 C)	3.16							;	
THE SENSITIVE OF SEN (LARE CONE PROTOREE FOR FIGHERY) 90-117 319-344	(OLICODENDROCYTE-MYELIN GLYCOTROL EIN FRECORDON		Ī						L	
CHEEN-ENGINITY CORN (FIGER) CONTROLLED CONTROLLED	BLUE-SENSTIVE OPSIN (BLUE CONE PHOTORECEPTOR PICHEM)	Ţ							L	L
### PER SENSITIVE GONG THAT COLOR PHOTODICES FOR PROPERTY 199-149 #### PER SENSITIVE GONG TO COLOR PHOTODICES FOR PROPERTY 199-149 #### PER SENSITIVE GONG TO COLOR PHOTOGEN TO THE TO THE THAT THE THE COLOR PROPERTY 199-149 ### PER SENSITIVE CALGADAD VITALIST PROPERTY 199-149 ### PER SENSITIVE CALGADAD VITALIST PROPERTY 199-149 ### PER SENSITIVE CALGADAD VITALIST PROPERTY 199-149 ### PER SENSITIVE PROPERTY RECURSOR (REC. I.A.I.) ### PROPERTY OF THE VALUE OF THE THAT THE CURSOR (REC. I.A.I.) ### PROPERTY OF THE VALUE OF THE CURSOR (REC. I.A.I.) ### PROPERTY OF THE VALUE OF THE CURSOR (REC. I.A.I.) ### PROPERTY OF THE VALUE OF THE CURSOR (REC. I.A.I.) ### PROPERTY OF THE VALUE	GREEN SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PICHENT)	1	37.4						L	-
CHECKONTEN PRESCUESOR GOORE SIALOPRICIEN 1) (RENAMAY STONE PROTECH) 170-204	-	T	987						ľ	ļ
17.10	NV.	239-266							1	1
177.507 177.504 177.	т	130.204							1	1
ONTSTEED LINGUIS PROTEIN 196-111		173-207								
ACKTOCCH RECEPTOR (014) ALEXACEN RECEPTOR (014) ALEXACEN RECEPTOR (014) ALEXACEN RECEPTOR (014) ALEXACEN RECEPTOR RECURSOR (014) ALEXACEN RECEPTOR (015) ALEXACEN RECEPTOR (015) ALEXACE		1213	90-217	190-317	23.65				-1	
Matthem Matt		116-377								
PATRICESTEM (PAT) PROTECTION PROTECTIO		T	23-449			L				
NACKATRAN (PAT)	-	T	17.464					L		L
PLECTRIN (P.1)	_	T								L
MOSTIVE ALTRIANCE ALTRIA SEGUED IN PROCESS 17-19 11-19			91.318			L			Ŀ	L
PHOSTHALTER TABLE ANTILE ROLLE OF THE CURSON (POST LAW PROTEIN) 134-15		T	90-							L
PROSENTED TRANSCRIPE AND PROTECT IN STATES 17-104 1	1	1	2						-	ļ
AMCREATHIS ASSOCIATED ROTER! PRECINSOR. 13-18	L	٦	272						1	-
PAIRED BOX PROTEIN PAX 3 (B-CELL SPECIE FRANSCHITON PAX(18) 18-48 PAXTEET SEGULATE ACTOR A CHAMPEGREOR (PGG A CHAIN) 18-48 PAXTEET SEGULATE ACTOR A CHAMPEGREOR (PGG A CHAIN) 18-48 PAXTEET SEGULATE ACTOR A CHAMPEGREOR (PGG A CHAIN) 18-48 PAXTEET SEGULATE ACTOR A CHAMPEGREOR (PGG A CHAIN) 18-48 PAXTEET SEGULATE A PRECINCIA CHAIN (PGG) 18-48 PAXTEET A SEGULATE A PRECINCIA CHAIN (PGG) 18-48 PAXTEET A SEGULATE PROTEIN PRECINCIA (PGG) 18-48 PAXTEET BASIC PROTEIN PRECINCIA (PGG) 18-48 PAXTEET BASIC PROTEIN PRECINCIA (PGG) 18-48 PAXTEET BASIC PROTEIN PRECINCIA (PGG) 18-48 PAXTEET BASIC PROTEIN PRECINCIA (PGG) 18-48 PAXTEET BASIC PROTEIN PRECINCIA (PGG) 18-48 PAXTEET BASIC PROTEIN PRECINCIA (PGG) 18-48 PARTICAL AND AND ASTAINAGE CAN'H FACTOR (PGC) (PGG) PARTICAL AND AND ASTAINAGE (PGC) (PGG) PARTICAL AND AND ASTAINAGE (PGC) (PGG) PROGECANTA (PGG) PRECINCIA (PGC) PROGECANTA (PGG) PROTEIN) (PGC) PROGECANTA (PGG) PRECINCIA (PGC) PROGECANTA (PGG) PROTEIN) (PGC)		3							\downarrow	-
RATELET DEBUYED GROWTH FACTOR, A CHAIN PRECURSOR (PECALI)		157-187								-
ALTELET ENDOTHELLAL CELL ADJESSION MOLECULE PRECINSOR (PECAN: 1) 419-119		30-65								4
142-178 142-		612-510								1
FORTHCOME PECTORIOR PECTORIOR PECTORIOR PECTORIOR		142-176								4
FEBTORIA PRECISSOR (P1), CAPADROCYTE PORE FORLEND (PFF) 411-434	-	306-335								
ALTELE ALSE PROTECT PRECUESOR (PRI) (CONTADNS: CONNECTIVE-1155 11-35	-	411-438								
CATEL GOES PECTRE PROTECCE, VEAN TOTALN PRECINSON (CSPCP) CATEL GOES PECTRE PROTECCE, VEAN TOTALN PRECINSON (CSPCP) CATEL GOES PECTRE PROTECCE, VEAN PECTRSON (CSPCP) ESTATEMENT AS PROTECCE, VEAN PECTRSON (PECTRSON) ESTATEMENT AS PROTECCE, VEAN PECTRSON (PECTRSON) ALTHOR PLATELET DELIVED CROWNH ACTOR RECEPTOR PRECINSON ALTHOR PLATELET DELIVED CROWNH ACTOR RECEPTOR PRECINSON ALTHOR PLATELET DELIVED CROWNH ACTOR RECEPTOR PRECINSON FROSTAL AND ON SYNTHAGE PRECINSON (RC 1.14 P.) (11.11) (PCTLODY CORNAS P.) FROSTAL AND ON SYNTHAGE PRECINSON (RC 1.14 P.) (11.11) (PCTLODY CORNAS P.) FROSTAL AND ON SYNTHAGE PRECINSON (RC 1.14 P.) (PAN) (PRE 4. 11.11) FROSTAL AND ON SYNTHAGE PROMINE (PCT. 1.14 P.) (PAN) (PRE 4. 11.11) CLAYCOGEN PROSTHORY LASE LIVER FORM (CC 2.1.1.1) CLAYCOGEN PROSTHORY LASE LIVER FORM (CC 2.1.1.1) CLAYCOGEN PROSTHORY LASE LIVER FORM (CC 2.1.1.1) CLAYCOGEN PROSTHORY LASE BRADE FORM (CC 2.1.1.1) CLAYCOGEN PROSTHORY LASE BRADE FORM (CC 2.1.1.1) CLAYCOGEN PROSTHORY LASE BRADE FORM (CC 2.1.1.1) CLAYCOGEN PROSTHORY LASE BRADE FORM (CC 2.1.1.1) CLAYCOGEN PROSTHORY LASE BRADE FORM (CC 2.1.1.1) CHAPTER CONTROLLED (PROSTHORY LASE BRADE FORM (CC 2.1.1.1) CHAPTER CONTROLLED (PCTRSON (CC 2.1.1.1) CHAPTER CONTROLL		21-55		L						
130 131 130 131 130 131 130		3.180								
11170ACKYPNOSTAGLANGN DEHYDROGENASE (NADR.) (PC 1.1.141) (PGDH) (17.114		2.3	1390-1417	1553-1500						
SET ALTEET DELIVED GROWTH FACTOR RECEPTOR PRECUISOR (EC. 2.7) 1.111) 394-311 134-314 445-491		87-118								
BET AT ILLE IT JULY OF COOK THE FACTOR PRECUISOR 44-94 147-191 461-418 131-131 PROSTACE AND OM SYNTHASE PRECIASOR (EC. 1,14 %) 1) (CYCLOOXYCENASE) 131-131 PROSECARTE AND OM SYNTHASE PRECIASOR (EC. 1,14 %) 1) (CYCLOOXYCENASE) 131-131 PROSECARTE AND OM SYNTHASE (EC. 114 # 1.) (CYCLOOXYCENASE) 131-134 PROSECARTE AND CHARGE (EC. 114 # 1.) (CYCLOOXYCENASE) 131-134 PROSECARTE AND CHARGE (EC. 114 # 1.) (CYCLOOXYCENASE) 144-135 CLYCOGEN PHOSPHORYLASE LIVER FORM (EC. 2 4.1.) (114-13) 111-13 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CLYCOGEN PHOSPHORYLASE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 2 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE AND CHARCE MASCLE FORM (EC. 3 4.1.) (114-13) 131-340 CHARCE		200	34.34	465.495			L	L		
MATAILE LE BOUNDO ON STITULE PRECADOR (CC 1.19 PL) (CYCLOOXYCENASE) 311-318 BONG-CARTILAGE PROTEOCLY CAN I PRECADOR (RALYCAN) (PC-51) BONG-CARTILAGE PROTEOCLY CAN I PRECADOR (RALYCAN) (PC-51) FRESTYALANDE CHARGE (CC 1.10 Is.) (PAN) (PRE-4 1148 FROGENING (ST. PROTOTIVANS BUCK (R. P. 1.1) GLYCOGEN PHOSPHORYLAGE (LIVER FORM (CC 2.4.1.) GLYCOGEN PHOSPHORYLAGE BALAN (CC 2.4.1.) GLYCOGEN PHOSPHORYLAGE BALAN (CC 2.4.1.) GLYCOGEN PHOSPHORYLAGE BALAN (CC 2.4.1.) GLYCOGEN PHOSPHORYLAGE BALAN (CD 3.4.1.) FROGENING (CC 2.4.1.) GLYCOGEN PHOSPHORYLAGE BALAN (CD 3.4.1.) FROGENING (CC 2.4.1.) FROGENING (CC 2.4.1.) GLYCOGEN PHOSPHORYLAGE BALAN (CD 3.4.1.) FROGENING (CC 2.4.1.)		277	147.105	197-199	524-551	916-1031		L	L	L
PROSTAGLADON ON STRINGS PROCUED IN PRECINSOR (EC. 1): PROFICE CONTROLL PROCUEDS PROFILED IN PROCUED IN PROFILED IN	-4							L		
BOOKCANTLAGE MOTERAL TOAT PRECING MEAN CONTROL OF THE MOTERAL AND CELLANDS AND THE MOTERAL AND CELLANDS AND THE MOTERAL AND CELLANDS AND THE MOTERAL OF THE	=									L
PHENTALANDE-AHTDROXTLASE (EC. 1.19 IS.) (FANGURE-E- PHOSIDIEN B. ED PHOTOTIVANSBUCING PROTEIN) (AEKA PROTEIN) GLYCOGEN PHOSIHORYLASE, LIVER FORM (EC. 2.4.1.1) GLYCOGEN PHOSIHORYLASE, AUSCLE FORM (EC. 2.4.1.1) GLYCOGEN PHOSIHORYLASE, BALDIK FORM (EC. 2.4.1.1) GLYCOGEN PHOSIHORYLASE, BALDIK FORM (EC. 2.4.1.1)	ļ					\downarrow				+
PROMBITIN. PHOSDICIN (1) KD PHOTOTIANSBUCING PROTEIN) (AEKA PROTEIN) GLYCOGEN PHOSPHORYLAEE, LIVER FORM (EC 3 4 I. I.) GLYCOGEN PHOSPHORYLAEE, MISCLE FORM (EC 3 4 I. I.) GLYCOGEN PHOSPHORYLAEE, BRADN FORM (EC 3 4 I. I.) GLYCOGEN PHOSPHORYLAEE, BRADN FORM (EC 3 4 I. I.) GLYCOGEN PHOSPHORYLASE, BRADN FORM (EC 3 1 I. I.)	1	200							1	ļ
PHOSOUCH (1) KD PHOTOTRANSUKING PROTEIN) (MEKA PROTEIN) (GLYCOGEN PHOSPHORTLASE, LIVER FORM (EC. 8.1.1) (GLYCOGEN PHOSPHORTLASE, MISSEL FORM (EC. 3.1.1) (GLYCOGEN PHOSPHORTLASE, MISSEL FORM (EC. 3.1.1) (GLYCOGEN PHOSPHORTLASE, BRADH (EC. 9.1.1) (GLYCOGEN PHOSPHORTLASE, BRADH (EC. 9.1.1)	F							1		1
GLYCOGEN PHOSPHORYLARE, LIVER FORM (EC 2 4 1.1) GLYCOGEN PHOSPHORYLARE, MUSCLE FORM (EC 2 4 1.1) GLYCOGEN PHOSPHORYLARE, BALDIK (EC 2 1.1) GLYCOGEN PHOSPHORYLARE, BALDIK (EC 2 1.1) F. PHOSPHATIDYL INOSITIOL. 4.3.81SPHOSPHAT TE PHOSPHODIESTERASE BETA?	÷=	14-235								4
TGLYCOGEN PHOSPHORYLASE, MUSCLE FORM (EC 2 4 1 1) GLYCOGEN PHOSPHORYLASE, BRÅDN FORM (EC 2 4 1 1) 1-PHOSPHATTDYLINOSTIOL-4.3-BISPHOSPHATE PHOSPHODIESTERASE BETA 2	+=	100						\downarrow		1
GLYCOGEN PHOSPHORYLASE, BRAIN FORM (EC 2 4 I I) - PHOSPHATIDYL INOSITOL 4.5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2	-	5)2-559								1
1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2		S				\downarrow			1	1
		\$66.806								1

PCGENE 1671	1871/78s4 Next Search on All Human Protes Sequences	ΙT	_	-				_	
LILENAME PROTEIN	PROTEIN		20070	_	APIA 2	20126		4	0
PPLAK HUMAN PLAK	PLAKOGLOBIN (DESMOPLAKIN III)	t							
PILST NUMBER LIPL	-PLASTIN (TILBIN)	507.534							
PPLST MARAN T.PL	T.PLASTIN O'IMBRIN	10.361							
+=	PEAUPHERAL MYELM PROTEIN 22 (PAP-22)	===							
-	PHOSPHOGLYCERATE MUTASE, BRAIN FORM (EC 5 4 2 1) (PGAM-B) (EC 5 4 2 4)								
	PHIOGLYCELATE MUTASE MUSCLE FORM (EC 5 4 2 1) (PGAM-M)		<u>. </u>	<u> </u>					
	PROBABLE TRANSCRIPTION FACTOR PAL-1.	581-585							
	PROBABLE TRANSCRIPTION FACTOR PML-X	\$81-385							
	AUTOANTICEN PM-SCL.	103-130							
-	DNA-BINDING PROTEIN PO-GA.		117.209 610.637	137 667-699				_	
PPOLI HUMAN METR	LETROVIALIS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE	174-804							
	LETROVILUS-RELATED FOL POLYPROTEIN (FRAGMENT)		171-205						
PION HUMAN OUTE	OUTER MITOCHONDRIAL MEMBRANE PROTEIN FORM (VOLTAGE-DEPENDENT ANIC) 33-76	Ē	89-216					_ ,	
PPAN HUMAN PROS	PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2)	335-269	_						
PPPAS HUMAN RED	LED CELL ACID PHOSPHATASE 1, ISO2YAGE 3 (EC 11.) 2) (ACP1)	26-53	_					ŀ	
PPPOL HUMAN NADO	MADI(+) ADP-RIBOSYLTRANSFERASE (EC 2 4 2.30) (POCY (ADP-RIBOSE)	624-649	12-1003	_					
-	PROTEASOME COMPONENT C2 (EC 3 4 99 44) (MACROPAIN SUBUNIT C2)	86						-	
-	PROTEASOME COMPONENT CJ (EC J. 4.99 44) (MACROPAIN SUBUNIT CJ)	14-61						,	
PPRCS HUMAN PROT	IOPAIN SUBUNIT C9)	192-602							
_		146-1990							
PPRIS HUMAN VITA	TTING) PRECURSOR.	111.111							
-	-DEPENDENT PROTEIN Z PRECURSOR.	39.62							
PPSOR HUMAN PSOR	PSONIASON	26-59							
MANUAL DESIGNATION PURLY	AECURSOR (PSP-D) (SP-D)	124-151	_						
	PARATHYROD KONKOKE PRECURSOR (PARATHYRIN).	(11.98			L			•	
=	PROTEIN-TYROSINE PHOSPHATASE 18 (EC 3.1.3.44) (PTP-1B).	136-177	_					-	
PPTNO HUMAN T-CEI	T-CELL PROTEIN-TYROSINE PHOSPHATASE (EC.).13.40 (TCPTP)	39-86	136-176						
-	PROTEIN-TYROSINE PHOSPHATASE IC (EC.) I.3 48) (PTP-IC) (NEMATOPOLETIC	227-261	512-580						
	PROTEIN-TYROSING PHOSPHATASE 2C (EC 3.1 3.43) (PTP-2C) (PTP-1D)		218-245						
_	EDETYNOSDÆ PHOSPHATASE GI (EC 3 1.3 48) (PTPGI)	┪	695-722	_				•	
_	PAKATHYROID HORMONE/PARATHYROID HORMONE. RELATED PEPTIDE	168-195		1					
-	PENTAXON-RELATED PROTEIN PIX PRECURSOR.		1				1		
PURE RUMAN PROS	PROSPERIORIST CAMPAGET CINE LIGASE (EC. 0.3.1.1) (UALS) (GET CINAMAGE)	017.10	$\frac{1}{1}$	1	1				T
-	ADENY OFFICERATE I VACE (FC 4) 2 31 (ADENY) OFFICERASE) (ASI)		+	-	-		Ī	Ī	Ī
-	REMANDE C. MONAPORTOCORA TE CONTRACE A DAY CONTRACE (CONTRACE)	95.16					T	1	
PYRO HEBANICTP	CTP SYNTHASE (EC 6.3.4.2) (UTP-ANOMINA LIGASE) (CTP SYNTHETASE)	۲	300-334				T		
PPZP HUMAN PREG	PREGNANCY ZONE PROTEIN PRECURSOR.	215-354	1162	1162-1189 1405-1432	170				
PEAN HUMAN TRAN	LPHA SUBUNIT (TFIIF, ALPHA SUBUNIT)	474-501							
		18-65							
	ATED PROTEIN RAB-6.	Т	П						
	RADIXIN.	200	414-463 510-537	6					
PARENT MANANT POPULA	P. 3) GRA. BINDING PROTEIN EVE. 1)	1	166,131		1			1	T
	Τ	7					1	1	
1	REPUBLICATION REVAIL (EC.) 423 153 (ANGIOTENSINOGENASE)	34.16		1	+			1	T
+-		Ţ	333.370 445.472	919-11.5	144.771	784-652	1023-1050	1001	1157-1184
		10	ī	Ī	Т				
	REPLICATION PROTEDY A 10 KD DNA-BINDING SUBUNIT (NP-A) (NF-A)	П	425-455				T	Γ	
	TRANSFORMONG PROTEDI (NEP) (RET FINGER PROTEDI)	113-217							
П	ВЕООБ СВОИР ВН(В) РОСУРЕРТВЕ								
	ALBOPHORIN I PRECURSOR.	\neg	496-530						
7	RIBOPHORIN II PRECURSOR		61.30	-					-
PRINCI HUMAN MUSO	GPSTEIN-BARR VIRUS SMALL BNA ASSOCIATED		1,0400	$\frac{1}{1}$	1		1	1	
PEL 26 HIMAN 605 P	Τ	Τ	101-111	<u> </u>	\downarrow		1	1	T
		1]

PCCENE	1671/316 Modif Search on All Human Protein Sequences			1,194	7484	7 5 7487	/ / / / / /	AREA?	VUEZE	AREA 9
П		т	Т						_	
	605 RIBOSONIAL PROTEIN L9	36.65	T							
ΞŤ	VEC A ANTIGEN (SCA)	T	205.265	Γ						
_	STRONG PROJECT STRUKOME TITE A APRICE (Service)	Ť								
_	SO KO KO PROTEIN (MOUREM STRUKKANE TITE A KINTUKI (45 A)	3								
7		\$01.528	-							
	-	630-657					-			
	PALESCOCKINGS CONTROLLED TO THE POLYPEPTIDE	T	665.720	179.906	1314-1341	1311-1394				
		T	1001-1015							
-+		:	:	:			:			
	MANUAL TION	28:31							_	
PREUM, HUMAN	RETINOIC ACID RECEPTOR DXX.ALPHA									
PRAXIB HUMAN	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM I		i	i :	:	İ	-	1	:	!
ı	(R.BETA ISO) ORM ?		Ī				T			
PRS12 HUMAN		3	Ì						1	
_	AS RIBOSOMAL PROTEIN SIG	2					-		٠,	
PRS35 IRINIAN	405 RIBOSCHALL PROTEIN S15	3				Ì				Ī
+	ANG RINDSOMAL PROTEIN \$27A	7.7		i	:					
+	ANG BIRDGOLAL PROTEDS \$7.581	33.100			:			: ::::::	:	:
+	AND SOUTH ON THE PROPERTY OF T	16.163	į		:					
٦,	A STATE PROTEIN TOTAL	2	!							
	III CALAIT MACHEAR BIRONINCI EOPROTEIN A (UI SNRAP A PROTEIN)	17-								
	THE CLASS WATER AND MONITOR FOR COLUMN STATES AND	13.44								
-	OL SPORT PROPERTY OF STATE AN ICC. E	154-188	495.522	169.93	11.0.111	1820-2847	1104-1111	3529-3556	1013-3910	4921-4948
	NYAMONE MELETION, SALLE I AL PIOSCLE	1								
PSION HUMEN	S-100 PROTEIN, ALPHA CHAIN									
PSIGE HUMAN	S-100 PROTEIN, BETA CHAIN	2	Ī				Ī			
PSIOD HUBLAN	S-1000 PROTEIN									Ī
PSANGH HELMAN	SAJOH HIMAN ADENOSYLHOMOCYSTEINASE (EC)) I I) (S.ADENOSYL-L.HOMOCYSTEINE	314-416								
PSATI HUMAN	DNA-BDODG PROTEIN SATBI	709.736								
PSCCA MIMAN	PECCA MEMAN SOUAMOUS CELL CARCINOLA ANTIGEN (SCCA) (PROTEIN T4-A)	78-105								
PACT MINAN	STEM CELL FACTOR PRECURSOR (SCF)	74.101								
12	SELENDACEL THE PROTEIN PRECURSOR (SGI) (CONTAINS SEMINAL BASIC	84.98	176-236	200-120	334.366				•	
	SENDINGED IN II PRECURSOR (SGII)		113.236	304.35	405-439	519-575				
-	SET PROTEDY		154-181							
PSG1 HUMAN	SECRETOGRAMM I PRECURSOR (CHRONOGRAMIN B)									
PEGS HUMAN	SECTIE TOGRANTN II PRECURSOR (CHROMOGRANIN C)		290-317	534-561						
PKIAL MAKAN	BONE STALOPROTEIN IS PRECURSOR (BSP 11)		185-193	256-283						
PSYCH HONSE	POSSIBILE CLOBAL TRANSCRIPTION ACTIVATOR SNF 11.	П	25.53							
PSNOB HUNAN		7								9,00
PSPCA HUMAN	SPECTIÓN ALPHA CHAIN.	۵ آ	370.621	217.669	1040	70(1-10#1	AX 1.781	7707-98A	2070	2
		-1					1000	7	700 700 700 700 700 700 700 700 700 700	1991
PSPCB_HUMAN	SPECTRUM BETA CHAIM, EXYTIONOCYTE	-	200	076-070	649:013	701-108		200		
PSPRE HUMAN	SEPLAPTEAIN REDUCTASE (EC 1 1 1 151) (SPR)	2								
PSRF HEDGEN		3 :	480.30							
PSILTA HIDAN										
PSSRI HUMAN	SOMATOSTATIN RECEPTOR TYPE I									T
PSTHOM MUMAN										Ī
PSUIS HUMAN		140								
PSYB! HUMAN		•								
PSYD3 HIDAAN		1/-1/								Ī
PSYEP HUMAN	MULTEUNCTIONAL AMENDACYL-TRNA SYNTHETASE (CONTAINS: GLUTANYL-TRN		740 77							
PSYH HUBAAN			704-105							
PSYTI KISKAN		140-167	25.27							
PSYTC HUMAN		497-524	98-989							
PSYV HUBCAN	VALYL-TIMA SYNTHETASE (EC 6.1.9) (VALINE-TIMA LIGASE) (VALRS)	230-237	37.60				-	!		
PSY'N HUBAN		14.46								
NOW A		961-691	245.272							
TAPA HUMAN	HATSULTION FALLS A CONSTRUCT									

PCCENE	1071 17814 Atoti Search on All Haman Praids Sequences	П	\boldsymbol{T}	_	_		_	т		
THE PANE	PROTEIN	AREA!	1	AKAA	A KIN	24110	4	i dan	1	4
PIAN HUNIA	THE ANGLESTION CAPTON THAT IS	201.102					T		1	
PANTO HOMAN	PRANSITION FACION 108-10	274.305				Ī	Ī	Ī	-	
TAU HUNAN	MICROLOGIC E-ASSOCIATED TAIL FETAL			Ī						
PTCOI INMAN	-	201:34	330-357							
PICE HUNAN	7-COMPLEX PROTEIN I (TCP-1)	316-343								
PIDI HUMAN		\$6.19								
PTEK HUNAN	RECEPTOR TYROSINEPROTEIN KINASE TEK FRECURSOR (FC 2 7 1 112) (III'K-6)	П	966-696	1007-10%						
PTF28 HUNGA	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB)	135-162								
PTE HUNKN		43.70	122-149	178.226						
PTFS3 HUMAN	TRANSCUPTION ELONGATION FACTOR S-II.	36-58							-	
PTF HUMAN	TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)	148-175								
PTGFI_HUMAN	TRANSFORMING GROWTH FACTOR BETA I PRECURSOR (TGF-BETA I)	148-183						:		_
PTG#2 HUMAN	TRANSFORMING GROWTH FACTOR BITTA 2 PRICURSOR (TGF-BITA 2) (GLIOHLASTO	241-270							7	
PTGFA HUMBAN		17.114							·	
PTCLK HUMAN	PROTEIN-GLUTAMINE GANOVA-GLUTANIYLTRANSFERASE K (EC 2) 2 1.)									
PTHBS HUMAN		9 9	2						-	
THIX HOMEN	1-KETOACYL-COA THIOLASE PEROXISOMAL PRECURSOR (EC 11.1.16) (BETA-	22.5					1		1	
PTKNB HUMAN	PROTACITYKININ BETA PRECURSOR (CONTAINS SUBSTANCE P. NEUROKININ A						Ì		+	
FILE HUNAN	INAMEDICATION OF THE PROPERTY I	160-070				Ī	T			T
PILES MUNKA	TRANSPORTING FRANCE PROTEIN A	21.21								T
PILES MUMON			(1)				1	Ī	1	T
TOTA HUMAN	DAY TOTALSOMERASE II, ALTER 1902 THE (C. 2.37 1.3)	T	416.647					Ī		T
NAME OF THE PARTY	THOSOLAYORN FIRMON ACTIONAL TAIL	Τ	12.116		T		T		T	
PTPAIN MINIAN	TROPONYOSIN ALPHA CHAIN SKELETAL MUSCLE	Ī	47.74	911:0	147.174	191-217	20.277	T		
PTPACS HELMAN	POPOMYOSIN BETA CHAIN SKELETAL MUSCLE	Ĺ	193-240	Т	Т	Т			-	
PTPMC HUMAN	FROPONYOSIN ALPHA CHAIN, CARDIAC MUSCLE	16.74	3.116	193-277						
PIPM HIMAN	TROPOMYOŚTN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TNI)6) (TMEI)	17.116	110-240							
PTPMO HUMAN	TROPOMYOSIN, FIBROBLAST NON-MUSCLE TYPE (TM30PL)	46-30	11:13		207-234				-1	
PIPALI JEMAN	TROPONIYOSIN, CYTOSKELETAL TYPE (TMIONM)	2		<u>\$</u>		Ī			1	
PIPAIS HUMAN	TROPOMYOSIN ALPHA CIIAIN, SMOOTII MUSCLE (FRAGMENT)	\$	10.17	***			1			Ì
PIPP HOLLAN	TRIPEPTIONL/PEPTIDASE II (EC.) 4 14 10) (179 II) (INJPEPTIONE)	137-121	100	8			1	Ī		Ī
7	THE CALCULATION OF THE CALCULATI		347.340				T		1	Ī
PER HIDAN	THOROTHOPIALEL FASING HORMONE RECEPTOR LIRALRITHYROLIBERUN	146.183		Ī			1	Ī		T
PTRIC HIDNAN	TROPONTN I CARDIAC MUSCLE	16-61		Ī					T	
PTRXA HUMAN	HIGH AFFINITY NEAVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2 7 1 112)	(6-9)	117.148							
PTRSR_HIDAAN	TANSFERION RECEPTOR PROTEIN (TR) (ANTIGEN CD11) (T9)		166-193							
PTSHOT MUMAN	HYROTROPIN RECEPTOR PRECURSOR (TSH-R)	T	П							
NAME ATT	PROTEIN KINASE TXK (EC 2 7 I ·)	T	34-38	20.244	249.58)		Ì			
TANKA HUMAN	MON. RECEVIOR TYRUSING-PROJETY RIVASE LYRI (EC. 2.7 1 112)	20.00				Ī	Ì		1	
PURE MOKAN	MICHER AR TRANSCRUPTION FACTOR I (UPSTREAM BINDING FACTOR II (UBF-1)	187		Ī	Ī	Ī	T			Ī
PUDPO HUMAN	UDP-GLUCURONOSYLTRANSFERASE PRECURSOR, MCROSOMAL (EC 2 4 i 17)	127-754		Ī		Ī				
PUTO HUMAN	RECEPTOR TYROSDIG-PROTEIN KINASE UFO PRECURSOR (EC 2.7 1 111)	411-522								
PUSFI_HUMAN	UPSTREAM STEAMLATORY FACTOR I.	2								
PVATC MUMAN	VACUOLAR ATP SYNTHASE SUBUNIT C (EC.) 61.34) (V-ATPASE C SUBUNIT)	╗	13.16							
TYEL HENCY		╗	13.461	717.744						
PVDG HOMAN	VDGNTD	7	237.760							
VUNC HUMAN	VINCULIA SEL VERS BEOTE LE CE 1 11 1	£ 1	1		1					
PUTET MINAN	MEDIATION PROTEIN PROTECT 3 3 1 121	2017	1	T		1		1		
PWT! HUNCAN		147.374		Ī			\dagger	T	T	T
PXBPI HUMAN		97.135					T			
PXPAC HUMAN	I DNA REPAIR PROTEIN COMPLEMENTING XP.A CELLS (XERODERMA PIGMENTOSLIM 180-311	П			П					
PXPCC HUMON	PXPCC HUMAN IDNA-KEPAIR PROTEIN COMPLEMENTING XP-C CELLS (XEXODERMA PIGNENTOSUM 114-160	П	101-120							

PCT/US95/16733

* AREAS AREAS AREAS AREAS AREAS				١	300 2013-2017 2146-21#D			
ABEA 3 AREA		1047-1081			4 1071-1098 1469-1500 20	301-328		
If Searb on AB Human Protein Sequences	DAMA DAMA DESCRIPTION NO. 196-791	PROTEIN CONDITION OF DIGHTS (AEADORINA FIGHTS CONDITION 115-700	PROTEIN COMPLEMENTING AT 10 CELTS (MANCHES IN 1975)	PROTEIN XROC!	I ENITANCIER. 17-62	PROTEIN 40 (110 MACA CHILDEN CONTROL TO 101-120	PROTEIN 45 (BRC1 144) (FIXACRES 1)	PROTEIN 44 (ZINC FINGER PROTEIN ROTE
M 1.07.17011 10.00	FILE MANIE PROTEIN	PYPDC HEBAN DNA-REPAIR	YOOC HUMAN DNA REPAIR	PXRCC HUMAN DNA-REPAD	PENIO HUMAN ZONC FONCE	PZN40 INDIAN ZINCFINGE	PZN15 IIUNIAN ZINC FINGE	PZN46 HUMAN ZINC FINGE

WO 96/19495 PCT/US95/16733

TABLE X

Search Results Summary for PCTLZIP, P1CTLZIP, and P2CTLZIP Motifs

PCTLZIP LIBRARY FILE PENV POAMV PENV HVIMA PENV HVIMA PENV HVIBC PENV HVIBC PENV HVIZZ PENV	401-406 439-463 183-188 445-460 189-201	LIBRARY FILE PENV BIVOG	434-460			PENY BIVOD	626-642		
	401-406 438-463 183-198 445-460	PENV BIVOG	434-460			PENY BIVOS	626-642		
	481-486 438-463 445-460 188-201	PENV BIVOS	25.5				KEA. R.71	_	
	438-463 183-188 445-460 189-201				-	PENV BIV27	10000		-
	183-188 445-460 186-201	PENV BIV27				DENY FENY!	3047	630-047	
	166-201	PENV FOAMV	401-400	200.000		PENV PIVPE	781.708		
	188-201	PENY HVIKB	752-708			DENY FIVED	770-786		
		PENV HVIMA	437-463			PENV PIVTZ	780-787		
	123-138	PENV HVIMP	163-106			DENV FIVE	39-55	624-641	
	436-463	PENV HVIRH	4418			BENV ELVOI	605-622		
	760-765	PENV HV181	738-764	j		TENT TENT	A25.A13		
	741.760	PENV HV18C	186-201			PENV FLVES	603.610		
	349.384	PENV HV122	123-138			PENV PLVBA	200	100.00	
	349.969	PENV HV1Z3	117-133			PENV FOAMV	//2//	2	
	76. 700	PENV HV1ZH	437-463			PENV FBVDA	040-044		
	749 769	PENV HV28E	760-768			PENV FBVOB	220-925		
	20/27	Beny Mysos	741.756			PENV FBVBM	808-628		
	745-760	ACIN' HVADE	741.750			PENV HV10Y	123-140		
	104-118	PENY NYAU!	349.7K7			PENV HV122	410-427		
PENV MMTVB	616-633	PENV HVZNZ	750.700			PENV HV123	164-171		
	616-633	PENV HVZHO	00/.10/			PENV HV2CA	760-767		
PENV BIVMIK	139-164	PENV HV258	163/00			PENV MCFF	600-617		
	139-154	PENV HV28T	746-760			PENV MCFF3	801-618		
>	391-408	PENY JBRV	10-116	/66.190		PENV MIVAV	630-647		
	391-400	PENV MOFF	307-413			PENV MIVES	025-042		
	391-406	PEND MOFF3	307-413			DENV MIVES	639-656		
	301-400	PERV MLVAV	427-443		-	OCHY AN VER	639-656		
T	402-417	PENV MLVCB	422-438			and the same	A10.AEA		
	403-410	PENY MLVHO	423-430			COUNTY TO SOLD	A2A-A43		
T	286.310	PENV MLVMO	420-442			PEN MINE	147.484		
T	815.00	PENV MLVRD	424-440			PENV MLVAI	200		
T	202-208	PENV MLVRK	424-440			PENV MIVMO	070-070		
	000.00	DELIV MATOR	616-633			PENV MIVRD	924-041		
	301-316	BENN MANTO	018-633			PENV MLVRK	624-641		
	286-301	FENV MINITO	884.880			PENV MSVFB	170-167		
1	206-311	PENV Brvi	A61-877			PERV RMCFV	603-620		
PHEMA INBHK	293-308	PENV BPV3L	200			PENV BFV1	710-727	067-074	
PHEMA MBIB	268-303	PENV SIVUS	201-50	010.00		PENV BFV3L	707-724	064-071	
PHEMA INBID	289-314	PENV BIVMK	201-851	200		PFNV BIVM1	766-783		
	302-317	PENV BIVML	130-104	100		PENV BIVME	765-762		
5	202-307	PENV BIVE	1000-000			PENV BIVML	764-761		
	286-311	PENV BIVEP	010-070			PENY BIVAL	769-766		
	288-303	PHEMA COVO	30-62		+	97/40	272.700		
	301-318	PHEMA CVBLY	301-400			PENV BIVOT	636.83		
PHEMA EVER	301-318	PHEMA CVBM	391-406			CAMP AND	49.60		-
BURNA MEAL	208-313	PHEMA CYBO	201-400		-	PENV BM3AV		300.513	
MEMA INDE	304.300	PHEMA CVHOC	391-408			PHEMA COVO	30-03) (300)	
PHEMA INBUB	200	PHEMA CVMAS	402-417			PHEMA CVBLY	391-408		
1	11000	PARTY CAME	403418			PHEMA CVBM	391-408		
PHEMA DIBVK	303-316	LUE MY CAME	227.28.2			PHEMA CVBO	301-408		

BURNA WILLIAM 1133-148		PHEMA LABAN	221-237		LUCIAN CANOC	200	
T		PHEMA LABUD	234-250		PHEMA IMAIC	322-338	
T		PHEMA IACKA	234-260		PHEMA IABAN	300-323	
T		PHEMA IACKO	231-247		PHEMA IABUD	320-337	
PHEMA PINHW 348-350		PURMA IACKV	230-248		PHEMA INCKA	320-337	
8-8		STATE OF THE PARTY	914.980		PHEMA LACKO	316-333	
		PHEMA INC.	222.282		PHEMA IACKP	302-310	
PHEMA RINOK 366-363		PHEMA IADAS	207.727		PHEMA IACKO	302-318	
		PHEMA IADICA	200.000		PHEMA MCKB	319-336	-
		PHEMA WOR!	767-177		PHEMA MCKV	316-332	
PHEMA BV5CP 7-94		PHEMA IADKZ	221-23/		DURWA IADA1	270.237	
PHEMA BYBLN 7-04		PHEMA LADHO	221-237		CON CHILL	22.220	
PVENV DHVII 42-57		PHEMA IADHA	221-237		PHEMA IAUAS	34.6.338	
		PHEMA IADHS	221-237		PHEMA IADCZ	320-33/	
		PHEMA LADING	221.237		PHEMA IADH1	308-323	
Ī		PHEMA IADH7	221-237		PHEMA IADH2	306-323	
		PURILA IADMO	217.283		PHEMA IADHS	306-323	
PVGO! MBVEB	212 223	BURNA 145W7	234.250		PHEMA IADH4	306-323	
PVGO! HSVII	377.	THE MAN AND AND AND AND AND AND AND AND AND A	991.933		PHEMA IADHO	306-323	
		PHEMA WEND	227.087		PHEMA IADH7	306-323	
		PHEMA INCN	207.767		PHEMA IADM2	322.330	
FVG08 HBV11 134-148		PHEMA LAFPR	230-240		MURITA IANUT	270.947	
PVG10 BPPH2 183-188		PHEMA INHAL	230-252		THEMA INDIA	277.430	
PVG10 BFPZA 163-198		PHEMA JAHAR	235-261		PHEMA IADUS	344.336	-
PV010 H3V8A 109-124		PHEMA LAHCO	230-246		PHEMA WENG	275.000	
		PHEMA IAHC7	230-246		PHEMA IMEN/	372:378	
468-483		PHEMA MANCO	230-246		PHEMA INFIR	316-332	
67:112		PHEMA LANDS	230-246		PHEMA LAGRE	320-337	
		PHEMA LAHFO	236-252		PHEMA MOU2	320-337	
		PURMA JAHKA	236-262		PHEMA LAGUA	319-336	
T		CALLED MALEY	228.282		PHEMA LAHAL	321-338	
		THEMS MAIN	220,246		PHEMA IAHCO	316-312	
₹		PHEMA MARLE	200.240		PUFMA IAHC7	316-332	
		PHEMA INTE	226.262		PHEMA IANCO	316-332	_
		PARMA LANGO	400 400		PHEMA TANDE	316-332	
	2	Prema Annua	224.282		PHRMA TAMPO	321.338	_
		PHEMA IATIO	420,404		OUFUA IANKA	221.918	
		PHEMA IANDA	200 000		PURLLA IANE?	321.338	 -
		PHENEX INTO	200.000		PUFMA IANIE	318-332	
		ביינו איינות	200		PHEMA IANIO	318-312	_
FVGB BPPH2 234-248		PARMA IARIE	200.000		BURMA IANUI	321.336	
		PKEMA IAHIO	707-067		PLEMA IANNA	321.338	
PV08 8PV1R 67-72		PHEMA IAHUM	730-707				
		PHEMA IAKIE	236-251		PHEMA LAHING	010-075	
FV01.2 CVBF 264-278		PHEMA IALEN	236-261		PREMA IANTH	775-015	-
PVOL2 CYBL9 284-279		PHEMA LAMAA	233-240		PHEMA LAHRO	321-336	-
		PHEHA IAMAB	238-264		PHEMA LANGA	321-338	-
-		PHEMA IAMAO	237-263		PHEMA LANSP	316-332	-
		FHEMA LAME!	237-263	-	PHEMA JAHBW	316-332	

					T							<u> </u>																															I	-	-	_		
													621.638																			803.820	A03.820															
701.00		101-101	101	101-101	280-297	280-207	201-208	176-193	176-193	209-226	173-180	646-666	Τ	T	801.1/1	1252-1200	3073-3080	1094-1111	736-763	675-692	736-763	736-753	736-763	597-614	607-624	607-624	180-187	469-486	401.418	14K.182	200.781	346.363	248.263		90.18	81.08	319.730	319.330		24.50	200	38.84	12.04	12.04	12.04	12-04	280-287	3AA.987
PHEMA SV41	PHEMA BVD	PHEMA BV6CM	PHEMA BV6CP	PHEMA BV6LN	PVF08 VACCC	PVF05 VACCP	PVF08 VACCV	PVF09 VACCC	PVP09 VACCV	PV027 H8V8A	PV028 HSVII	BYONG URVIN	TANKS CANA	2007 COVE	PVGB/ HBVII	PVG72 HBVII	PYOF! BYB	PVDL2 IBV6	PVOLB HBVE1	PYGLB HGVE4	PVOLB HOVEA	PVQLS MBVEB	PVOLR MRVEL	PVGIE ILTVE	DVOIR II TVR	TATE BIOM	PVOLC PRVIE	Pydie Cyn	BVO! E BVE	M/01/2 UCAN/A	באשטע שמאל	PVOLH NOW!	אפוע אפאנו	TVGLA NOVIC	SVOLVE BILLI 7	SAVOI M BILINES	STATE SOLICE	TACE TOOLS	FYGEN FOOMS	PVGLM HVPV	PVOLM HVPV	PVOLY LASSO	PVOLY LABBJ	PVOLY LYCVA	PVOLY LYCVW	PVOLY MOPEI	PVM1 REOVD	MA11 DECAM
																								-																								200
																																												204-279	264-279	204-279	264-270	
	-																			212.212													143-168			330-346		618-633						174-180	174-190	174-190	174.180	
324-340	324-340	324-340	324.340	324-340	324-340	324.340	924.340	200.707	3			7.84	7.04	42.67	26-41	101-104	89-104	39.87	100.101	200.000	277.00		108-176	103-118	270-280	70-92	20-38	22-37	108-123	284.200	244-260	1244-1260	22-37	209-263	101-117	130-146	267-282	362-378	89-105	234-240	234-240	67-72	2210-2220	123-139	123-139	123-130	132.130	-
PHEMA PIDS	PHEMA PISHA	PHEMA PISHA	PHEMA PISHT	DUEMA PINKU	PUELLA PITHV	PLIEST BITTIN	FREMA FISHER	PREMA FISHA	PAEMA KIRUA	PHEMA BVB	PHEMA BV5CM	PHEMA SVECP	PHEMA BVBLN	PVENV DHVII	PYENY EAV	PUEDS FOWING	BATES CABAC		TANGE VALLE	PVGO1 MSVED	PVGO) MBVI)	PVG08 HSVII	PVG10 HBVBA	PVG11 H9VII	PVOR 2 HBVII	PVQ1 SPV1R	PV029 HBVII	PVGBG BPOX2	FV036 HBVBA	PVC37 HBVII	PV041 HBVII	PVG48 H8VII	PVGES HBV11	PVCE6 HBVII	PVGED HBVII	PVG66 HBVSA	PVGB9 HBVII	PVOGE HBVII	PV071 HBVBA	PVGB BPPH2	PVGE BPPZA	PV08 BPV1R	PVOF1 BVB	EVOLD CYBP	PACE 9 CARLED	VIEW C 10/20	1000	באמוד האמש
28.40	36.40	9,30	25.07	200	05.02	28-60	26-40	226-241													•																											
AVAITA 141.61			Ţ		1			PVMT9 MYXVL																																					•			

PVGLF TRTV
278-283
355-371
400.616
489-515
743-758
600-628
366-371
166.371
826-642
960-985
12.84
12.04
12.84
12-04
12.04
12-04
1021-1037
621-638
191-207
136-161
135-161
166-205
189-205
10.134
110-134
119134
118-134
110-134
116-131
360-398
187-202
376-393
363-388
383-398
363-398
383-368
234-248
26-40
25-40
V 24

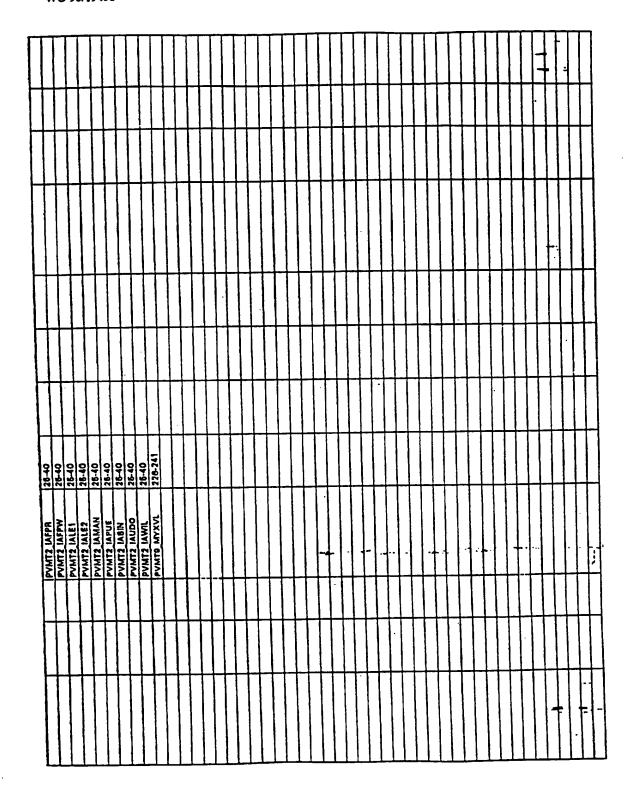


TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP, P5CTLZIP, and P6CTLZIP Motifs

						05.711.710			TOC. I.A.			ĺ
Pachaip			PACTIZIP			BOAGY ENF			LIBRARY FILE			
LIBRARY FILE			LIBRARY FILE			LIGARY TILE	280.400		PENV BIVOS	47.09	626-646	
DELLY BIV97	147.186		PENVI FRSFV	360.300		PENVI PHSFV	200		PENV SIV27	47.68	147.160 564.575	1.575
TO STATE OF THE PARTY OF THE PA	R10.828		PENV AVIBU	08-117		PENV2 FRSFV	3000		DENIV BEAVI	235.248	630.061	
2000 000	AC		PENV BIV27	147.188		PENV BAEVM	1/0/100		בנות ביינה	834.64		
PENV CARVO			PENV HV12H	1123.142		PENV FIVPE	781-601		בניים ביים	200	ACE. 828	
PENV HVZBI	90/30/		DENV HV202	0.20		PENV FIVSD	779.700		PENV PLVUL	000.788		
PENV HV2DI	741.768		Sent under	378.707		PENV FIVT2	780-800		PENV FLVL®	407-488	0.0.070	
PENV HV201	741.769		בניים יים	64.6		PENV FLVOL	0.20		PENV FLVSA	444-405	602-623	Ī
PENV HV2NZ	742.780		PENV JSKV	200		PENV FOAMV	266-276	924-944	PENV FOAMV	163-174	967-978	
PENV HV2RO	751.760		PENV RSVP	293.662		Service Comme	9.20		PENV FSVOA	467-488	026-040	
DENV LIVER	743-781		PHEMA VACCC	173-102		ACIA LINGY			PENV FEVOR	447.460	805.626	
ביייי איייי	746.363		PHEMA VACCI	173-102		PENV HVICE	D		Devis caves	480.471	A09.839	
יבואר ארצהי	236.304		PHEMA VACCT	173-102		PENV HV2CA	/60//09/		LENA LINA	467.488		
VENV JOHN			PHEMA VACCV	173-102		PENV MLVF6	400-420		TENY TOVO!		. 079 013	
PHEMA FIZH	07.0		BVENV REV	62-61		PENV MMTVB	043.663		PENV GALV	57:20		
PHEMA PIZHT	116-138		מינבויי ביינו	01.80		PENV MMTVO	043-663		PENV HV28E	780771		•
PHEMA BV41	66.73		TVENV MCV	2		PENV OMVV3	96.94		PENV HV201	741-702		
PVENV THOOV	473.401		PVENV MUV			PENV RSVP	42.62		PENV HV2NZ	742-763		
PV010 8PP22	83.101		PVFUS ORFIX	200		DENV REVI	024.044		PENV HV2RO	781-772		
PV024 BPT4	116.133		PV001 HSVEB	100.100		16773	021.041		PENV HV28T	746-766		
PUNTA MEVSA	344-362		PVG01 VACCC	376-385		FENV OF VAL			DENV LICE	800-621	_	
	14.33		PVGOI VACCV	316-334		PENV SIVMI	100/00		TENA MICH.		<u> </u>	
PVG40 H3VII			PURCH VARV	376-306		PENV SIVME	765-785		PENV MCF13		1	
PV050 HEVBA	10.0		DYON BOTA	A27.848		PENV BIVML	764.764		PENV MLVAV	930-00	-	
PVOE1 BPT4	63.81		1000	18.84		PENV GIVB4	769-769		PENV MLVCB	026-040	- -	
PVD61 MSVII	84-102		TOIO HE		160.189	PENV SIVSP	773-703		PENV MLVFB	639.660	-	
PVOSE HSVII	166-173	- 1	PVQ11 H3VII	103.144		PHEMA COVO	403-613		PENV MLVFF	639-660		-
PVOF1 18VB	2788-2806	3374-3382	FVO! BPPH2	20.15		SUELLA CABIN	117-100		PENV MLVFP	030.000		
PVQL2 CVH22	1063-1071		PVOI BPVIR	969-679		PHEMA CVOLT	301.411		PENV MLVHO	626-647		1
PVGI 2 BVB	1066-1074		PV020 8FT4	231.260		MOAD WELL	100		PENV MLVKI	167-168		
PVOL 3 IRVE	1066-1073		PY032 VZVD	90-109		PHEMA CVBU	2000		PENV MIVMO	629.650	-	
1010	1056-1074		PVG36 BPK3	132.161		PHEMA CVHOC	1000		DENV MI VRD	024.046	-	
1015 BVC	1056.1073		PV037 8PT2	10.36	620.648	PHEMA CVMAS	402-422		BENY MI VOT	A24.645	-	
PVGL 2 IBVA	1066.1071		PVQ37 BPT4	10.38	926.644	PHEMA IACKO	101.101		PENV MINTE	197191	-	
PVGLZ IBVM	600 630	AAD. 207	PVG39 H9VII	1038-1067		PHEMA IADMA	101-101		PENV MOVED		- -	
PVQLB MSVB1		1	PUGA1 HSVII	62-81		PHEMA MUMPM	397-417		PENV RMCFV	903-076	-	
PVOLB HEVBC	27.70		DUCA TAPPES	380-309		PHEMA MUMPA	307-417		PENV 9FV1	967-978		Ī
PVOLO HSVSA	664.002		DUMAN RPPF1	337.350		PHEMA MUMPS	307.417		PENV BFV3L	167-170	979:66	
PVOLB ILTVB	740-76B		PAGE DAVID	142.181		PHEMA PHODV	403-613		PENV BIVA1	437-460		
PVOLD ILTYS	760-788		Primer Levis	117.138		PHEMA PITHW	322-342		PENV BIVAG	442-403	+	
PVOLB ILTVT	760-788		1000	200	1073.1081	PHEMA PIZH	13.33		PENV BIVAI	421-442		
PVOLC VZVD	431-440		PVG07 H3VII	200	2108.2122	PHEMA PIZHT	13.33		PENV BIVAT	436-450		
PVOLC VZVS	431-440		PVGP1 IBVB	200		PHEMA RINDI	407.817	_	PENV BMSAV	42-03	-	
PVOLF PISH4	2.04		PVGLZ CVBr			PHEMA SENDS	322.342		PHEMA CVMAS	402-423	-	
PVGLH H6V60	314-332		PVOL2 CVBLB			PUEMA AFNDE	322.342		PHEMA INDET	200-207		
PVOLH HBVE4	614-832		PVOL2 CVBLY	0.01.100		DUELLA RENOW	322.342		PHEMA MUMPM	226.246		
PVOLH HEVED	807-626		PVQL2 CVBM	001-1010		SUSTAN SEND I	332.342		PHEMA MUMPA	226-240	_	
BVO I MAVI	6-04		PVOL2 CVBO	991-1010		PACINA BENDO	333.373		PHEMA MUMPS	226-246		
7410	676-696		PVOL2 CVBV	991-1010		PHEMA BENDA	344.324	901	PUEMA PHODY	213-234	-	
AMIN OLINA	134.183	177.106	PVDL2 CVH22	766-787	1116-1134	PVENV LELV	75.72	1140-100	LUCIUV LUCO.			

7									Ī			Ī							-										Ī	T					-							T	T	T							
		370-400	378-400	379.400	370.400		<u> </u>	-	-		1		_			-	·			ŀ		.	-	-						+				-								1	+	1						463.474	
13.34	13.34	7.20	7.28	7.20	7.28	160.100	688.610	314.336	200	00.00	167.178	266-309	901-98	1165-1170	266-287	30.61	218.260	1000	10000	10/-1/0	1269-1200	1269-1260	1269-1200	1269-1260	1260-1200	1269-1280	1317.1338	13AR. 13AA	200	11/0/11	93.50	82.103	82-103	83-104	136-160	448-487	1338-357	224-246	227-240	224.246	440.407		440-40/	440-407	306-326	460-4771	460-171	460-471	450-471	405-420	
PHEMA PIZH	PHEMA PIZHT	PHEMA 6V6	PHEMA GV6CM	PHEMA BV6CP	PHEMA SVELN	PVOOL MSVEB	PVOOT HEVIT	Aves trevis	MACH CZDY	FVU37 BPOX2	PV043 H9VII	PVGEE HSVII	PVOE6 HSVBA	PVQ56 HBVII	PVG58 HSV8A	PVG60 HSVII	מעספי ניפעון	1100 000	OCT I INCO	PVGH3 HCMVA	PVOL2 CVBF	PVGL2 CVBLB	PVOL2 CVBLY	PVOL2 CVBM	PVOL2 CVBG	eval 2 CVBV	EVOLUE CVIA	TARIA CARA	CAMAD PARA	PVOL2 CVMJH	PVOLB HBV11	FVOLD HGV1F	PVOLB HBV1K	PVOLD HBV1P	PVOLB MCMV9	PVOLC PRVIP	PVOLF COVO	PVOLF MEAGE	PVOLP MEAB!	PUDIE MEARY	OLOGE ALLIABAL	VOLT MOM! A	PVOLE MUMPR	PVOLF MUMPS	PVOLF PHODY	PVOLF PITHC	PVOLE PIZH	PVOLF PIZHO	PVOLF PIZHT	PVOLP PISS	
¥	Ĭ.	Ě	٤	Š	É	1	1		1	0 70-990	٤	٤	۵	اهٔ	١	16	İ			-	378-398 P	٥	ā	۵	1						۵	ă.	6	4	d		-		٩					-	•	٥					
366-370	298-318	237.267	208-318	19.16		36.46	12.131		300 320	648-868	20-40	336-356	117.137	124-144	128.34R	333.343	7575	378-348	328-348	327-347	327.347	310-330	732.752	750-770	761.771	70.00	90.07	78.00	99-99	72.02	270-280	63-63	738-768	283-303	464-474	454.474	464-474	484.474	464.474	000	200-0/0	1326-1346	1326-1346	996-1016	9101-000	1000-1020	1001-1021	1001-1021	1166-1170	1000-1020	
PVENY THOOV					Ī	LAGO AVA	PVGO BYTT	PVG12 HSVII	PV022 H9VII	PVG38 HSVII	PVGE1 H3VII	PVG63 H9VII			6/01 & 10/0			PVOL2 IBVD2	PVGL2 IBVD3	PVGL2 IBVK	PVGL2 18VM	PVGL2 IBVU2	PVGLB EBV	PVOI B HCMVA	BYOLD MINNT	CC//417 4:07	PVOLB HSV23	PVGLB MBV2H	PVOLB MSV28	PVOLB HBV6U	PVOLB HSVB2	PVGLS HBVBA	PVOLB MCMV8	PVGLF PISH4	PVOLO RABVE	PUDIO BARVA	DVOLO DARVO	PVOLO BABVE	TV810 010/10	VOLU KABY I	FVGLM MCMVB	PVOLM BUNL7	PVOLM BUNSH	PVOLM BUNYW	PVOLM HANTB	PVOLM HANTH	DVOIM MANTI	PVOLM HANTV	PVOLM RVPVZ	SVOI M SEOIIB	VOLEN SECON
٩			630.000	1	7	1		١		770-789 P	771.700 P	Γ	Τ	T						٩	467.488 P	Γ	Γ	١				•	-																						7
8101.000	04.7.0AA	000	Ť	1	1	814-833	614-833	9		_		T	T	T	100/100/	92/-/0/	117.136	260-276	266-285	200-206	Γ			146.66	430.400	3/2-381	44.03	276-207	117-136	162-171	007-1010	166.174	166.174	830.849	910.010	200	-10.000	201.00	1100-1104	621.640	171.180	136-166	174-193	174-103	174.103	121.100					
PAYOF 4 PAYA	SEASON OF THE PERSON OF THE PE	CVMAD	CVMJH	CVPFB	CVPPU	2 CVPR8	5		PVGL 2 18VB		BVD2		YAD.	M/BI	HCMVA	PVQLB HCMVT	PVOLB HSV&U	PVQLB ILTVB	PVGLB ILTVS	PVOLS ILTYT	PVOI C MEVI 1	9V01 C 44V1E	שולאים הפולטו	PVOIC MSVBC	PVQLG CHAV	T		PVOLI VZVD				PANIS M PRINCE	CHOCK BOOK	PVOLET FOOMS	PVOLM NATA	PVULM MVIVE	PVGLM UUX	PVGLY LYCVW	PVQNB CPMV	PVM3 REOVD	PVME1 CVBM	PVME1 CVH22	PVINE! CVPFB	PUMEI CVPPU	SYNE CVPRM	TAMES COUNTY	PVME1 CVING				
	120.14																												_															1					_		-
	101-00	227-248	227-248	44-62	100-208	180-208	183-201	183-201	183.201			102.50	103-201	160-106																																					ļ .
	,		PVMI REOVL	PVMAT HRBVA	PVMAT NDVA	PVMAT NDV8	PVMP CAMVC	PUMP CAMVD	DYM CAMVE		T	1	PVMP CAMVW	PVMP FMVD																																					

						_					+			1														239-260				1	1														
	22022	220-241	460-481	160-161	460-481	460-461	480-481	482.474		/D0-00	217.100	117-000	304-326	207-310	060-670	2.23	2.23	107.218	180-211	160-211	103-214	237-269	236-269	67-88	261-302	230-251	189-160	200-221	122-143	64-86	201-222	70-01	244-205	244-266	244-268	233-264	10-01	233-264	233-264	233-264	70-01	233-264	244.206 1	244-205	70-01"	233-264	114.964
	PVOLF RINDK	PVOLF RINDL	PVOLF BENDS	PVOLF BENDF	PVOLP GENDH	PVQLF BENDJ	PVOLF BENDZ	AVA. 6 4744	PVOLF BVA	PVOLF BVB	PVOLH HCMVA	PVOLH HCMVT	PVOLH HBVE4	PVQLH HBVEB	PVOLH HBVSA	PVOLI HBV2	PVQLI H9V23	PVOLM BUNDE	PVOLM BUNL7	PVOLM BUNSH	PVOLM BUNYW	PVOLY LABBO	PVOLY LABBU	PVGP6 EBV	PVM01 VACCC	PVM01 VACCV	PVMAT HRSVA	PVMAT RINDK	PVMAT TRTV	PVME1 CVHOC	PVMBA HPBDB	PVMBA HPBVO	PVM8A HPBV2	PVMBA HPBV4	PVMBA HPBVB	PVMBA HPBVA	PVM6A HPBVD	PVMGA HPBVI	LVBAH ARMVA	PVMEA HPBVL	PVM8A HPBVN	PVMBA HFBVO	PVM8A HP8VP	PVMBA HFBVR	PVMSA HPBV8	WARA HPBVW	WASHING A STREET
800-1010	026-046	12-32	12-32	12.32	161-161	066.016	900-900	37.	309-329	308-328	312-332	312-332	308-328	308-328	74.04	74.04	74.04	74.04	201-221	200.228	202.313	307.227	919.232	212.232	919.932	212.232	63-63																-	-			
PVOLM BEOUS	PVOLM UUK	PVOLY LYCVA	PVOLY LYCVW	DVOIV BIABV	PVOUR CRIMY	The state of the s	PVMAI MUMPS	PVMAT NUVA	PVMAT NOVB	PVMAT PIZHT	PVMAT PICHA	PVMAT PIANB	PVMAT 9V41	PVMAT 6V6	DVMF1 IAVA	DVAIE 19VB	DVMF1 IRVA?	DVMC1 INVE	DVIVA HIPADR	SUMPLY MEDICE	DIVAGE LIBRUE	BULLET WANT	DVALOA WAVED	PULLA WAV	DUMA WILL	FVMEA WHVBI	PVM9A WHVW8																				
																										\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\			-																		
																			-																												
										-		1-1-1-1													4		.	+		+	1	-	-	4	-	-	1	1		-	1	1					_
-																																+	+			†	+									-	
																																												-			

																												T			
233-264	28-46	26-40	26.40	25.40	28.40	26.40	26-48	26-40	26.40	25.40	25.40	26.40																+		=	
i																															
L																															
																													-		
																				•											7
									-																						
																			,			•				1					-
																															•••

WO 96/19495 PCT/US95/16733

TABLE XII

Search Results Summary for P7CTLZIP, P8CTLZIP, and P9CTLZIP Motifs

			PACTIZIE			POCTLZIP			_	+			
770178			LIBRARY FILE			LIBRARY FILE							
LIBRARY PILE	400 400		PENVI FRSEV	360-403		PENV BLVAF	303-327			+			
PENV BARVM	277.707		PENV3 FREN	300-403		PENV BLVAU	303-327			-			
PENV HVIBI	020000		DENV BINDA	178.201		PENV BLVAV	303-327						
PENV HVIDO	010.70			367.330		PENV BLVB2	303-327		_				
PENV HVIBN	010-00		PENV EGANV	604.687		PENV BLVBG	303.327						
PENV MVIBA	979-509		PENV MV123	176.108		PENV BLVJ	303-327		-	-			
PENV HVIEL	10000		oruv uvans	3.26	761.804	PENV FIVPE	781-605						
PENV HVIH2	486-620		PENV NV3CA	150.22	1	PENV FIVSD	770-803						
PENV HV1H3	488-620		FENV NV CA	Τ	772 706	PENV FIVT2	780.604						
PENV HV1J3	610-632		PERV HVZDI	200	!	PHEMA CVBLY	391.415						
PENV HV1JA	480-612		PERV MYZUI			BUENA CVRW	301.416			•••			
PENV HVIKB	604-620		PENV HVZNZ	277.600		CAN AND AND	101.416			_			
PENV HVIMA	600-522		PENV JSRV	541.554		THE MA CAGO	301.416						
PENV HVIMP	480.616		PENV BEVI	864-867		PHEMA CANOC			<u> </u>				
PENV MVIND	488-610		PENV GFV3L	861.004		PHEMA INCCA	447.400			-			
מפווא וואופא	49A.520		PENV SIVMI	603-626		PHEMA INCEN	430-454						
בעה שב	, ,		PENV BIVMK	802-825		PHEMA INCOL	430-464			1			
PENV HVIBI	T	406 617	DENV BIVILL	801.824		PHEMA INCHY	420.463						
PENV HVIZZ	1	10.00	PONT OF THE	BOA 879		PHEMA INC.H	443.467						
PENV HV128	407-519		PENV BIVOS			PUEMA BUCKY	420-463						
PENV HV128	606-627		PENV BIVSP	2000		BASE MENA	420.467			_			
PENV HVIZH	498-520		PHEMA COVO	577.002		THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON AND	99-99		PHEMA MUNA	202-076			-
PENV MPLN	213-236		PHEMA PIZHT	66-68		PHEMA INC.	430-484						
DRIVE GOVE	213.236		PYF11 VACCC	161-164		PHEMA INCP2	430-464		-				
PLEASE AND IN	17.60		PVF16 VACCC	26-48		PHEMA INCP3	430-464						
CALETA ABAN	21.43		PVP18 VACCP	3-20		PHEMA INCTA	430-464						
PHEMA WOAR			PVG1L AMEPV	313-336		PHEMA INCYA	430-484						
PHEMA IADAS			BV038 MEVNI	401.514		PHEMA MUMPM	101-126						
PHEMA IADK2	21-43		MAN PAGNE	122.346		PHEMA MUMPA	101-126						
PHEMA LADHS	21.43		2000	230.363		PHEMA MUMPS	101-126						
PHEMA LADHA	21-43		TAGE VENT	339.746		PHEMA PITHW	20.63						
PHEMA IADHS	21:43		TARK YORK	10.33		PVENV REV	62.60						
PHEMA IADHO	21-43		TAGE CABL	AK1.674		PVF05 VACCC	280-304						
PHEMA IADHT	21-43		7107	10.33		PVF08 VACCP	280-304			_			
PHEMA IADMZ	37.68		PVOL 2 CVM4	1267-1280		PVF05 VACCV	201-306						
PHEMA IADMA	0007		DVOL 9 CVMAE	1216-1230		PVF00 VACCC	176-200			-			
PHEMA IADUS	3/.00		2013 CVM IN	1126.1140		PVF00 VACCV	176-200			-			
PHEMA LAENO	21:43		- 10/6 - 10/6	1974.1207		PVG01 VZVD	60-02						
PHEMA IMEN?	37.60		PVGL2 CVFT	1272-1205		PVQ10 H6V8A	366-370						
PHEMA IAMAO	37.68		PACI 9 CARDS	1060-1073		PV012 H8V9A	00-07						
PHEMA LAME!	37.00		EVOL 2 CVERA	1060-1073		PVG18 H8VII	00.112			_			
PHEMA LAME 2	37.60		- CO CO.	1377.1300		PV028 HSVII	173-107		-	1			
PHEMA HIMEO	27.5		200			PVD43 MEVII	108-133		-				
PHEMA LANTO	37.50		ביסוק שאפ	106.318		PVG67 HBVII	108-132	1006-1029	-				
PHEMA MOUT	21-43		אמר ז ופאפ	200.0		PV022 HEVIT	720-744						
PHEMA INTRM	33-66		LVGLZ IBVDZ	917.00		PVGF1 BVB	3601-3626		_	_			
PHEMA LAUDO	37.69		The Contract of the Contract o										

PCT/US95/16733

17-60 17-6			֓֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֡֓֓֡֡֡֡֡֜֜֜֜֜֡֡֡֡֓֜֜֜֡֡֡֡֓֡֡֡֡֡֡	PVOL 2 INVE	196-210	PVOLB	PVGLB HSVMD	669-613		+	1	
13-16		20 20		MARI & INVA	106-218	PVQLB		607-621			†	
11-13		37.60		100 A 100 M	178.201	PVOLB	ILTV8	607.031		1		
21-43 VVOIL BUAD 176.201 PVOIL BUAD 19.401 19.437 19.431 19		97.60		אמר ז ופאסו	100.00	PVOLB	ILTY!	607-631		-		
17-93 VVOID B (MENAT) 615-666 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) 615-667 VVOID B (MENAT) VVOID B (MENAT) CVOID B (MENAT)		21:43		VOLZ IBVUZ	100.00	PVGLE	H9V11	413.437		1		
17-56 PVOLE HENRY 10-50 PVOLE SV6 PVOLE HENRY 10-50		21-43		PVOLZ IBVUS	1/040	PVOLE	OVEN	469-493			+	
20-86 VOLUE MCAN'S 405-60 VOLUH HCMYA 12-60	IA IAZUK	37.60		VOILE HCMVA	20.00	PVQLE	976	401-426				
Color Colo	IA PHODV	30-60		PVGLB HCMVI	487.604	MIDA	HCMVA	674-598				
05-67 PVGLC H8V1K 463-460 PVGLM H8V1E 443-467 172-44 PVGLC H8V1K 453-460 PVGLM H8V1E 443-467 172-45 PVGLC H8V23 436-460 PVGLM BLMSH 31-56 172-51 PVGLC H8V23 436-460 PVGLM BLMSH 31-56 172-51 PVGLM BLMSH 325-1410 PVGLM BLMSH 344-386 172-16 PVGLM UNK 362-3410 PVGLM BLMSK 344-386 172-16 PVGLM UNK 362-3410 PVGLM BLMSK 344-386 172-16 PVGLM UNK 325-3410 PVGLM BLMSK 344-386 172-16 PVGLM UNK 325-3410 PVGLM BLMSK 344-386 172-16 PVGLM UNK 325-3410 PVGLM BLMSK 344-386 172-16 PVGLM UNK 32-36 PVGLM BLMSK 344-386 172-16 PVGLM UNK 32-36 PVGLM BLMSK 344-386 172-16 PVGLM UNK 32-36 PVGLM BLMSK 342-386 172-16 PVGLM UNK 32-36 PVGLM BLMSK 342-386 172-16 PVGLM UNK 32-36 PVMR BLMSK 32-36 172-16 PVGLM UNK 32-36 PVMR BLMSK 32-36 172-16 PVGLM BLMSK 32-36 PVMR BLMSK 32-36 172-16 PVMR BLMSK 32	IA PIZN	66-67		TOTAL MOTOR	500-589	PVOLH	HCMVT	673-687		+	1	
17-316	IN PIENT	66-67		TARREST TO A COLOR	447.480	HIDA	HEVII	443-407	003-827			
12-84 PVOLE HSU23 436-469 PVOLE BUN17 130-1410 PVOLE BUN19 150-72 PVOLE HSU23 436-469 PVOLE BUN19 150-72 PVOLE HSU23 436-469 PVOLE BUN19 150-72 PVOLE HSU31 150-72 PVOLE HSU31 150-72 PVOLE BUN19 PVOL	7 CAPVR	2	1	איסור שפייוני	447.480	PVOLH	HSVIE	443-407	603-627			
17-336	9 VACCO	72.04		PVOLC HOVIN	436.464	PVOLM	BUNL?	31.66				
C 5672 PVOLIM BUNNY 1397-1410 PVOLIM HANTH C 11-33 PVOLIM BUNNY 1397-1410 PVOLIM RVPV 11-33 PVOLIM BUNNY 1397-1410 PVOLIM RVPV 11-33 PVOLIM UUK 66-819 PVOLI	II HEVII	317-336		PVOLC MEV2	436.460	PVOLN	BUNSH	31.66		-		
C 11-33 FVGLM BUNSH 1367-1410 FVGLM RVFVZ 11-33 FVGLM BUNSH 1367-1410 FVGLM RVFVZ 11-33 FVGLM LUK 12-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPMV 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 17-35 FVGLM CPM 18-35 FV	3 VACCC	50-72		PVOLC HSV23	0177	PVOLN	HANTH	694-718				
11-33 PVGLM BUNSH 130-101 11-30 PVGLM BUNSH 12-56 PVGLM BUNK 10-10 PVGLY JUNIN 12-36 PVGLM BUNK 175-166 PVGLY LASS 12-36 PVGLM BCNV 13-16 PVGLY LYCVA 12-36 PVM1 REOVO 13-16 PVGLY LYCVA 12-36 PVM1 REOVO 13-16 PVGLY LYCVA 12-36 PVM1 REOVO 16-2-26 PVGLY LYCVA 12-36 PVM1 REOVO 16-2-26 PVGLY TACY 12-36 PVM2 REOVO 17-2-26 PVGLY TACY 12-36 PVM2 REOVO 17-2-26 PVGLY TACY 12-36 PVM2 REOVO 15-2-26 PVGLY TACY 12-36 PVM2 REOVO 15-2-26 PVGLY TACY 12-36 PVM2 REOVO 15-2-26 PVGLY TACY 12-36 PVM2 REOVO 15-2-26 PVM1 REOV TACY TACY TACY 15-2-26 PVM1 REOV TACY TACY 16-2-107 PVM8 HEDC TACY TACY 16-2-107 PVM8 HEDC TACY TACY 16-2-107 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACY TACY 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC TACK 17-136 PVM8 HEDC 17-136 PVM8 HEDC 17-136 PVM8 HEDC 17-136 PVM8 HED	3 VARV	56.72		PVOLM BUNL?	0170	PVG! I	I AVEV	344.368				
11-33 PVGLY LASS 12-36 PVGLM UUK 12-36 PVGLM UUK 12-36 PVGLY LASS 12-36 PVGLY EBV PVGLY LASS 12-36 PVGLY EBV PVGLY LASS 12-36 PVGLY EBV PVGLY LASS 12-36 PVGLY EBV PVGLY LASS 12-36 PVGLY EGV PVGLY LASS 12-36 PVGLY EGV PVGLY TACVY 12-36 PVM1 REOVD PVM1 REOVD PVM1 REOVD PVM1 REOVD PVM2 TACVY 12-36 PVM2 REOVD PVM2 TACVY 12-36 PVM2 REOVD PVM2 TACVY 12-36 PVM2 REOVD PVM3 TACVY 12-36 PVM3 REOVD PVM3 TACVY 12-36 PVM3 TACVY	M VACCC	11.33		PVOLM BUNSH	138/12/10	N IONA	RVEVZ	344-368				
175-166 PVGLY_JUNIN 12-36 PVGLY_CONT PVGLY_LONN 12-36 PVGLY_CONT PVGLY_LONN 12-36 PVGLY_CONT PVGLY_C	A VARV	11.33		באסרא חחצ	100000	10/0	TITIE	601.686				
175-195 PVGLY LASSO 12-15 PVGLY EBV 20-42	D HSVI	66-110		PVOLY JUNIN	97.2	1200	A CPMV	311-335				
10-16	INOH BE	173-186		PVOLY LABBO	12:30	600/10	789	057.081				
134-166	M M M	20.42		PVOLY LABSJ	12:30			REA. R78				
11-83 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE 12-36 PVMI REOVE PVMI REOVE 12-36 PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE REOVE PVMI REOVE PVMI REOVE PVMI REOVE REOVE PVMI REOVE REOVE PVMI REOVE REOVE PVMI REOVE REOVE PVMI REOVE PVMI REOVE REOVE PVMI REOVE REOVE PVMI REOVE PVMI REOVE REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE PVMI REOVE REOVE PVMI PVMI REOVE PVMI PVMI REOVE PVMI PVMI PVMI PVMI PVMI PVMI PVMI PVMI	1707	134.160		PVOLY LYCVA	12.36	PVGP	ruv Tu	200				
100	A WOVE	11.03		PVOLY LYCVW	12.38	₽VM:	REOVO	200				
13-1-13-15-15-15-15-15-15-15-15-15-15-15-15-15-		104.300		PVOLY MOPEI	12.36	PVM1	REOVE	205-002	-			
13-7-1369	WAN BE	462.380		PVGLY TACV	12.36	PVM2	REOVD	166-102	+	+		
13.75 PVALY TACY7 13.36 PVALY REOVL 13.47-1368 PVALY TACY7 13.36 PVALX REOVL 13.47-1368 PVALY TACY7 13.36 PVALX REOVL 1066-1078 PVALI REOVD 324-347 PVALT GEPUS 1066-1079 PVALI REOVD 237-360 PVALE CVRC 1066-1077 PVALI MUMPS 237-360 PVALE CVRC 1066-1077 PVALI MUMPS 237-360 PVALE CVRC 1066-1077 PVALI MEDC 236-292 PVALE CVRC 1066-1077 PVALI MEDC 236-292 PVALE IBVE 1066-1077 PVALI MEDC 236-292 PVALE IBVE 1066-1077 PVALI MEDC 236-292 PVALE IBVE 1066-1077 PVALI MEDC 236-292 PVALE IBVE 1066-1077 PVALIS APBUL 236-292 PVALE IBVE 1066-1077 PVALIS APBUL 236-292 PVALE IBVE 1066-1077 PVALIS APBUL 236-292 PVALE IBVE 1066-1077 PVALIS APBUL BVALIS APPUL 1066-1077 PVALIS APBUL BVALIS APPUL 1066-1077 PVALIS APBUL BVALIS APPUL 1066-1077 PVALIS APPUL BVALIS APPUL 1066-1077 PVALIS APPUL BVALIS APPUL 1066-1077 PVALIS AP	HBVII			PMOLY TACVE	12.36	PVM2:	2 REOVO	10B-18Z	+			
1347-1366	NA S	36.55		PVOLY TACY?	12.36	PVM2	REOVJ	100-102		+		
00-02 00-0	NAME OF	2		PVOLY TACVT	12.38	PVM2	REOVL	168-182	†	\mid		
1066-1079 PVM1 REOVD 324-347 464-477 PVMAT GEPVB 1066-1079 PVM1 REOVL 464-477 PVME! CVHOC 1066-1079 PVMAT MUMPA 227-250 PVME! CVHOC 1066-1071 PVMAT MUMPA 237-250 PVME! CVHOC 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD 268-292 PVME! BVB 1066-1071 PVMAA HPBD PVMAA WHVB 1066-1071 PVMAA HPBD PVMAA WHVB 1066-1071 PVMAA WHVB 1066-1	N HOVE	200		PYDNM CPMV		_	T MEASI	07-111	†	-		
1066-1072	BLAIR.	9000		PVAI REOVD		┪	T CEPVB	314-338		+		
1006-107 1006-107 1006-107 1006-107 1006-107 1006-107 1006-107 1006-107 1006-107 1006-107 1006-107 117-130 1746-70	7 HV6	1000-1070		PUMI REOVI	464-477	PVME	CVBM	137-161	1	+		
1056-1077 PVMSA HPBDB 269-202 PVME1 CVTKE 1056-1077 PVMSA HPBDC 266-201 PVME1 IBVG 1056-1077 PVMSA HPBDC 266-201 PVME1 IBVG 1076-107 PVMSA HPBDC 231-264 PVME1 IBVB 266-201 PVMSA HPBDW 266-202 PVME1 IBVB 266-201 PVMSA HPBDE 236-202 PVME1 IBVB 266-201 PVMSA HPBDE PVMSA HPBGS 266-202 PVMSA HPBDE PVMSA WHV5 266-203 PVMSA WHV5 266-203 PVMSA WHV5 266-504 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-506 PVMSA WHV8 266-507 PVM	2 BV6	1000-10/		PUMAT MIMPS	227.260	PVME	CVHOC	107-101		+		
1056-1077 FVMBA HPBDC 268-291 FVME1 IBV0 1056-1077 FVMBA HPBDC 231-264 FVME1 IBVB 1056-1077 FVMBA HPBDU 231-264 FVME1 IBVB 236-292 FVME1 IBVB 236-292 FVME1 IBVB 236-292 FVME1 IBVB 236-292 FVME1 IBVB 236-292 FVME1 IBVB 236-292 FVME1 IBVB 236-292 FVMBA HPBDB 236-292 FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPBDB FVMBA HPWBB 464-609 FVMBA HPWBB FVMBA H	12 m/02	1056-1078		EVILA MPRDR	269-202	PVME	1 CVTKE	137-101				
1056-1077 PVW9A HPBOU 231-264 PVME1 IBVB 117-139 PVW9A HPBOU 231-264 PVME1 IBVB 126-107 PVW9A HPBOW 269-2 PVME1 IBVB 126-421 PVW9A HPBUE 236-26 PVME1 IBVR 126-421 PVWBA HPBUE 236-26 PVWBA WHVI 126-207 PVWBA WHVI 126-207 PVWBA WHVI 126-207 PVWBA WHVI 126-208 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI 126-209 PVWBA WHVBI	2 IBVR	1056-1077		JOSEPH SELLING	268-201	PVME	1 1876	74.00				
117-139 FVM83 HPBDW 268-292 FVME1 IBV82 246-197 FVM84 HPBDW 268-292 FVME1 IBVR 230-420 FVM84 HPBDW 268-292 FVM84 HPBDB 269-202 246-202 FVM85 HPBDW 268-292 FVM85 HPBDB 269-202 246-203 FVM85 WHVS PVM85 VM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM85 WHVWS PVM85 PVM8	2 IBVM	1086-1077		TOUR TOWN	211.264	PVME	1 (5/6	14.00				
246-707 PVME1 BVK BVK	B HBV6U	117-139		MODEL VEWA	249.202	PVME	1 (6/62	24.08				
100-421 PVMSA HTGHE ASSETT PVMSA HTGGS 100-420 PVMSA HTGGS 100-420 PVMSA WHYS PVMSA WHYS S 100-420 PVMSA WHYWS 100-420 PVMSA W	B HEVE2	746-707		TOPLE VOICE	226.950	PVME	- BVK	74-99				
1 350-420 PVMBA WHV! 200-121 PVMBA WHVS0 200-127 482-504 PVMBA WHVS0 404-500 PVMBA WHVS0 404-500 PVMBA WHVBI 404-500 PVMBA WHVBI 404-500 PVMBA WHVBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500 PVMBA WHVWBI 404-500	C HBVMB	300-421		PVM3A HFBME	-	SW>4	A HPBGB	271-206				
399-421 PVMEA WHVEG 205-287 482-604 PVMEA WHVEG 484-606 PVMSA WHVEG 484-606 PVMSA WHVEG 484-606 PVMSA WHVEG 484-606 PVMSA WHVWEG 484-60	C HBVMG	396-420			1	BVVO	A WARVI	200.203				
266-287 402-604 464-606 PVMSA WHV8I 484-606 PVMSA WHV8I 484-606 PVMSA WHV8I 484-606 PVMSA WHV8I 484-606 PVMSA WHVWB 484-606 PVMSA WHVWB 484-606 PVMSA WHVWB	IC HOVEN	389-421			-	PVME	A WATVED	274.290				
464-600 PVMSA WHV6 PVMSA WHV6 A64-600 PVMSA WHV8I PVMSA WHV8I A64-600 PVMSA WHVWI A64-	P BABVA	205-287	482-604		+		A WANT	274.208		-		
464-606 PVMSA WHV8I 494-606 PVMSA WHV8I 494-606 PVMSA WHVW8 494-606 PVMSA WHVW8 494-609 PVMSA WHVW8 494-609 PVMSA WHVW8 494-609 PVMSA WHVW8 494-609 PVMSA WHVW8 PVMSA WHV PVMSA WHVW8 PVMSA WHV PVMSA WHVW8 PVMSA WHV PV	F BRBVC	464-506			-	2	WALLA A	274.208				
464-606 484-606 484-606 484-606 484-609 484-609	LE BROVE	484-606		-	1	2000	A WANGE	974.208				
484-606 484-606 484-606 484-606 482-474 77-09	I P MRGV1	484-608			+	2000	A WAYNA	128.140		-		
	I P MRBVA	484-606			1	E	2			-		1
	I HAEVI	464-606			+			+		-		
	THE MARKA	484-606			+							
	VERT 41	462-474			1	1						
I	200	22.00				+						
	VANA 0.018	408-428		1	_	-						

																																			-		-		
																																				4.			
																																							-
					+			-								+	+	+								1	•												1
																										,							-						1
				1540-1569							-	+							-			+	1							•	-			+				+	
014-636	807-828	166-160	743-766	430-482	420-440	427-440	426-447	967-679	854-876	114.436			304-328	188-21/	132-164	106-217	105-217	196-217	132-154	131.181	200 000	203-310																	
PVOLH HBVR4				Γ		١		PVGP2 EBV		6				T			PVMAT BENDH	Г	Γ			PVMP CEMV																	

PCT/US95/16733

TABLE XIII

W 96/19495

SEARCH RESULTS SUMMARY FOR PIZLZIPC MOTIF

PCCEME	PLICTIZIP	All Vinesas (No Destance Lane)	ŀ		-						
1	PROTEIN	VIRIO			-	_					
PISK TRVSY	POTENTIAL 194 KD PROTEIN	TORACCO RATTLE VIRIS ISTRAIN SYMI		<u>.</u>	- 10 min	3	7	1	6	4 64	- \$ 63 ii.v
PIBHS VACCC	18E1A-11SD	VALCINIA VIBIG COPAIN CONTRACT NA			1	_		E	100	i	
PIBILS VACCV		VACCINIA VIRIS (CIR AIR) IN IN	!			: :					
Punis VARV			•	:	_	-				•	
PATER PRINCIPAL					_						
		TOWING VIRINGINA AND THE AND THE REST	43.69					•			
			187.410	<u> </u>		İ				1	.
AVA (VARIOLA VIRIIS	10.431		į	!					
- 1		IEBPES SMIPLEX VINIS (INFL 1/5 IBARE 17)	20.01	<u> </u>	: <u> </u>	-			::::::::	:	
		HERFES SIMPLEY VIRILS IIVIT 1/ STRAINI	25								
PATO 115VEU	2	FOUND IDEAL COURT INTO A PARTY AND A PARTY		_		•					
	i	CACCAST COMPANY CONTRACTOR CONTRA				••		1	i		
	į	ACCOUNT OFFICE OF THE STANDERS				-			i		
		VANICELLA ZOSTER VIRUS (STRAIN DITAIAS)	2	111.197	:			i	:	:	
A ID A YOU		VACCINIA VIRUS (SIRAIN WR)	15.51	!	:	¦.	i	:	ì	:	:
PATEN ICSVED	Ī	BOVING HELPECVIENCE TYPE LICENSINES IN THE PROPERTY OF THE PRO			:	٠.	:				
PATEN INCVEA	İ		2			•					
	ı	EQUING HEATESVIALIS LYFT. 4	2.5			, .					
LAILM HISVES		EQUINE HEAPESVIRI'S FIFT ILSTRAIN ANATH	130.148	!		:	:		:		
PATCH VZVD	Ī	VARICELLA 2007FB CIBIC CORAIN CHINAS		1	:			: !	!		
Y THE COMPX	Ī	MILES ACCORD	2		:					:	:
200	1	CONTON VINIS	386.412					i !	: ;		
		MLACK BEETLE VINUS	2 =	;					!		
Parol HSV60	TRANSCRIPTIONAL REGULATURY PROTEIN	GAPES SEMPLEX VIRIUS CIVEL 67 STR VINCIN		:	•	:	1				
7000 EBV	Ì	THE PARTY OF THE P				• ;					
201	ĺ	The second with the second sec	62134								
			١	2007	: İ	:	!	İ	:	!	i
LAB VACCC		VACCINIA VIAUS (SIBAIN COPINITACIEN)	10.10	1	:	!	!		:	::-	:
PCALBI VACCV TO	Ī	VACCINIA VIEW CONTINUES.				:	-				
VALUE VALUE	Ī	ALCINIC VIALS (SIRVIN P.F.)	2						!	: :	:
1		VAMOLA VIRITS	181.201		:	:		!	:	1	,
MON MOVSA	i	ERPES VIAUS SAIMINITION IN				:				-	
PCELF HSVII	l			-							
POST & SECURE	Ī	LAFES SUULEA VINUS (1978 1/5) PAIN (1)	2	33.33	386 100			! 	:	:	
	Ī	GATES SWOTER VIRUS (TYPE I / STRAIN KOS)	78:18	212.211		į			-		- - - -
5		GAPES SOULEN VINUS (TYPE 1/ SIRAIN HGV)	2	212.211	11.10	1			ļ		
		HEADES WAUS TYPE I (STRAIN KENTUCKY A)	1								
MAN CED	CELL PUSION PROTEIN PRECUASOR	VARICELLA POSTER VIBILS (STRAND PURIAS)									
PCOR MSYSA IT	Ī	LEGISTER CANADAR CANADAR CONTRACTOR	2		!						:
Т			3.6	216-242							
T.		SE VINUS	91.110						Ī	i	-
-		(STRAIN AS)	3.5		13.00			Ī		-	
			23.5	97.13		-	Ī	Ī	1	-	
_			94-120			Ì	Ī	Ì	i		!
-	PROTED VF:	LAMSTER POLYCHANIBUS									
PODA! POVIC		POLYDALA VIDIT IF									İ
		The North Marie	1	2	22.24					İ	
PCDA! POWA			97-123								
7		HOUSE FOR TURN VINUS (STRAIN KILITAN)	43.160	231.249					İ	İ	İ
7		SPECAN VIRUS 40	37-44	\$21.86	235.251		Ì	Ì	İ		
		HELMOTROTEUS TENAX VIRIIS I (STRAIN KRAI)	101.03		İ			Ī	İ	İ	i
	COAT PROTEIN VY		77.104				Ì	Ī			
- 1			2	İ	1				ļ	-	
MOAL POWED		MOUSE POLYDMA YIRUS (STILAIN 1)						I			
KON TIVI	12	THE EMOPROTE US TENAN VIRILE LACTRAIN VENT					_				
PODAT ABLOW											
PCDAT BOOLV	PAFCINGOS		- 1				İ		İ	İ	
PCOAT GIVE!			183.401					İ			İ
TO A CO	roteur.		14.33	192.409			Ì	Ī		İ	-
1000			3		-		i	<u> </u>	i	!	;
1		CASSAVA LATENT VIRUS (STRAIN MIGERIAN)	100			-	Ī		<u> </u>	-	· :
=1	COATPROTEIN	CYNGIDIUM MOSAIC, VIRUS (STRAIN STRICAPORE)	21.76	-				i		İ	-
		CUCUMBER NECROSIS VIRUS		1	:		Ī	-			
ī	OLEY	218		!						_	:
MOAT CTVS					İ				<u>-</u>	- i	į
			Ī	İ				-	<u> </u>	<u> </u>	
	COAT PROTEIN	THE CALL COVERS CONTAINS TO SECURE STATES	٦	79.73					İ	İ	
1			564-587	647-657		<u>-</u> !		<u>!</u>			-
								1	1	1	7

PCCLME	PIICTIZIP	All Viruan (No Bestresphages)	П	\Box		- 4 - 4 - 1	_ :	2.4.19.2			
THEHAM	PROJECT			9	i	i	1		_	-	
PCOAT FCVF	COAT PROTEIN	PEI DE CALICIVINOS ISTRAIN IN	ī		1	1		-	1	:	•
PCOAT FPV	COAT PROTEIN VP	FEI ONE PAM EUXOPENIA VIRUS	2			-		1	•	:	•
PCOAT FPV10	COAT PROTEIN VP.	FEI DE PAM EUROPENIA VIAIIS (STRAIN 191)	640.703	:	- 	-		-		i	:
200	COATBOOKEN		43.66						į	i	
		MINK ENTRAITS VIRIS (STRAIN ABASHIRI)	685.700								:
4		AND AND PROPERTY CONT. VIETE	5	-	-						
YOY MAN	COAT PROTEIN		18.19	204.233	:	į	<u> </u>		! !		:
MOAT MST	COATPROTEIN	MALE SINGLE VINO	ì	-	:		:	•			
MOAT NOW	COATPROTEIN	NAMCISSUS MOSAIC VIRIIS		1 - 1				:	:	:	1
12	COAT PROTEIN PRECURSOR	HODAMURA VIRUS	76.78	į						-:	
200	TIST COLUMN TO THE PROPERTY OF	COONTOCLOSSUM RINGSPOT VIRUS	2							1	!
- 1		DADATE VELL DA ACTAIN VIBUS	2		i						
KOAT OTH	COATPROTEIN		141.64							-	İ
MOAT PAVCE	COAT PROTEIN VP3	CANINE PARVOVINIS (117E 2. STRAIN AT)		1	!	Ī		-	:	:	i :
PCOAT PAVCS	COAT PROTEIN VPI	CANINE PARKOVIRUS (STRAIN MONTO)			:	.!	:	:			
PERIOT BAVER	COAT PROTEIN VPI	CAMINE PARYOVIRUS (STRAIN CIV.I) COUNTIL 130)	28. 2.		-	•	ļ	1	į	:	
2		CALINE DAG CALIBRE CLIDADA	32.11								
MCOAT PAVEN	COAT PROTEIN VFI		1	i	-	-			: :	:	:
PCOAT PELAY	COAT PROTEIN PRECURSOR	PEPPER MOTILE VIRIES		İ	i		!	: :	:	:	
YEAT PAC	COATPROTEIN	PAPAYA MUSAIC POIF XVIAUS	9	!	į	- :	-	1 :: 1	: :	:	
PCOAT PPMVS	COAT PROTEIN	PEPPER MILLD MOTTILE VIRUS (STRAIN SPAIN)	-	101.13			1	1		:	:
	701.1 banser.	POTATO VIRUS S(SIRAIN PERINIAN)	179-147			-					
		BIOS CABIBE CIBILS		İ		-					
Y04	COAT PROTEIN			:		İ			İ		
PCOAT SECUL	COAT PROTEIN	SATELLITE PLAIZE WILLE LINE MUSAIC VINUS		Ì		1		i			
PCOAT SMATEA	COAT PROTEIN	STRAWBERRY MILD VELLOW FOCE ASSOCIATED VIRUS	27.72	-				1		!	į
PCOAT TAMP		TAMABLE DESCRIC VIRUS	223.233		-	İ				İ	
200		TOMATO BUSHY STUNI VIRUS ISTRAIN BS 11	186-381		- !						
		CONTRACTOR CONTRACTOR	1		;	-		!			:
PCOAT TCV	COATPROTEIN	IUMIT LAMALE VIACO		-					-	!	İ
MOAT TOMY	COATPROTEIN	TOWATO CALDER MOSAR, VIRUS				1			-		!
PCOAT TIMEMY	COATPROTEIN	TOBACCO MILID CREEN MOSAIC VIRUS (TNIV STRAIN U.I.)	201.00		i	۱				i	:
MOVI INV	COATPROTEIN	TOBACCO MOSAIC VIRIS (VUI CARE)	20.0	İ	i			!		:	:
PCOAT TMYOR	COATPROIEIN	TOBACCO MOSAIC VIRUS (STRAIN 06)	107-128						i	:	
MOVE TAVOR	COAT PROJECT	TOBACCO MOSAIC VIRUS (STRAIN DAVIL ENTENSE)	102-128					-		:	
PCDAT TWVF	COAT PROTEIN	TOBACCO MOSAIC VINUS (STRAIN ER)	103.138			7					
	100 4 PEO 18 PE	TOBACCO MOSAIC VIRUS (STRAIN HOLNICS RINGRASS (11R.))	101.13			-					
200	201 t and the Co.	TOBACCO MOSAIC VIBUS (STRAIN O)	103.130			İ					
	CA: 0 ES CHEM	TORACCO MOSALC VIBING STRAIN ONLY	20.00		:				:		:
MOAI INCH		TOTAL CONTRACTOR CONTRACTOR I	103.130		!					İ	l İ
XOA INV		CONTROL OF THE PROPERTY OF THE PARTY OF THE			-	1		-	:	:	!
MOAT TAVA	COAT PROTEIN	TOBACCO MECADOS VIRIOS (STRAIN A)		i	1				i 	!	
MOAT TAND	COATPROJEIN	FUBALLU MELHUSIS VINUS (SINAIM U)				İ				İ	!
MOLL HOVE		DERFESTRUS SALMIN (SUBGROUP C.) STRAIN 418)				İ					
PCORA HOBYI	CORE ANTIGEN	INC. PATITIS & VOIUS (SUBTITIE ADWZ)	8		į					į	
PCCRA ICENA		SEPATITIS & VIRUS (STRAIN ALPITAT)	=		-					Ì	i
PCORA IDBVI	_	IEPATITIS B VIRUS (SUBITY E ADYW)	9 18		-						
PENSI ADENI	_	INDIAN ADENOVIRUS TYPE 2	71.93								
POND! EBV	MAJOR DNA-BRIDGING PROTEIN	EPSTEIN-BARR VINUS (STRAIN 895-8)	640-673								
AVADA HOLOY		INDIANA CYTOMEGAL OVIRUS (STRAIN AD169)	691.708								
PONCE HIS VIEW		ICAPES SOOLEX VIAUS (TYPE 1/STRAIN 17)	459-476	\$97.620							
TIVEL LICENSE	MINISTER BRANCH PROPERTY	TIGAPES SOUTEX VIAUS (1YPE 17 STRAIN SI	459.436	367.620	!						:
AIAM INVIN	NI SI COLO DI SI	INCRPRES SUMPLEX VIRUS IT YPE I / STRAIN KOS)	459.476	507-670	-	į Į					!
	NISCOS CANCELLA MANAGEMENT	ROVING HERPESVIRIS TYPE 1 STRAIN DAIN	653.433	96.616	<u>.</u>				i 	!	
		FORTING DESCRIPTION OF 1 ACTOR IN ADJAN	110	-	Ī		-				
POWER	MAJOR DNA BINDING FROIEIN	INTERESTRICT AND THE TANKS AND THE	Ī	01.4.01.4	100 000	W. 160					
HSVSH HSVSA		Married State Control of the Anna Children	Ī	-	7						
		MULION CALL CONTROL CONTROL SMITH		- 511				-		İ	
PUNBI SOUNC	MAKIR DNA-RINDING PROTEIN	SOUTH CTTONE GALOVINUS (STRAIN COLIDRA)			-						
PERCHASI VARY	DNA LIGASE	VARIOLA VIRUS		1	!			i	-		i
PDPOL ADE01	DNA POCYNEAASE	INDIAN ADENOVIRUS TVPE 1		93							
Poror ADES	7	HUMAN ADENOVIRUS 177E S		•						Ī	
POPOL ADED!	- 1	MUNICAL ADEROVINOS 1 TTE 7	2	-							
PDPOL ADELL	DNA POLYKERASE	INDIAN ADEMOVIALIS TYPE 13	167-701	20.50	200]]			1	

PCCTNT	916.10.10	All Contract the Breast and an artist the									
	PROTEIN	VIRUS	Ī	ARCAI	ARTA	- NAC	ARCAS	AREAG	AHEA 3	ANTA	ARTA :
PDPGL CBEPV	LIMA POLYNGRASE		j	650.678				•	i .		ļ
POPOL CHYNJ	THA POLYNGRASE	(10 ONELLA VIRUS NY 1A									
PDPOL CHVPI	DNA POLYNGAASE	PARAMECITAL BURSANIA (10 INEL 1 A VINUS I	П	474 442							
PDPOL EBV	DHA POLYNGRASE	I PSTITIN BAKK VIREN (SIRAININS B)	2	7	36.50	P67.687	073.670				
PDPOL FOWPV	DNA POLYMERASE	FOWL PUR VIRIUS	1	230-241	:						
ADIO TOTAL	DNA POLYMERASE	HUNGALI C'YTOME GALOVIRUS (SERAIN ALVI69)		3	1030-1013						
- i	POLYNERAS	DACK HEPATIBLE AVEUS (BPOWN SHANGILAL DUCK ISOLATE SV)	Ī	2.12	╗	2					1
	DNA POLVAGRASE 1	DINCK HEPATHES B VIRIES (STRAIN CHINA)	5	2.5	_	3					
_1	DNA PUL YMERASE	OUCK HEPATITIS B VIRUS	300	11.211							
POPOL MODOW	DNA POLYNGRASE	DUCK IE PATITIS B VIRUS (WILLIE SHANGHAI DUCK ISOLATE \$11)	2	2	3.5	25.					
200	DNA POLYMERASE	GROUND SQUIRREL ILPATIIIS VIRUS	-		!	-		į	!	-	:
POPOL IDENIE		HERON HEPATHIS IN VINUS	2	25	:	:	!	:	:		
POPOL INDIAN	DNA POLYMERASE	TEPATITIS DVINIS (SITELLA INC.)	:	=======================================	£ ;						
PINCH. IPBV	INA TRE VARIENASII	INPAINS II VIEIK KIIDI MEANA	===			•					
MUNCH CHEBY	INA MA YAR HASII	INTERTITIS IS VIBITS (SUBIT VER AND FAIRARY WILL	413.414	11 4.1	Je. 180	• •					
PDPOL JEBVA	DNA POL YMERASE	IEPATITIS B VIBUS (STRAIN ALPITAL)	2.0	199.426	434.430	150.760		!	· 	1 :::::::::::::::::::::::::::::::::::::	!
PDPOL HEBVI	DNA POLYMERASE	IEPATITIS B VIRUS (SUBLYPE ADW / STRAIN INDONESIAPIDW (20)	90.08	410-417	105.461	1			Ì		
POPOL MEBVI	DNA POLYNERASE	HEFATILIS B VIRUS (SUBTYPE ANW / STRAIN IAPAN/PIDW/11)	86.0	10 411	445.468	161.33					
POPOL LOBOVI	DNA POR VACEBASE	INPATITION VIRING SCHRAIM COLVENING AND FINE ATT.	3	100.434		1.0 16.			:	! !	:
AND SOUTH	DAY BOY VANCE ACE		1			:					
	TOTAL PARTY AND THE PARTY AND						:	:	•	: :	!
	UNA FUE I MERA SE			410.437		10.77					Ì
	DRA FULTHERASE	HETAILIS & VIRUS (SITEL ADM / STRAIN PHILIPPING POW PM)	4								
TOTAL POST	DNA POL TABUASE	7	200	10.0	761.738						
POPOL IDBWW	DNA POLYNERASE	_	22.00	105.432	450-450	•					
PDPOL HEBVY	DNA POLYMERASE	IEPATITIS & VIRUS (SUBTYPE AYW)	20.02	13.42		76767				İ	i
POPOL IDBV2				369.436	25.55					İ	
POPOL HSVII			797.817	877.897	1071-1000	-			İ		
POPOL HSVIA	POLYNEAASE	Ī	ĺ	131.101	000	-					i
POPOL IISVIK			ī	111.161	100	-			ļ	: -	
POPOL HSVIS			Τ	11.69	90			1			:
PDPOL HSV31	POLYMERASE		Ī	100	1074.1023		1	İ	;	:	•
POPOL ISVAU		Ī	413.433	784.101		Ť				İ	İ
POPOL 165VEB	POLYNERASE	FOUNE (GRAPE SVIBUS 1 YPE 1 (STRAIN ANGE)	Т			208.816	12.00		İ	Ī	
POPOL ISMI	POL YMERASE	T	1		İ					1	İ
POPOL MSVSA	DNA POLYMERASE	BAININ	Т	100	ī	110.710	110			Ì	
POPOL MONYS	ONA POLYMERASE	AIN SAUTH	Т					Ī		Ì	İ
POPOL NOVAC	DNA POLYMERASE	IF DROSIS VIRUS	Ī	476.407	-	!			Ī	İ	
POPOL VARV	INA POLYNCERASE		Τ						Ì	İ	
POPOL VZVD	DNA POLYMERASE		111.11	161.107	440.461	111.140	167.791	711	Ī	İ	
POPOL WITH			446.473		ī					Ì	
POPOL WITYSS			21.478							Ì	
PDPOL WHYT			11715						Ī	İ	
PDPOL WHY			120-473	386.511						İ	
PDPOL WHYE!	DNA POLYMERASB		121-151						İ	İ	
POPOL WHYWG	DHA POLYMERASE	WOODCITUCK HEPATITIS VIRUS W64 (ISOLATE PWS2))	133-150							İ	İ
POPOM POBYY	DNA POLYMEDASE	IEPATTIS B VIRUS (SUBTYPE AYW)	38.426	414.450	150.767						!
POST HOWA	DUTPASE	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	107.126							1	:
POUT HISVE	DUTPASE		X 0								
POUT HEVEB	DUTPASE	AIN AB4P)	130-149								
EVEL IES	DUTPASE	ICTALURID ICTALORIO I	13.95							i	Ì
PDUT HSVSA		PEAPESVINUS SAIMINI (STRAIN II)	Ş.	79.104	1						!
- 1		MAJASE ADENOVIRUS 1YPE I	14.47								:
TE AS AUES	EARLY ELA 6 JAC PROJECT	HINGARA ADEMOVIEWS I YPE 7	=	-							
		THE MAN ALLEMONING STATE A	2							İ	-
ŧ.				,,,,					Ì	İ	
18191 ANS13	ELB PROTEIN I APCE T ANICCEN		Т		-				Ī		
			1431-469]

ı									l		
PCGENE	417112114	All Viranes (No Bacterlophages)	Ī	•		-	ī	1	i	ı	i
FILE NAME	PROTEIN	VIRUS	Ī	O E CAL	AMEAL	- FOTAV	AREA.	SPIGI	SAIA.	ALLAL.	ABLA.
PEIBL ADECT	EID PROTEIN, LARGE T-ANTIGEN	CANTAE ADENOVIDIUS TIPE 2	22		Ì	1				-	ļ
PEIBL ADENT	EALLY EIB 44 KD PROTEIN	TUPAIA ADEMOVIRIIS	25.101						-	_	
PEIBS ADECT	EID PROTEIN, SMALL T.ANTIGEN	CANINE ADEMOVIRUS TYPF 2				-			-	-	
PEIBS ADEM!		MONISE ADENUVIRUS LYPE I	10.03		i	Ī		į			1
PESIO ADEOS	EAALY EIB 10 4 KD PROTEIN PRECUMSOR	IN PALAN ADENOVIBLIS TYPE. 2	=	3							Í
relie ADEOS		INDIAM ADENOVIRUS TYPE S	-	3					i	1	İ
		RINGAN ADEMOVIRUS 179E 7	-		1					-	-
	-	RIMAN ADENOVIBUS TYPE 1	3	ĺ		Ì		İ	-	į	
PESSI ADEOS		ISTALAN ADENOVIAUS TYPE 1	19-03			Ì			-	- : :	į
		HUNIAN ADENOVIRUS TYPE S	30 4					ļ			
PENI ADEON		IRIDAAN ADENOVIRUS TYPE 1	16-62			7					
PEDIT ABER		INDIANA ADENOVIBUS TYPE S	103-135								
	EARLY ESE TO SKD PROJECT PRECIASOR	INPARA ADENDVIRUS 1YPE 1	2 22	:	:					İ	1
PETER ADER		INDIAN ADENOVIRUS 1976 9	3.33		:					İ	: :
		THE PLAN A DRIED COURSE IN THE PROPERTY OF THE	100	İ		!				!	!
2	EAST TO REPORT OF TOTAL			1	1	1		† 	:	1	!
TELM ADEOU	EARLY ES TO SED CLYCOPROTEIN	IN DAMA ALIZACIONIS ITTE J		İ		-				i	!
PENI ADED	EAMLY ET TO SIND GLYCOPHOTEIN	HUMAN ADEMOVIRHIS 17PE /		:	: !	.		-	i	-	İ
	EALLY ES 32 2 KD GLYCOPROJEIN	CAMINE ADEMOVIRUS TYPE I (STRAIN GLAXO)	2		į	-			İ		
PECE ADDA	EALLY ED 19 7 KD GLYCOPROTEIN	MOUSE ADENOVIRUS TYPE I	105-127						-	-	-
reall ADEas	PROBABLE EASLY E4 11 KD PROTEIN	INDIAN ADENOVINUS TYPE 2	ž.3			-					
ī	PROBABLE EAST V EA II KD PROTEIN	INCALAN ADEMOVIRUS TYPE S	26.73							İ	
L	PROBABLE EASLY EATH RD PROTEIN	MOUSE ADEMOVIRUS TYPE I	01:10	į					<u> </u> 	<u>-</u> 	
a	EALLY EASINED PROTEIN	HAMAN ADENOVIRUS TYPE 2	20.00		!						! !
Ī	FARLY ANTICEN PROTEIN D	EPSTEIN BARB VIRUS (STRAIN BOS.D.)	263.286			-			<u> </u>	İ	
200	EAST VAUNCEMBER PER	FPCTFILE AND VIBILITY SECTION OF THE PROPERTY				Ī		İ	<u> </u> 		1
	CALL A LANCE A MACRETA	CENTRE LAND CARLES AND BOLDS				İ			i	Ì	
Ī	EBNA-J MUCLEAR PROJECT	CONTRACTOR OF THE PROPERTY OF THE PARTY OF T	Ī			L		Ī	1	İ	
Ī	EBMA-J MALLAM PROIDIN	CARLO A SOUTH	ī		İ	1		1	i	i	
T		TAUGUS STATES OF THE STATES OF				Ī				-	1
PEW PROV	ENV FOLVER PRECURSOR	THEN STATE TOURS CHANGE VINE	20.00		i			Ī		-	!
AN MEN	ENV POLYTROTED PRECURSOR	PRIDATE STREET FOLUS FIRMING VINCS	100								!
PEN AVID	ENV POLYTROTEGY	AVIAM KETRUVIKUS KIL 10	8			-			-	į	
DSV AVEU	COAT PROTEIN CP37	AVIAN SARCOMA VIRUS (STRAIN URL)	ī			-		-			!
PDV BAEVA	ENV POLYPROTEIN	BABOON EXOCEROUS VIRUS (STRAIN ACT)	اء	22.00		į		İ	-	i	
PEN BING	ENV POLYPROTEIN PRECIASOR	BOVINE DARGRODEFICIENCY VIRUS (ISOLATE 106)	Ī	-	2	3.5			_ <u>;</u>	_ <u>'</u>	-
PENV BIVZI	ENV POLYPROTED PRECUNSOR	BOYDAE DEALMODEFICIEMY VIRUS (ISOLATE 127)		97.168	207.330	63.479	\$54.575				
PDW BLVA	ENV POLYPROTEZN	BOVING LEUKEMA VIRUS (AND RICAN ISOLATE FLK)	101.127								
POW BLVAU	ENV POLYPROTEDI	BOVINE LEUKEADA VIRUS (AUSTRALIAN ISOLATE)	101.131								
PDIV BLVAV	ENY POLYPROTEDI	BOVINE LEUXEAGA VIDUS (AMERICAN ISOLATE VIDA)	2								
TOW BLVBS	ENY POLYPROTEEN	BOVING LEUXEMIA VIAUS (BELGIUM ISOLATE LB205)	101-111								
PENV BLVBS	ENV POLYPROTEIN	BOVINE LEUREMIA VIRUS (DELGIUM ISOLATE LBS9)	101 111								
H	EXV POLYPROTEEN	BOVING LEUREAGA VIAUS (IAPAINT SF 150LATE BLV-1)		-							
. 1	ENV POLYPROTEIN PRECURSOR	FELDIE EMOCEMBLY VIRUS FCE I		1	5000		İ			<u>-</u> : !	!
- 1	DAY POLYTHOTE BY PRECURSOR	PELINE EMDUCEMBIS VINUS F.C.E.		ī	6,00.651	i			-	į	•
-1	DAY POLYTHOTE DA PILECURSOR	FELTING LEUKEMIA PROVINCIA (LONG CYE 4)	_	_	1		:::	1		i	
- 1	ENV POLYPROTEIN PRECURSOR	FELME LEUKEMIA VIRIUS (STRAIN AGLASCOW. 1)	7	-	M31 A 20			,			
- 1	ENV POL YPROTEIN PRECIPSOR	FELDE LEUREMIA VIRUS (SIRAIN LANGOA III)	Ī	475 646							
	ENV POLYPROTEIN PRECURSOR	FELDIE LEUKEMIA VIPUS ISTRAIN SARAIA)		602-623					_		<u> </u>
- 1	ENV POLYPROTEDI	FUNAN SPURABE IROVINUS (FORMY VIRUS)		35.315	56 00	80.18	110.111	E 130	150 020	11.978	
	ENV POLYPROTE IN PRECINSOR	FEI DE SARCOMA VIRUS (STRAPH GARDNER ARMSTEIN)		625.646						: :	:
	ENV POLYPROTERN PRECITISOR	FEI THE SARCONIA VIRIUS (STRAIN GA)		103-676						<u> </u>	!
_	ENV POLYPROTEIN PRECIASOR	FE DE SARCENIA VIRUS (STRAIN SM)	Ī	60 63°				İ		:	:
PEN ISVST	ENV POLYPROTEIN PRECURSOR	BUS (STRAIN SNATTE THE HE PA	467.488		:	!	1	!		i	:
	ENV POLYPROTEIN PRECURSOR	IIA VIRUS	\$19.500		!	İ	1			:	
PDV WIE	GP146 PRECURSOR	ICIENCY VIPIUS TYPE I (BIIIO ISOLATE)	498-570				!		:		
PEN HVIE	CPIEG PRECURSOR	ICIENTY VIRUS TYPE 1 (DIB ISOLATE)	497-515								
NIA NO	GP160 PRECURSOR	3	94.516	ĺ							
ILEAV BYIER	INTER TREE URAIN	THE PROPERTY OF THE PARTY OF TH	301 323		1				1	1	7

	1171171	All Virgan (No Botteriophistes)									
1	Control of the contro		3		7 7 11 1	1111	VII.V	7 111 7 4	, HI , 1	ANIAN	*****
- Indiana						-					
	CONTRACTOR CONTRACTOR					•	:	•			
- 1	OT THE COASON	HIMMAN INTERMEDIATION OF THE STATE OF THE ST	21.20	:	:	1					
- 1	CTIES PRECLIES OF	ICIENCY VINCIS TYPE !	25.52								
- 1	CATION PRECINISON	ICIEMCY VIPUS TYPE I	20.0		1				i		
	OF THE LIES OF	CIENCY VIRUS 1YPC			:						
- 1	GP140 PRECURSOR	CIENCY LIBES 11F	\$04.126	£ 05	11.76.8		:				
. !	GP140 PRECURSOR 1	ICH NCV VINIS IVE	60.533	:	_						
	GP160 PRECURSOR	ICIENCY VIAUS 1YP	536.518	i					ĺ	:	!
- 1	CP 140 PRECURSOR	HUMAN INDAINADDEFICIENCY VIRIS TYPE I (MEW YORK S ISOLATE)				1				-	!
_	GP160 PRECURSOR	ICIEMCY VINUS IYP	440.510	<u>.</u>	:	1		1	!		i
	CP 140 PRECUPSOR	KIFKEY VIRUS IYP	21.60		! :	-	i	İ	:!	:	;
PEN IIVIPY	OPI BO PRECURSOR	CHACK VIRIA IVE	- 01	:	:	i	:	:			
L	Carles Program Con				:	-		1	!	:	;
1	SOCIAL PROPERTY OF THE PROPERT	ILIENCY VIAILS TYPE I	3			7				:	;
1		CIENCY VIRUS TYPE	40.511	75.74							
1	STATE OF SUR		38·33		_	•					İ
	CATEGORISCON SOM	_	23-165		11110	-	-				
-1	GP 160 PRECURSOR	-	13.00	175.100		į-	Ī		İ	-	į
	CP160 PRECURSOR	4-	407.410	1		•				İ	
•	CP140 PRECURSOR	VIBIR TVPE		Ì	-	+					
	CP160 PRECURSOR	VIET PARE			,	•					
		INDIAN INGREDIES CONTRACTOR OF THE CAME OF THE PARTY OF T	7	ī	200						
PDW WOCA	Chiches	TOWNS DESCRIPTION AND STATE A HOUSE SERVICE SE			8						
1		MUNICAL CANES	-								
- 1		INDIAN BONDRODE (CIENCY VIRUS 1'YPE 1 (150LATE D194)	3.26	741.764	111.775		i		!		!
TOTAL MARKET	UP 100 PRECURSOR	HEMAN INDICATION OF THE 1 (150LATE DIOS, 7)	12.4	i	!	<u> </u>				-	
٦		INDIAN BEAUNODEFICIENCY VIRUS TYPE 1 (ISOLATE GILANA-1)	741.786	171.795					Ì		Ī
٦	GP186 PRECURSOR	INDIAN BORDNODE PICIENCY VIRUS TYPE 2 (ISOLATE MILLZ)	143.767	111 800		-			1		
_		INDIAN DEAMODE KIENCY VIRUS TYPE 1 (150LATE NOD)	351.776		-	İ				Ī	
1		INDIAN BERNODERCIENCY VIRUS TYPE 1 (ISOCATE SBLISY)	745.768	208-07		-			İ	-	
		HUMAN MORINODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	÷	İ	-			Ī		j	
		SHEEP PULMONARY ADEMONIATOSIS VIRUS	96.19	399.139	176.308	100	Ī	Ī		!	
	ENV POLYPROTEIN PRECURSOR	MANK CELL FOCUS FORMING MURINE LEUKENDA VIRUS	-	T	i						
	ENV POLYPROTEDY PRECITISOR	MAINE I ELIKEMIA VIRUS (150LATE CI		İ		İ		Ī		İ	
7	ENV POLYPROTEIN PRECUISOR			İ	-	İ	Ī	Ī		-	
_	ENV POLYPROJEIN PRECLINSON	Γ	613.646		1	Ì	İ	I		- !	i
٦	ENV POLYPROTEIN PRECIDISOR	Ī	079-619	-				-	1	-	İ
	ENV POLYPROTEIN PRECIMSOR	Γ	099 619				İ			Ī	
7	ENV POLITING FILE CLASSIN	MEND MURINE I EUXEMIA VIRUS (150LA LE PVC. 211)	077 619		i	<u>-</u>	İ	1	-		i
7	ENVIOLENTALISM FROM THE STATE OF THE STATE O		676-E27		i	ĺ				İ	
	ENV POLITICISM		107-166	i	-					Ī	
	ENV PALTAGLES FRECURSOR		439-650		-				Ī	İ	
PEN LA VAR	DAV BOX VEROTETA SECTIONSON		620.645				-				ļ
POV LATIVE	SAV POLITICAL PRESENTATION	MANUAL MANUAL LEUNE MICH VIRUS (STRAIN KAPLAN)									
PEN LACTVO	PAV POL VPB OTERA		3								
+	COUNTY AND THE PARTY AND THE P	NUS ISTRAIN GR)	3					Ī		Ī	
Ī	ENV POLYPROTECT		113-235							İ	
7	ENV POL VPROTEIN PRECIDENT	DOWN CARDINELL SERVICES OF STATES	2	-							ĺ
PENV MACOV	DAV POLYPROTECH PRECIDENCE		9 10		-						
Т	ENV POL VPROTEDA		•								
Τ	NA POR VERNIERA		╗	_		ī				İ	
Ī.	7041016A NO ANI		٦	19.73	184 187 93	934.051				İ	İ
ī	CONTRACTOR		- 1				931.948	110.01	<u>-</u> 	İ	i !
PENY SIVAG		SOUTH STATE OF THE	5							<u></u>	! !
1	CP140 PRECINSOR		9							- 	
	GP140 PRECURSOR	SPARM DAGNAM INTENCT VINUS (ISOLATE AGM CLONE GR. I)	7	j	-						
PENV SIVEB	CPISOPRECIENCIA	Ť	***								
1		7	6)	1							

	PROTEIN Grido Precinsor Grido Precinsor	YIRUS	Ī	4	_	310	1	Torus	4		791
	O PRECURSOR		t	ï	1						
	o PRECURSOR		26.74	607.03	1	-					!
1 1 1 1 1 1		SIMIAM INDITINODE FICIENCY VIRIIS (KOW ISOLATE)	139-154	765.792	52 60					į	į
1 1 1 1 1 1	CP 140 PRECURSOR	SINGLAN INDALITACIONE TO VINIUS (R.70 ISOLATE)	36.154	764.781	101.134						
T 1 1 1 1 1 1	A PRECISEOR	CLASS MICHAEL PRINCE OF SERVICE OF SECRES OF ATES	26.788	20.00					!		! !
7 1 7 7 7		CHAIN MAN AND THE PRINCIPLE CORP. A. CO. A. P. C.	101.101	110.011	!			!			
	THE CONTROL OF THE CO						İ	1		1 :: :	į
177	PROTEIN	SINIAM SARCIMIA VIRUS		:	1			-			!
7-1-	ENV POLYPROTEIN	SEMINA METROVIRILY SRIV.	61:00								
	A ONCOCEME PRESTITIVE	AVIAN ERYTIROBLASTOSIS VIRUS (STRAIN ES4)	11.10		1						1
1	LY TRANSCRIPTION FACTOR	FOWLPOX VIRUS (STRAIN FP.1)	1-4	11.01					1	;	
	EARLY TRANSCRIPTION FACTOR	SHOPE FIBROMA VIRUS (STRAIN KASZA)	1			!.				: :	:
t	2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -	VACCINIA VIBILE (CIBAIN CON MIACILIA)		i	i	-		:	:		
7	TO THE PROPERTY OF THE PARTY OF										!
-	LY IMANSCRIPTION FACTOR		-							į	
PETER VACCO EAR	LY TRANSCRIPTION FACTOR 32 KD STIBLING	VACCIDIA VIRUS (STRAIN CIPP MIACI N)	2			201.10	28.38				
	LY PRANSCRUPTION FACTOR 13 KD SUBURIT	VACCIDIA VIRUS (STRAIN WA)	4.72								
_	EARLY TRANSCRIPTION FACTOR 12 KD SUBUMIT	VALIDLA VIRIIS	16.73	101.111	145.167	301.10C	\$38.503				
PEXON IBVII ALK	ALKALINE EXONUCLEASE	HEAPES SIMPLEX VIRUS (TYPE 1/ STAAIN 17)	165-180			•				į	
1	ALINE KOMICHEASE	HELPES SIMPLEY VIRING CLYPTE 21	2013		-			:	:		•
je	AT KAR DAF FROM MILE A CE	FOUNDE AND APPROVIDES TYPE 1 CYBAIN ABAP.	136.301	!!!	1	j .			-	i	!
A VOI POWER	AT DATE EXCHANGE EASE	PACIFICON AND STATES VINE STATES NA. 11	1	İ	1	1	i	-		:	i
	AT INE EXCUSED BACK	VARIOUS A. 7043- VIETN CARAMAN MARKAN	:	317.34.2		•					
THE APPEAL	And the partition	THE PARTY OF THE P	:=			;					
PERSONAL APPEAR	ALARO BIRE PROTEN	INDIAN ADENDUE (1 VPF 4)					Ī	1		-	ļ
-	Linca harriera	THE ACCUSAGE LAND 1					Ī		: : :		:
	FRUILIN	HUMAN ADEMONIACIO	1			İ	-	1		!	!
VIBY ADEOS	HOER PROTEIN	III WAAM ALDENOVIRIIS I VIE)			Ì	-	-	-		į	i
MIEN ADER)	R PROTECT	BOVINE ADENOVIRUS 18PE 1 (MASTADENOVIRUS 11051)						:		:	
MIN ADECI	T PROTEIN	CAMINE ADENOVIAUS TYPE I (STRAIN GLAXII)						_			
PFIBP ADEM! FIBC	PROJETY	MOUSE ADEMOVIRUS 1 YFE I		200	=	10.50	14.5.1	:	:		!
PGAO AVEVI GAG	GAG POLYPROTEIN	AVIAN ENDOCENDIS VIRUS EV.1			i					- 1	
ı	POLYPROTEIN	AVIAN ENDOCENDUS ROUS ASSOCIATED VIRUS 0	2.2		!			1		:	
	GAG POLYPROTEIN	AVIAN MYELOCYTONIA TOSIS VIAUS MC19	53.78								
	GAG POLYPROTEIN	AVIAN MYELOCY TOMATOSIS VIRUS HIN	53.78								
POAD AVISU COR	CORE PROTEIN P19	AVIAN SARCOMA VIRUS (STRAIN URZ)	93.76								
_	GAG POLYPROTEIN		2.3	i							
POAD BAEVIN GAG	GAG POLYPROTEIN		397.422								
П	POL YPROTEIN		11.11						j		
Ì	GAG POLYPROTEIN	BOVINE LEUR EMIA VIRUS (IAPANESE ISOLATE BLV.!)	2			ļ					
ال	GAG POLYPROJEIN	HALITIS VIRUS (STRAIN CORK)	102-119								
٦	GAG POLYPROTEIN	٦	2.2								
1	GAG POLYPROTEIN	ILITATAN T.CELL (ELIKEMIA VIRIIS TYPE I (STRAIM ATK)	2								
1	GAU POLITICAL	٦	2								
J	CAUTOLYROIEM	HIMMAN I CELL LEURENIA VINUS ITTE ((ISOLATE NIT.)	2								
T		Ī		i					İ		
POAC IIVIBI GAG		Ī	16:01	-							
1		Ī		-		1			-	İ	!
- 1		1		:		1	1	İ	i : !	:	
POAG INTEL GAG		Ī			:	1		: : :	1	:	:
ł	GAG POLYPROTEIN	Ī	15	-	!	İ	-		İ	:	!
1		INDIAN BORRODEFICIENCY VIRUS TYPE I (TH) ISOLATES					Ī	Ī		$\overline{ }$	
		Ī	16.59								
	POLYPROTEIN		263-289	1	-	!		İ		İ	
POAG IN ING	POLYPROTEEN	(AIN ISOLATE)	-		:	İ		!	!	:	į
	GAG POLYPROTEIN	(KA1E)	Ī								
	POLYTROI ELN	(NOK ISOLATE)	Ī	2							
	POLITICAL SIN										
TO THE PARTY OF TH	TOUR VIEW CENT			1	j						
ŧ	TOUR IT A COLUMN	1	18.60								

	PAGIZIN CADEN YEARS		ARCAI	A REA 3	V V V	3776	ORIA 2	4554	1 7387	OBIA!	ANTA?
	Mai Cean To UT				т						
	AU MULTIPLICA	ध्रा			Ì	-			1		
	DAG POLYPROTEIN	INTERIOR CONTINUES IN TERM, Y VINUE I (WM) I SOULATE)									;
	AG POLYPHOTEIN	IVEL I (ZUCDL-E14 ISOLATE)			!!!	-		:	:		
	RETROVIRUS-RELATED GAG FOLYFROTEIN			:		: :	:	:		-	_
	GAO POLYPROTEIN	MOUSE MANIMARY HINGH VIRUS (STRAIN URA)									
	TAO POLYPROTEIN		- i								
	ING POLYPROIEIN B		13.97								
	GAG POLYPRO I GIN		11.18								
	MAKIA COAT PROTEIN	SACCHAROMYCES CEREVISIAE VIRUS L.A	618-645								
П	DAO POLYPROTEIN	-	10.7	:							
ī	AC POLYPROTEIN	:	101.0	į	_	~	:				
Ī	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CHAIRM MAG Monte (Ciency Vibrie (ACADIS (Cit) ATE)	160.311		-				-		İ
		THE PROPERTY COMES AND		Ī		1					1
٦	AU POLITICIA	SEMIAN CONTINUE TOTAL TOTAL STATES		Ī					ĺ	-	İ
٦i	GAG FOL YPROTEIN	SINITAM INDUTINOSINE ICLEMA, Y VIRUS (170-1150). A LE		!	1	7					
POAG SIVE	JAG POLYPROTEIN	CHINGANZER INDAMENCE FORMA VINIS (SIVICES)	r t			- :					
	IND POLYPROTEIN	SIMIAN MINIMAN I CHIM Y VINUS (SCIM, A 11: CHII)	7								
ì	DAO POLYPROTEIN	SIMILAN INCOMMENCE OF YORKS (MATER) TO ISOLATE		!		:-		i	:	:	:
i	CAC BOX VPROTEIN	SCHIEBET MONEY BETROVIRUS (SMRV.III)	286-107			-		-			
Ī	Control of the American	TOTAL CHARLES AND CONTRACTOR AND CONTRACTOR AND CONTRACTOR			!	1					!
<u>ار</u>	COSTELLE CLUT ALEBOATION	TACENS THE STATE OF THE STATE O				-		Ì			
ī	POSSIBLE GLUI ARELDOXIN	VARIULA VIRUS		:	. :	:		٠	:		
	Ca ANG B. IN	ACROSTS SECETIFIA CRAINS UNIS VIRUS	301:338								
PORAN OVTN	GRANGE IN	TAICHOFLUSIA MI CIRANIII JUSIS VIRUS	26.23								
PGHTA VACCE	GROWTHIFACTOR	VACCINIA VIRUS (STRAIN COLEMIAGEN)	2		!						i
١.	- NOWTH FACTOR	VACCINIA VIRUS (STRAIN WR)	200							İ	
	Canwrite Factors	VARIOU A VIBISE	2			1					
	PODANI BIRE ICACE	SPETS DE LEAST COTE AND INC. BY	100.00	18. 161	797.160	ŀ					
						<u>آ</u> 				İ	İ
VIEL IN MY	MODALLE IEL ICASE	HUMAN CTION COLUMNS (STICKIN AUTON)	Ī	3		1				-	
	PROBABLE JELICASE	HEAPES SINGLEX VIRUS (TYPE 1/STRAIN 17)	Ī	27.00							
	PROBABLE SELECASE	HEAPES SOCIEX VINUS (TYPE 27 STRAIN HGS)	1	370-554							
	PROBABLE (TE) ICASE	EQUINE HEAPTSVIXUS TYPE I (STRAIN AB4P)		143.266	394-413	- T					
L	ROBABLE IEL ICASE	INERPESVIRUS SABGIRI (STRAIN 11)		180-411	638-683						
HELL VEVD	PROBABLE ICLICASE	VANCELLA-ZOSTER VIRUS (STRAIN DUMAS)	•	183.403	\$61.57	761-786					
- -	IEMAGOLUTININ-NEUKAMINIDASE	CANINE DISTEMBER VIRUS (STRAIN ONDERSTEPOORT)	34-53	100.223							
=	EMAGGLUTININ-ESTERASE PRECURSOR	BOVING CORONAVIRUS (STRAIN F15)	291-415			•					
-	REMANDALUTININ-ESTERASE PRECIRSOR	BOVINE CORONAVIRUS (STRAIN LY-138)	\$1716								
-	REMANCE UT DOWN ESTERASE PRECINSOR	BOVING CORONA VIRUS (STRAIN MERUS)	21-13					j 			
-	EMADOLUTININ ESTERASE PRECIRSOR	BOVINE CORONAVIRUS (STRAIN QUEBEC), AND (STRAIN L9)	31718								! !
_	REMADOLUTINON ESTERASE PRECURSOR	INDIAM COROMAVIRUS (STRAIN OCA)	391-413								
-	IEMAGOL UTDATH-ESTERASE PRECURSOR	PATRIME CORONAVIRUS KOIN (STRAIN ASO)	401-411								
-	IEMACOL UT DATA-ESTERASE PRECURSOR	MURING CORONA VIRUS MOIV (STRAIN S)	403-418								
≔	IEMAGGI UTOTA PRECURSOR	DELUCIZA A VIDUS (STRAIN AVAICHUZMA)	25.22	122-330							
ᆖ	IEMAGGI LTIDAN PRECURSOR	DELLEGEA A VINUS (STRAIN ABANCKOWINS)	7	104.13							
HENA MACO	IEMAOGLUIDEN PRECURSOR	INTLUDICA A VIRUS (STRAIN ABUDGERIGARHOKKAIDOVIAT)	110-111								
=	TEMACOL UTDAIN PRECIDENT	POFLUDICA A VIBUS (STRAIN ACHICKENALABAMAINS)	110-117								
-	HEMACOL LITINGS PRECURSOR	DOLUENCA A VIDUS (STRAIN ACHICKENGERMANYAVA)	101-101	131.347	16.333						ĺ
-	IEMAGGLUIDUM PRECITISOR	DOTUBLE A VIRUS (STRAIN ACHICKENPENNSYLVANIA))	303-319								
-	INTERNATION PRECIDENT	DOTI LENZA A VINUS (STRAD) ACHICK ENPENNSY! VANIALI PORT!	102.310								
PIEMA IACK	IN MACHINTON PRECITS SOR	VINUS	10.11								
	TELLA COLL IN DATA PRECIDE COR	PATHERON A VIBIG GURADA ACIDOMENACTORIA/1955	T	116.113							
7	IEMACC INVINEECE CO	DATIENTA A VENIC CORAN ACHICA DE LA CARACA	Ī			Ī					
÷	TENACCI IT DAM PERCI DI COR	DOT SENT A VIBIG (CIDAD) ANDICE/AS BEBLACOOK		911.00		Ī					
-	HAVE COLUMN SECTIONS	INGLIEUTA A VIBILE (CIBANI ANIMERATECINOSI OVACILADA)									
1901	HEMACO LOUNTA PRECIDI COR	INCHESTA A VIRIE COMMUNICATION AND INCHESTAL	Т	110 114		Ì					
PIEMA IADITI	IEMAGGI LITEMIN PRECURSOR	INFLUENZA A VIRUS (STRAIN A/DUCK/NORKADOCY/7)	T							ĺ	
	HEMA OCE LITORIN PRECURSOR	INGTUENZA A VIRUS (STRAIN ACHICKAROK KAIDOMAG)	Ī	100							
۳	HENZAGGE LITORIN PRECISESOR	INGT LIENZA A VIRUS ISTRAIN AMUCKANORKAIDON VIDI	T	104-123					Ī		
-	HEMACKS INTON PRECINCOR	PARTITIONS A VIBILIC (CIRAIN AMIN'R AINCHE AINCHAIN	T	100							
_		fat. Manual Control of the Control o								$\left[\right]$	

The Country	Terrentation	All Viruses (No Besser isphoges)		П	\Box	$\boldsymbol{\Box}$	П	П	П	$\overline{}$	
TILERAME			AKAL	,	ARCA.	- 4018 v	SEGS	08541_(4	AMENZ- A	AMEAS .	AMEA
PENA ANDIES		ENZA A VIRIIS (STRAIN	9	≘: ≘:		7		j	Ì		İ
PIESTA IADIO	IN MARCE LITTON PRECIESOR	INTI (TENZA A VIRUS (SIRAIN ADUCKAIOKKAIDOMAS)	21.40	120					i	Ì	1
		A A VINIS (SINANA	31.43	100	i					-	İ
		MANUAL VIDENTA	===	113.130							
		MA WIND A COMPANY	2.5	101.10							
NEW AUT	INCHARGE UTININ PROCESSOR		110.00		!	İ		Ī	<u> </u>		
MENA MONZ	PENACCALIFIENT PRECINSOR			- 011				Ī			
PREMA LADUS	HEMAGGLUTTININ PRECURSOR	INTLUENZA A VIRINI SINAIN AUDUMONAMINENI			Ī				Ì		1
	MENTAGOR UTINUE	VIRUS (STRAIN		3	1			İ	İ		-
PHEMA IAPRO	HEMACICLUTING PRECUTSOR	INTLIENZA A VIRIUS (STRAIN AFINGLAND/11/17)	37-39	123.119		į			-		
	HIS MARCEL LITTE ON PRECITE SOR	A VIRUS (STRAIN	330-346	118.333							
		A VIBIR (SIBAIN	110.011								
VIEW MARK		1			İ						ĺ
PENA INOCI	-	VINUS CONTRACT		Ī				-		Ī	-
PIEMA IAGUA	=	INTLUENZA A VIRUS (STRAIN A/GULL/ASTRAKHAN/117/14)	119 176								1
SIMPLE INUAL	÷	INTI LENZA A VIEUS (STRAIM A/EOUINE/ALGIERS/72)	321.338			•					
	-	BASE STATES A COMPANY AND	310.344			Ī					
MENA MICE	-	THE COUNTY				1					
PIEMA IAIC!	_	2	2	7		-				:	:
PIEMA (ANCID	-	INTLUENZA A VIRUS (SIRAIN ACQUINEAC DETROIT/184)	330-24	115-332		•					
	THE PARTY AND THE COMPANY OF THE COM	MAN	230-246	18.19		ŀ		Ī			
1	-		116.36								
MENA INGO		A VINUS (SIRAIN			Ī	-				Ì	Ì
TIEDA MAS	HEMADGLUTINDA PRECUASOR	A VINUS (STRAIN			İ	.		İ	Ì		
PIESTA LANK?		A VIRUS (STRAIN	236-252	2		,		į	i		!
PHEMA IAIR F		INTLUENZA A VIRUS (SIRAIN AFQITINTA EXINGIONUM)	310.24	115.112					-		
		A VIEW AND A	200.346	115.00							
			1	111111111111111111111111111111111111111		j-	İ	İ	-	1	
MEMA MIND		A VIAUS (SIPAIN		_	-				-	İ	
MENT MOST	-	INTLUENZA A VIRUS (STRATH AZEQUINEME W MARKE 1776)	10-01		1	••				1	
MISSA IAIDA	INTERACTION PRECIASOR	INTLUENZA A VIRUS (SIRATH AEQUINEMEW MARKETHITY)	315-332								
		MANUAL STREET	115.332			L			i		
NOW YOU	HEMACOL OLIVIN PAECINGSON	2	114.341							i	
MENA MINO	PENAGGE UTININ PRECIESOR					L	Ī		:		: :
PIEMA MISA	HEMAGGLUTININ PRECIMSON	A VIEWS (STRAIN				-				1	:
PIEMA MISP	HEMAOCI, CTONIN PRECIASOR	A VIRUS (STRAIN	130-246	15:112		-					
PIEMA IAIRW	IN MACCALLINGS PRECIESOR	INTLIENZA A VIRUS (STRAIN A/EQUINE/SWITZERLAND/17/72)	230-246	211.112		-					
100	HENVACOL PRINTED PRECINCOR	A VINUS (STRAIN	336-351	11.11							
CHILL ALMA	THE ALL ANCE THE BASE OF SAME	A VIEUS (STEAN)	136.131	111111							
	-	A VARIABLE ACTION A	116.36	131.161	i	İ					
TIENA MAGE	HENCELD SINK PRECURSOR								İ	-	
MENA MAY		INTERFER A VARUE (SIRVIN VIVA NEW VI)									I
PIEMA MACA	HEMADOLUTING PRECURSOR	NAME OF THE PARTY			İ						
PIENA LAMAB	HEMAGGLUTHAN PRECURSOR	A MINIS (SIBAIN	207-218	374.301		Ī			Ì		
HENG WALKO	HEMAGGLUTOWN PRECURSOR	A VINIS (SIRAIN	1.5	2							
MEN WEI	HEMACCLUTIONN PRECURSOR	A VIRUS (SIRAIN	17.59	123.139						Ì	
MENA ME	JEMAGGLUTIND PRECURSOR	INTLUENZA A VIBUS (STRAIN AAGADHIS/102/12)	17.59	332.339							
MEN WES	=	A A VIRUS (STRABA	11-13	106.123							
MEN WAY	HEMACCLUTININ PRECIASOR	DIFLUENZA A VINIIS (STRAIN AMINICS WEDFINIA)	13.101	231.347	116.333						
PIESAA LANTIG	IEMAGG UIDER	A VINUS (STRAIN	37.50	133.330							
PIESAN LAPER		INTLUENZA A VIBUS (SIRAIN APILOT WITALITANEDINA)	110-111								
MENA IAOU		A VIBUS (STRAIN	17	106.133	!						
CION VALUE	LESTANCE IN TAINING DESCRIPTION	INSTITUTA A VARIUS (STRAIN AMUDDY TURNSTONEMEW TERSEY/47/	1120-111					 			-
		A VIETT A STRAIN			İ				İ	Ī	i
Mark War								Ī	İ		Ī
MENA INSHI			2						i	Ī	
PIEMA INSTA	IEMAGGLUTININ PRECITISOR	VELUS (STRAIN	230.746	? ?!					!	:	-
PIEMA LATRA		ا <u>ح</u>	11-55	130			-		-	:	
PIEMA LATRO		MILLENZA A VIPUS (SIPAIN AZIOPIE YADMIARIOTI) 2060)	233-249					1	į		
PHEMA LATER	-	A VIBIIS (SIRAIN	330-346		:			!			
MEMA INTEN	_	INTLIENZA A VIRIIS ISTRAIN ACTURKE YANISCUNSTAINA)	139.145								
HENG INUDO	HEMA GGLUTININ PRECIASOR	INTEREST A VIRIS (STRAIN ANIDORNIO)(1)	33.50		5						į
PIEMA IAMI		MES	3	33.140	i i						
PARTY INDI	-	PRECENSA A VINUS (STRAIN X.11)	2.2			ĺ		!			
200	HELLANDS LITTLEN DRECT POR	NIN I	17.50	133.110	-	İ	-				ļ i
THE PARTY	4										

נינים	riki 21	All Virgas Inc Bed in ophics					Ī	Ĭ			•
THERMS	PROTEIN	TABLE	4	7	V C	- 2070 d	45.64.2	08544	PRES	A#544.	7
PHEMA IAZUII	DEMACKALUTINAN PRECLIFISOR	A VIRUS		8	-	-		: ;	j	:	•
MEMA IAZII)	HEMAGGLUIMIN PRECURSOR	INTLUENZA A VIBIUS (STRAIN A/SWINI/AIDNG KONG/12/642)	5	2	:		::::	:	:	•	
PIEMA NZUK		I LIENZA A	17-59	22.119		-		į			
MEMA DUBAA		INTI ITEMA B VITUS (SIRAIN BIANN ARBORUMA)	13:13	293 210							
PIEMA INTER	IN MACCINITININ PRINCIPSOR	POLITENZA S VIRUS (SISAIN SOFTEING//17)	137.130	101							!
PIEMA PABO	HEMAGGI UTININ PRECIPSOR	THE LIENZA B VINIS (SINAIN BADANAS)	116-132	101 108							
PIEMA DRED	HEMAGGI LTININ PRECINSOR	INSTITUTION OF VINISAS IR AIN BENCHAND 2242)	131.130	917 101	:		- -		i i	:	! : :_
PITE AL PARTIE	HELLEN LITERAL	SASS STEAD A DIVIDIO STEAD AND DATINGTON AND VALLE	761	36. 30	<u>:</u>	:	:	:		_	
	The state of the s		L						!!!	•	:
TIENG INPRE	I EMAGALUI ININ PRELIMSOR	INTELLECTA OF VIRIOS (STRAIN GROUPS)			1					i	į
MEMA DANK	HEMAGG UTININ PRECIASOR	INTEREST BYTHIS (STRAIN BUILDING KONGA/3)	=	20.00	į		-		i		
PICEMA PABIB	HEMAGGLUIMIN	INFI LIENZA B VIRUS (STRAIN BADARAKUZES)	108-134	111 303						. !	
MENA MID	LIEMAGGE UT INTH PRECIASOR	DALLENZA B VIRUS (STRAIN BAD'86)	20.136	15.	1				; 		i
PLEMA MILE	HISTAGE LITTING PRECINCOL	DOLUGNZA B VIRIUS (STRAIN BA FE/10)	13.130	103.313					1		!
CALCALLE MONTH	CONTRACTOR PROCESSOR	PARTICIPATE VIEW STREET AND DAYS OF ANY AGO.		1							
- No.	TEMANOR. DI INTIN TRECORDOR					1					
MENT PARKE		INFLUENZA B VIRIIS (SI KAIN BAIEMPHISAIS)		2		-					
MENA CABAN	_		200	200.00		-	Ī				
PIEMA PRICA	HEMAGGLUTININ PRECURSOR	WIRLIS (STRAIN	123.139	301.316		•					
PIESAA INBSI	HEMAGGLUTOWN PRECURSOR	DATLIENZA B VIRUS (STRAIN BYSINGAPORE/12/19)	133-139	301.316		-					
PIEMA BASS	HEMAGGLUTINGN PRECURSOR	DELLENZA B VIRUS (STRAIN DISINGAPORESA)	18:03	31.33							
PEMA DAUS	-	DATLUENZA B VIRUS (STRAIN BAUSSAVIONI)	116-132	394.300		<u></u>					
PIEMA DOV	•	INGLUENZA B VIRUS (STRAIN BAVICTORIADAS)	16-132	1000							
PIGMA BUSY	NEMACCI UTDON PRECURSOR	INDICIENZA B VIRUS (STRAIN BANCTORIAZA))	13:13	303.316							
PHONA BANYS		INSTITUTE IN VIEW OF THE ATM RAY AND AGA TAVISCON	108.134	101.101							ĺ
PIENT NICE	INCLARCOL INTERNATIONS	INSTITUTE OF CORP. C.	777 (77			-					
	SECTION OF THE PROPERTY OF THE PARTY OF THE	THE PERSON OF TH				-					
-	I EMACULO INTERPREDICA					1					
JAC INCOL	ILEMANOCO I INTO PROCOUNTS ON	INTUCATA C VIATA (SIRAIR COREAL LAKESTIE)				ĺ				-	
MCMA DACHY	HEMAGGE UT INTO	INTELLEMENT CHILDS (STRAIN CATYOGOVIA))				1					
NEW PC	HEMAGGLUTININ PRECURSOR	INFLUENTA C VIRUS (STRAIN CIGILANNESBURG/IMS)	40.7								
MEMA DICKY	HEMADOLUT DATA	RELUENZA C VIRUS (STRAIN CR YOTOVIAT)	439-453			•					
MEMA INCM!	HEMADGLUTININ PRECURSOR	INTLUENZA C VIRUS (STRAIN CANSSISSIPINO)	479-453								
PHEMA DICHA	HEMAGOLITION	INTLUENZA C VIRUS (STRAIN CNARARZ)	439-453			-					
PIEMA DICPI	HEMAGGI. UTININ PRECURSOR	INTLUENTA C VIAUS (STRATH CPTC///DETITHG/10/11)	430-434								
PIEMA INCP.	HENIA GGI UT IMM PRECURSOR	INTLUENZA C VIAUS (SI RAIN CPICTE IIINGI I STI)	430.454							İ	
PIEMA INCP	HEMAGGLUTIBNIN PRECURSOR	INTLUENZA C VIDUS (SIRAIN CPIGBEITING/1941)	13707							Ī	
MEMA INCTA	HEMAGOLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CTAYLON/12)1/47)	430-454								
PIEMA DICYA	HEMAGGLUTININ PRECURSOR	INTLUENZA C VIRUS (STRAIN CYAMAGATA/10/11)	130-450							İ	
PIEMA MOO!	HEMAGGLUTIONIN-NEUTANDASE	MUMOS VINUS (STRAIN SBL-1)	101-125	100	225-246	167.394	197-417				
PIEMA MANON	INDIANAGE UT DAIN NEUTANDRIDA SE	MINOS VINUS (STRAIN MIYALIARA VACCINE)	101-123	131.141	225.246	147.104	107-417				
PIEMA LABOR	HEMACCI LITRIM METANIMIDASE	MANAS VIRIS ISTRAIN BWI	101.134	177	331,346	147.104	107.417				
PIEMA MONOS	IN MACALITY DAMENDE AND HIDASE	MARGE VALUE (STRAPH SB) 1	101.134	1							
MEMA NOVA	DE MARCELLE DOWN - NEL JE AMONIDA SE	NEWCASTLE DISEASE VIRUS (STRAIN ALISTRALIA. VICTORIA/17)	91.110								
PHEMA NOVE		MEWCASTLE DISEASE VIRIS (STRAIN BEAUDETTE CAS)	91.0								
MENA NOVO	I EMACCA UTDEN WEI MANUNDASE	NEWCASTLE DISEASE VIRITS (STRAIN DZG76)	91.00								
MEMA NOVICE	I EMACCLUTING WEURANDINGE	NEWCASTLE DISEASE VINUS (STRAIN BILIITCIDIE RAT)	93-110								
MEMA NOVI	IEMAGGLUTOTH-NEI TAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN ITALIENIAS)	99:110							Ī	
MENA NOVA	IEMACCI LITIMINI MEURAMINIDASE	NEWCASTI E DISEASE VIRUS (STRAIN MIYADERANS)	93.110								
PICEMA NOVO		NEWCASTI E DISEASE VIRUS (STRATH CHEENSLANDAS)	91:10								
PIEMA NOVTO		NEWCASTLE DISEASE VIRIIS (STRAIN TEXAS G BAR)	91:16								
PIEMA NOVO		NEWCASTLE DISEASE VIRUS (SIRAIN ULSTERAST)	93.110								
PICEMA PHODY		PHOCINE DISTENDER VIAUS	16.50	111.234	69).513						
PIESAS PILITA	IEMAGGI UT ININ NEUTAMINIDASE	INMAN PARAMFLIENZA I VIRUS (STRAIN WASHINGTOWINST)	78.53	200	_	486.501				!	
PIEMA PINI	HEMAGGI LITININ MELITAMINIDASE	INDICAN PARAINS (FENZA 2 VIRIIS (PIV. 2)	18:0	=	_	İ					1
PIEMA PIZHI	HEMACCI UI MIN-NEUTANIMIDASE	HILALAN PARAINFI UENZA I VIRUS (STRAIN TOSIBINA)	1.48	1	1 1 1 1			İ			
PIEMA PIDB	HEMAOGLUTININ-NEURAMINIDASE	•	111.121	3.0							
HENA PINA	HEMAGGI UTINNI NEURANINDASE	HUDGAN PARATURI UENZA I VIRUS (STRAIN MIL 47085)		272.799							
MENA MINA	HEMAGGLUTINGH-NEURAMINIDASE	~ +	111.121	272.209							
***************************************	The second of th	۰									

$\overline{}$	PARTIE	All Vicense (No Berteinsphager)	AREAI	ARTAI	Anias	ABIA	-1 1/1	ABTA 6	i i i		
אנוע אישוע	BENIAGGLUTININ NEURAMINIDASE	HENDAM PARAINTI LENZA) VIRUS (STRAIN TEXMINSTRE)	====	11.14	20 100	1	1	•			
=:	HEALACH UTININ MEURANIMIDASE	INDIAN PARAING LENZA) VIRIS (STRAIN TO COSE 1743)		2	2			:	! !		
PIEMA PIBLE	HEALAGGL UTIMIN MEURAAUMIDASE		11:130	¥.	24.140		:				
	HEATAGE UTING MELIAAHAIDASE	HIGHAN PARAINELIF NA A VINUS (CIRAIN WASIVISIO)	<u>= </u>	<u>وا</u>	D .	-		:		:	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ILPACALOLININ PREJITANINA SE	FICHAR PARAIN LUINA A A VIRUS (VIRAIN TUSHIBA)	9		ĺ					. :	:
Т	SECTION OF THE PARTIES OF	MINUTALES VINCE STRAIGHT IN CO.		į	:	į	!		; :		
Ŧ	SENANCE INTRICTUTE AND AND AND AND AND AND AND AND AND AND	CENTRAL VINCENTIA PRINCE AND AND AND AND AND AND AND AND AND AND	2	;		:				_	
1	HATTER COLUMN ST. IN A STREET, SEC.										
ī				;		٠					
7								-	!	:	:
1	CENCOLO INTERNATIONS		77.76		:::	1	Ī				
Ŧ		SERUM VIRUS (STRAIN Z)	30.00								
-		SINGAM VIRUS 41	2.5	15:102		٠					
≕			2.2	ē :	174 400	•					:
=		STALLAN VIRIUS S (ISON A I E CANINILA FI)	2.2	10.10	177 em		-	:			
MIEMA SVYCP		SINILAN VIRUS SUSCIL ALL CAMINIZATION	2.2	2	179 trū						
=	4 S.F.			101.7	in din			:::::::::::::::::::::::::::::::::::::::	:	•	
PHEMA VACCE			12:10	!	:	1		!	, !	:	•
			131.00		:	1	1	:			•
PIEMA VACOT	IEMACCI UTININ PRECIASOR	VACCINIA VIBUS (STRAIN TIAN TAM)	13.182	!		į.			Ì	;	
PIEMA VACCV			133.183		-	ĺ		İ	İ		
PIEDLA VARV			7	İ						,	:
MEXE ADER	Ī	VIDIOS TYPE 2	11 61	19.140			Ī	i			!
MEXI ADEO					-	1.	Ĩ	İ	1-1-1	!!!	
ī	Ī							1111			i
T		HOLEN ADEROVINING TOPE AL			i				-		1
		MOJEE ADEMONDE COME			1			1		!	!
PIGYS ABEST	IC KON A COCIATED PROTEIN	IN DAAM ANEMANCIBLIE TYPE 7 AVID 1		İ	1	^				1	-
					İ						-
1					İ						
PIERO COMPX				100	 3	Ī				1	į
÷				ī	-	-		-		-	· ;
PILM ASSES	LATE PROTECN 11962								i		!
Ī								-	111	į	!
ļ					:						
-	EARLY PROTEDUING	APERCAN SWING FEVER VIBIG CATE AND ACTION	3		:		İ			!	İ
7	2			1	:	:				:	:
Picis Eav	PROBABLE PROCESSONG AND TRANSPORT PROTEIN		Ī					:	:	į	
4	OTEN	ICHIAN CYTONE GALOVIRUS (STRAIN AD 149)	Ī	161	-	i	Ī			i	:
ſ		IERPES SUCH EX VIRUS (17PE 1/STRAIN 13)			1		-	İ	į	Ì	1
Г	Ī	ICAPES SOULEX VIRUS (1 YPE I / STRAIN ANGILOTTI)		Ī			İ	İ	İ	İ	
PICIO MSVSP	Ī	BEAPES SOULEX VIRUS (TYPE 1/STRAIN I)						Ī	Ī		
	II PROTEIN	BOVINE HEAPESVIRUS TYPE 2 (STRAIN PAIV)	11.11	9			-	Ī	i	İ	
PICIE HEVED	OTEN	EQUINE HELDESVIRUS TYPE I	3.	ı	- 375 571	-		i	1	i	1
	OTEN	IEWESVRUS SAININ (STRAIN !!)	97.6	ī	100						!
2	OTEN	MURANE CYTOMEGALOVIRUS (STRAIN SALITILI	Ţ	į,	-		Ī	Ì		j	!
PICIE PRVD	OTEN	PSEUDORABLES VIRUS ISTRAIN INDIANA FUNKTIALISE A DECKTOS	T	ī		1					İ
Ī	OFER	VABICEL A. 2057ER VIRIS (STRAIN DIRIGE)	Т	ī		Ì		Ì	Ī		
PICH HEVEL		GRAPES SINOR EX VIRIS (1996 17 STRAIN 19)	Ţ,	ī		Ì		Ì	Ì	į	!
Ĺ		Т					İ				
PICH PAY		ī		ļ			Ī	Ì			
Ĺ	Ī	1				Ī	-	Ī			
	PTIONAL PROTEIN	HENDES SOOLEX VIRUS (TYPE 17 STEATH IT)	Ī	169.63		İ	İ	Ì		1	
П		T	1=	16.73	!		Ī	Ī		-	
		i	ī	100		Ī	Ī	İ	İ	İ	
0	TRANS-ACTING TRANSACTIVATOR PROTEIN	Ť	105.22	-	100.101	Ì	İ	Ī		Ī	
PICY4 VZVO	7		147.565		<u>-</u> !	İ	İ	Ī	ĺ		İ
						1		1		1	

PCCFNF	3121311	All Vignes (Na Dacterleabaces)					Γ				
-	PROTEIN PARFIATE EAST V PROTEIN IT 100	TRUS ISTACIN INIMANA - UNIVERSITATION	7	1 6,110	Trang	No Take	AH LAS	- Time		i V inv	AHIA
PLE IL PRVKA	MAGDIATE EALLY PROTEIN IF 110	SEUDORABIES VIRUS (STRAIN KAPLAN)	130-111							İ	İ
PEGS INCHVA	HE 61 HOMOLOG (INCAN CYTOM	2	20.19		۱ ا					
	PANSCRIPTIONAL REGIN A TOR II 61	HERPES SIACHEX VIRUS (TVPE 1 STRAIN 13)			:		:		i		:
	TANSCHIPTIONAL BEGIN ATOM IS &!	COLD TABLE COMMENT TO THE PARTY AND THE PART		11.44							
	TAD INDICATE - FALLY FINSTHURGHIN	THE BALLY SAFETY OF THE PARTY O	92.	· .						•	
	ADEDIATE EALLY AOTEIN IEM	ICAPES SIMPLEX VINIS (1797 175 FRANK 17)	100.205		: :					!	i !
PIEGO IISVEA	MAREDIATE EARLY PROTEIN IF AS	EQUING HEAFESVINIS TYPE	를 등 -	-	!	!	İ			 	1
	ACCEDIATE EAST V PROTEIN	COUNTY OF PARTY OF PA				-					
	AMEDIALE CAME T PAULTIN	SCULOUGHIES VINITED IN MAINTAIN IN MAINTAIN AND AND AND AND AND AND AND AND AND AN		!	İ	-		-		:	:
7	CALCAL MACHINE	THE ALL CALLS AND		j	:	İ		1	:	:	:
PULL AVIET	FOR TYPOSINE PINASE TRANSPORTING PROFESSION	AVIAL BAVILLANDI ACTORIC CONTRACTORIC		100	;	-	İ	1	-	!	:
-	lo	FEI DE CARCOLA VIETA CETA CARLOTE A ANALTE IN		1	!	1					1
7	TYROSINE PROTECTION OF TRANSFORMING PROT	PELOG SANCONA VIRUS SIRAIN SYVDER TIETLEN	1								
L	CPROI	FELINE SARCOMA VIRUS (STRAIN GARDNER, RASHEED)	26.288			T-					
1_	FMS TYROSINE KINASE TRANSFORMING PROTEIN	FELINE SARCOMA VIRUS (STRAIN MCDONOUGH)	83.1	141-161	636.450	(41.16)	191.187	119.95			
	VROSINE PROTEIN KINASE TRANSFORMUNG PROT	AVIAN SARCOMA VIRUS (STRAIN PRCII)	30.3%			-				Ī	
	MASE TRANSFORMING PROT	FUIDAMI SARCOMA VIRIIS	230.27	14 170	600.470	19.19					
ī	INVAIDINE KINASE		1			İ		İ		†	1
PRITI EBV	131 YMDDWE KINASE	PSTEIN BADA VIRUS (STRAIN 895.1)	87F (Q)	97710	į						
	INTRIDINE KINASE	FISH LYNOHOCYSTIS DISEASE VIRUS	=======================================	33.33							
PKITH HSV11	HYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE I / STRAIN IT)	333.349							ĺ	<u> </u>
1	HYDEDRE KINASE	IEAPES SLAPI EX VIRUS (TYPE I / STRAIN CL. 101)	223.249			-					
1	INTHIDINE KINASE	ERPES SIMPLEX VIRUS (TYPE 1/SIRAIN HERAI)	333.240								
	HYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN KOS)	223.240								
	HYMIDINE KINASE	ICERPES SUADLEX VIRUS (179E 1787AAIN SCIA)	2								
ı	HYMIDINE KINASE	IGENES SUCLEX VIRUS (1775 1/51RAIN 1)1)	2	2	İ	·		1			
- 1	THE MINASE	BOVING REPERVIOUS INTE (STAND 8000)	1	2		-				į	
	INVESTIGATION OF THE PARTY OF T	BOVER REPRESENTED THE TARE TARESTON		17 857		-				İ	
1	DIVANDOG KDASE	SOVING REPREVIOUS 17PE 1 2 (78 AIN DIGIS)	9	1					-	i	!
1	HYMIDINE KINASE	EQUINE HERPESVINIS TYPE 4 (STRAIN 1942)	- :-	20.10							Ī
	THYMDONE KINASE	EQUINE IERPESVIRUS 17PE I (STRAIN ADAP) AND (ISOLATE HVS23A)	:-	134.193	174.398					Ī	
	HIYMDINE KINASE	FELINE HEAPESVIRITS (FEI ID HERVIRUS 1)	131-189								
1	THYMIDINE KINASE	IC I ALUMD HERPESVIRUS I	<u>-</u>								
PASTIN HISWOOD	TITMIDINE ROASE	MAJLMOSET FOUR ESVIRUS	1								
	HIT MININE KINASE	MELOTES VIAITS SALVING (STRAIN II)									
1	HIYMDAF KINASE	VARICELLA-205 FEB VIBILS ACYCLOVIE BEGISTANT CIBARA AGAST	10.10							Ī	
1		VARICELLA ZOSTER VIRUS JACYCLOVIR RESISTANT STRAIN 7:1.11	10.00	İ							-
PKITI VZVD		VARICELLA ZOSTER VIRUS (STRADI DUNIAS)	193.216								
١	HYMIDDE KIMASE	VARICELLA ZOSTER VIRLIS (ACYCLOVIR RESISTANT STRATN GK)	97.716								
FEITH VZVV		VANCELLA ZOSIER VIRUS (VZV)	197.216		ļ	i					
i	ALL LINGSING MANDE LANGE INCOME TO THE PROPERTY OF THE PA	THE BANCOMA VINOS ISTRAIN HARITY CITCAT RAINE 4									
Ī	CENE LA PROTECTION ROLLAND	ETAL GENERAL CONTRACTOR							İ	-	
ı	SERINE/TIMEOWINE PROTEIN KINASE	HELDES SDOLLER VIRUS (17PE 17 STRAIN 17)	20.78		Ī	Ī	T			İ	1
1	SEADME/TICHEONOME PROTEIN KINASE	HEADES SOULEX VIRUS (TYPE 3)	36.786	12.0			-				1
1	SERINE/TIGNEONINE-PROTEIN KINASE	EQUINE HEAPESVIRIIS TYPE I (STAAIN ADAP)	10.00			Ī		-			i
ادا	SERINGALINE PROFESS KINASE	EQUINE HEATESVIRIS TOPE I (STRAIN KENTIK KY A)	19.107					1	į	:	:
إ	SECING/THRECONNE, PROTEIN RINASE	VARICEL LA. 2051 I WIPLY COLLAND WANTER	•		: !					. ;	_
YKIL EBV	PROBABLE SERINE TIMEONINE PROTEIN KINASE	EPSTEIN-BARK VIRUS (S (RAIN ROS. I)	=	Ξ					İ		' i
- 1-	PROBABLE SERVICE TIME ONLY BEOLEN WINASE									İ	
. !	SERNETICE SOUNCE PROTEIN FINASE	PSECROBABITE VIRIS (TRAIN NIA.)			Ī					Ī	Ī
.1				100		1				1	

PCGENE	PIICTL21P	All Viruses (No Bocieriughanges)	П	\Box		П	П	\Box	П		
H	PROTEIN	53	j	3	3	3	48.62	-12.00	-rosso	4	37.0 V
PKRJ VZVD	PRUBABLE SERING/TICHEONINE PROTEIN KINASE VAN	VACH FILLA. 20STER VIRUS (STRAIN DUNIAS)	Ī			-				Ì	1
PKR11 HSVI	GENE 33 PROTEIN KINASE	KT ALIMID IG APESVIRUS I	2			1			-	-	-
PER MENT	CHAS MANDER KINA (F	A DI CIRCIO	150.160	148.575		-		į			į
		SURIN ANAILY		İ						-	
- WE WALL	INTITION AND THE PARTY OF THE P		8			 		Ī			į .
PERS VACCV	JOKES PROTEIN KONASE IENAMI, DO					İ		Ī			1
PKRBI VARV	10 KD PROTEIN KINASE 1 KNAUL OG	UOLA VIRIIS	7	:: !						-	-
PKAPI SFVKA	POSSIBLE PROTEIN MANASE CO	PE FIDROMA VIRUS (STRAIN RASZA)	9.0			Ī					
PKEE VALLE	POSSIBLE PROTRINGING FIG	CINIA VIRUS	83.100								
	SOCIET E DESCRIPTION PRINCE E 10	CIMIA VIELIS	23.63								
עאירי אירי	POSSIBLE PROJECT RAMASE TIV		2	i	-						i ;
PKRF1 VARV	POSSIBLE PROTEIN KINASE FIO	VAKOLA VIRUS	3		-	1				ļ	1
PKROS AVISU	BOS TYR KINASE TRANSPORMING PROTEIN	AVIAN SARCOMA VIRUS (SIRAIN UR.)	6.24	207-173	6	-				į	
TOTAL MARIE	TAN DECITED TOTAL TO A MATERIAL MINES PROJECT BY PROJECT BY PROJECT BY A MATERIAL MINES AND PROPERTY OF THE PR	AVIAN BETRUVISIUS RPL 30	154-172	23.241							
		Ë	1			-					İ
PKSEA AVET	TYR. PROFEIN KINASE TRANSFORMING PROTEIN SE	2: 5		i	-	1	İ			i	: i
PK SRC AVISS	TYR. PROTEIN KINASE TRANSFORMING PROTEIN SE	AN SARCOMA VIRLIS (ST	161.177			7		1		:	;
SULVE TO SE	PARTICIPATION OF THE AMERICAN CONTRACT PROPERTY OF	AVIAN SABCOMA VIBIS (SIBAIN BANVIAL)	161.111			•					
		200	146.133		:	-		İ	:	:	į
PRSEC AVISS	TABLESON FINASE TRANSFORMING FROIDING	10 CHO CHO CHO CH	1		_	:.		:		:	
PESEC AVIST	TYR PROTECN KINASE TRANSFORMING PROTEIN SH	AVIAN SARCOMA VIPUS (STRAILL SZ)	161.17				-				:
	S NITIONS CHANGE THANKS THE WAY WITHOUT BY	BOUG CARCOMA CIRILS AS IN 11.193	181.337			·					
TASAL ASVE	I TRITACIE IN A IN A SE LIANNA SE CONTROL SE	1			:					:	!
MEST REVE	TYR.PROTEIN KINASE TRANSFORMING PROTEIN ST	SAMCONIA VIRUS (SINA			: 1	7	ļ	!	į	-	
PKSAC RSVPA	TYR PROJECT KINASE TRANSFORMING PROJEIN SP	IS SARCOMA VIRUS (SIR	156.374			. !		İ		!	į
SACOL BOVE	TAN PROTECT TANKED BY AND PROTECT BY	BOUS SARCOMA VIBUS ISTRAIN SCIOUST RUPPIN	161.373								
	THE PROPERTY OF THE PROPERTY O			: 	!		i	į	ļ	<u>:</u>	
PKYES AVISY	TYR. PROTEIN KINASE TRANSFORKING PROTEIN Y	AN SARCONIA VIRIUS (ST			:	:	1	!	į	i	İ
71 100 ADEBY	LATE 180 KD PROJEIN	INDIAN ADENOVIBIIS 11FE 2	=					1		-	1
	A STATE OF THE PROPERTY OF THE	INTERIOR ADDITION TYPE 5	1	İ	!					!	!
2	LAIR IWAD FACIENT				; ;	:	İ		i	!	!
FIS ADEA	LATE 100 KD PROTEIN	INDICATE OF THE 41		:	-	:		:	:	:	:
N S ADFO	LATEL SEED PROTECT	INDIAN ADENOVIBUS TYPE 2	21.24		_	_	_				
		THE PARK ADDITION OF THE PARK	117.159				:				
	THE PLANT OF THE PROPERTY OF THE PARTY OF TH					:	:	:	:		
_1	JE PATIC LECTIV HOMOLOG	CONCEDE A MINISTER OF THE PROPERTY OF THE PROP	1		•	:	1	:	:	:	:
	LATENT MEMBRANE PROTEIN I	SPETER BARR VIRGS (STRAIN BO) ()			,	•	:	:		,	
ı	LATENT MEMBRANE PROTEIN	TOSTELY BAR VIETS (STEAM FOR 6)	=	8	_	_					
,	A TRIVE AGENCE AND PROPERTY.		2	8	:	•		!			
		2 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -		206 226	101 101	-	901.00	00.410			
	UENE TELMINAL PROJEIN				_			Ī		1	:
PACEL SFYKA	MOUNT CAPPING ENETTINE LANGE SUBLINI		3		•		-		1		:
PACEL VACCO	MANA CAPPING ENLYNIE, LARGE STEITHIT	VACCINIA VIRUS (STRAIN COPPINIAL.)	2			2	-		:		:
PHOEL VACCV	ADMA CAPPING ENZYME, LANGE SUBINIT	VACCINIA VIRUS (STRAIN W.F.)	103	269-202	200	2			1		
VANA ISTAN	MANA CAPPING ENZYNG LARGE SIGNIT	VANOLA VIRUS	101.10	169.312	211 011	101 119					
		TABLE AND THE PROPERTY OF THE PARTY OF THE P	117.701			-	İ	!	:		
	The state of the s	DECAMBLE (TABLE 1, CREATE DE ABINC)		447.486	314.341	-		!		: :	
THE REDVO	FOUND LAFTING ENC 1 FM					1			1	İ	-
PLOVE COLVS	MOVEMENT PROTEIN	CUCUMER CALENTION IL FINDAL VIRID WATERION STAND			!	-	-				
PAROVE COMMY	# MOVEMENT PROTECU	CUCUMBER CREEN MOTTLE ANDSAIC VIRUS (WATERUNG TON STRAIN	_	i	!		į				1
PLOVE ORSV	MOVEMENT PROTETN	ODOMIOGLOSSUM RINGSPOT VIRUS	ž	176.205							
PACY PROVE	MOVEMENT PROTEIN	PEPTER MILD MOTTILE VIRUS ISTRAIN SPAIN	25.30	100 901							
VALUE TATALA	MOVEMENT PROTEIN	TOBACCO MILD GREEN MOSAIC VIRUS (TNIV STRAIN UZ)	106.301	ł	- : 	:		<u> </u>	:	:	:
Contract of the	JUST CHAPTER TO THE PARTY OF A	TOBACCO MOSAIC WRITE STRAIN COMPEAN	101.101	146.191	ĺ		-		i	!	:
	The state of the s	CA DEST A VIEW NO. 14	130.144		İ					!	!
	MODIFICATION METATERASE CAIDS				1					!	Ī
שנים סואני	MODDICATION POLIMICASE CVIAII	PACAMACION BOILDAFIA CIRCUTA C					ļ				1
שיום סשיו	MODIFICATION METHYLASE CVIBILI	CHECKELLA VIRUS MC.1A	177.192	265 7116	1						1
	PINS GAG MYB-ETS TRANSFORMING PROTEIN (AVIAN LEUKEMIA VIRUS F26	104-124								
PLANT AVEG	MYN TRANSFORMING PROTEIN	AVIAN MYELORI ASTUSIS VIRI'S	11.11	9:1:01	!				!	:	
VOLUE A PARTY	MICH ENCLAPED PROTECT	AINO VIRUS	189.111	:	-						:
		AIRTY AVIDER I A CONCE	18		:	-	-		-		
3	MICHEUCATS TRUITING			-	i		Ī	i	!		İ
TCA BENSE	MIX LEOCAPSID PROTEIN	BUNTAVILLE SMUS SMUS SMUS SMUS SMUS SMUS SMUS SMU		-					i	1	
THEM COVO	MICLEOCAPSID PROTEIN	CANING DISTEMPTS VIRUS (STRAIN ONDERSTEPTION T)	2		:	į			-	!	i
	MICLEOCAPSID PROTEIN	FELINE INFECTIOUS PERITONITIS VIRUS (STRAIN 79 1144)	\$1.74								_
	MACLEOCAPSID PROJECT	TONTAAN VIRUS (STRAIN 76 110)	117.343	:	!				 	!	
	MACHINE ABOTEM	HAZABA VIBLIS (190) ATE ACTION	47.1.44	Ī	-		Ī				
	The second secon	THE CAN INC. ALL STREET, STREE				1	1		:	-	-
PACAP UON	MIN LEGGARSHI PROTEIN				1					1]

183534	1013(10)										
TILE NAME	PROTEIN	VIEW	ANTA	AMEAS	ABIA		100	1 1 1 1 1		1	
PHCAP DASV	MICLEOCAPSID PROFEIN	INDATIENS MECROTIC SPOT VIRUS	1000	1	7	Ť		0 200	1	1	1
PHCAP LIEASE	MICLEOCAPSID PROTEIN	ACE ASE ES VIRILS AS DANDES CONT	9, 00		-	1				İ	İ
PHCAD LGACH	_	ACE ACE DE CIPE AND MAINTENANCE	9	1	-	-					:
PHCAP LEASY	MAK LEOCAPSID PROTEIN	MCASIES VIRIS (SIRAIN YANIAGAIA.II		1	 -		:	1	•	i.	:
PHCA MADO	MICLEOCAPSID PROTEIN	ALINOS VIRIOS (STRAIN SOLL II	16.13	-	!	-		:	:	: 1	:
PC MONT	MICLEOCAPIED PROTEIN	ANDADS VIRUS (STRAIN MITTALIARA VACCINE)	2.0	İ		Ī				İ	!
	MUCLEOCAPSID PROJETY	PROSPECT HELL VIRIES	ī	311.336	14.117	100	Ī				
		INDIAN PARAMELIENZA I VIRIIS ISTRAIN CON	Ī	14.102	_						
MC MIN	MUCLEOCAPSID PROTEIN	HUMAN PARAINGLIF NZA I VIRUS ISTRAIN WASHINGTOWIEST	15.0	6.10						i	;
		BOVINE PARAINELIENZA I VIEUS	2	:	;	1.		!		:	
		INDIAN PARAINS (9 NZA) VIRIS (STRACK NIII 67865)	41:14			-	-	:	-	İ	i 1
İΞ		PUDDIALA VIRUS (SIRAIN HALL NAS RI)	ī	331.166					j		-
		PUDMALA VIRUS (STRAIN SOTKANO)	Ī	216.216	100	1		-	1		
PICCY RABVA		AABIES VIRIIS (STRAIN AVOI)	2		Ī	1	Ī			İ	İ
		AABIES VIRUS (STRAIN PV)	179.122					-	į	1	ļ
ŧ	MUCLEOCAPSID PROTEIN	AABIES VIRUS (SIRAIN SAD BIT)	790.122	:	!	-		-	-	!	
	MUCLE OCAPSID PROJEIN	RIFT VALLEY JEVER VIRIS (STRAIN 210. SAR A112)	2		: :	1			-	!	
PHCAN SENDS	MUCLE OCAPSID PROTEIN	SEKDAL VIBUS (STRAIN 2 / HOST ARTICANTS)	1	101.70		į.	!			•	:
THE STOR	MUCL EDCAPSID PROTEIN	SENDAL VIRUS (STRAIN FADERS)				. j					
!	MUCL EDGAPSID PROTEIN	SENDAI VIRUS (STRAIN HARRIS)	18.0	101		 					
PACAD SENDI	•	CENTAL CHICACOLAND	Ī		i				:	•	:
PACAP CERE	MANCHE CONTACTOR OF THE PROPERTY.	SECOND CAPACITOR OF THE CO.	ī			-			1		į
AND STATE	MICH GOCANGE BEOTECH	PANDEL VIEWE CHAIR SALLEY	Ī		!	1		1::1		i	:
PACA TAPU	THE CONTRACT OF THE PARTY OF TH	TATABLE COLOR			:	. !		*		!	;
100	Meritorial Maria	TACANGE UND				<mark>. </mark>		į			
STATE OF THE PERSON	March Rocketth Beatleto	CONCRETE STREET	_		!						: -
TANK AND	WALTERWANDS OF THE PRINT STRUKEN OF THE	20.75		İ	1		İ	ļ		ļ	
PNCAP VSVX	NAICI EOCAPCID PROTEIN		-	İ		-			1	•	!
MEAN VEVE					1			Ī			
PHET HAZEO	NEGATIVE SACTOR	HITMAN BRANDONE INTERNOV VIDITE SAFE SAFE SAFE BARN								1	
PAES MYSSI	NEGATIVE FACTOR	IN MAN WAS DATES HIS WAY VINITE A VICTOR A VICTO	1		Ī	1					ļ
۱.	NE URANDADA SE	INGLUENZA A VIRUS (STRAIN ARLACK DUCKIALISTRALIA/102/71)									1
•	MEURAMONDASE	INGLUENZA A VIRUS (STRAIN ACHILE/IN)		-	!						
ı	METIMAMENTO A SE	INTLUENZA A VIDIUS (STRAIN AMECKVAL BERTAZIO)	1		1				1	i	
PRAM LABOR	MEIMALINEDASE	┰		İ		1	Ī			İ	
PRIAM LAFPW	NE I'M ALUNID ASE	7	Ī	101.101				Ī		ļ	
MALM LAHCO	NE LIRAMINIDA SE	INTLUENZA A VIRUS (STRAIN AFOUINE/CONJECTA)	E			Ī	Ī			Ì	İ
PARAM MACK	MET MANIMIDASE	INFLUENZA A VIRLIS (STRAIN AEQUINEAL NI LICKY 1/101)		İ				Ī			
NAME INC.	METITAL AND A SE	< 1	3.34					Ī			
277	PECIFICAL STATES	INTUREZA A VIALIS (STRAIN AL ENINGRAINSCH)	7.74								
TANK WAY	VELIBARINIDASE	A VIDER AND A PARTY OF THE PART		İ	-		İ				
PRIM WILE	MEINAMMENTA	NOTIFICAL VIEW CORAC AGE TO SIGNATURE	2 2	İ	!		i		1	i	!
PHILAM MARUE	MEURANGMIDASE	A VIRUS (STRAIN ARUDDY TIRNSTONEMEN W IERSE YAR						1	-	i	
PHRAM LASHI	MEURAAGNIDASE	VIRIS (SIRATN ASILEARWATERAUSTRALIATI)		Ī	Ī	Ī			-	İ	-
PREAM LATER	MEURAMINIDASE	VIRUS (SIRAIN A/TURKE Y/ORS CON/7)	1	1	Ì			İ	Ì		.
PWRAM LATELA	NEURAMONDASE	VIRUS (SIBAIN ACTERNAUS TRALI COSOCIES)	=		!	T	Ī			İ	!
PNRAM IAUSS		VINUS (SIRAIN AAUSSIVOOTI)	2.5							1	İ
MACH LAWOR	NEURANDNESE	A VIAUS (STRAIN AWITAL EMAINE/1/14)	1		-	Ī	Ī	Ī			ļ
PAN IAWE	PET ILAMINIDA SE	A VINUS	2							-	1
PANA PANE	MEIRAMINIDASE	VIBITS (ST		<u> </u>				Ī	1	İ	İ
NAAL PRICE	NEITHAMINIDASE	INT. (IENZA & VIRIUS (STRAIN BATIONG KUNG-8/7))	2.0		-		İ				į
	NEUTA-GNEDASE	VIRUS (STRAIN B1 EF/40)	2.0				ĺ			İ	
A 100 M	VE DEAMINIANSE	16)	2							i	:
PARAM BOLLO	NE (BANDA CE		2								
PNRAH DOBO	ME LIM AND A CE	THE PARTY OF THE PERTY OF THE P	R								
			R								

- 1		All Virgas (No Bactersophoges)	П		-17	-					
THE WANT	CROILIN	YIRUS	7	PRINT.	7 7 7	25.27.40	AFEA.3	7		AMI A.	
		CALLE MAN BY VIEWS OF A STANDARD CONTRACTOR OF THE CALLES	2		ļ	Ī	i	-		: : ;	:
PRACT INC.	NEUKAPHINIDASE		12	-	1	ī	İ		:	į	:
	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAM	NOTICE OF THE COURT OF CHAPTER				•	İ	į	-		:
	THE PROPERTY OF THE PROPERTY O	THE PERSON OF TH	1	100 901	. 50	İ		İ	!		: !
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CONTRACTOR OF THE PROPERTY OF	MANAGE A LIGHT OF THE PASSAGE A LIGHT OF THE PASSAGE AND A	2	:	:			į	:	•	:
		TOWN TO SPOT IND WELL TVIBING THE AZILIAN INCH ATE CPATITUTE OF	50.00	11 435	į	İ	i		:	-	: i
	NOTICE THE PROPERTY OF THE PRO	MANTO COULTED WILL VIRILE AS BAIN IN	10.00	416.458	:	-		1		i	:
	MAIN STANCE OF THE PROPERTY IN SEC.	VACCING VINE ATM COLONIAGEN	12	107-101	:					İ	
1	ACCIONAL PRINCIPLE OF THE PRINCIPLE OF T		15.05	107(11	!					İ	
VALUE VALUE	MULEUSING INTERPRETATION	Pick & Welle	2		i	L		i			!
	MUCLE DSIDE TRIPHIOSPILATASE	MUCLA VIAITS					-		į		1
79100 MSV6U	MAIOR ANTICENIC STRUCTURAL PROTEIN	ILENES SIMPLEX VIRILS (1) FE & STRATE CICANDA-1101)	8	130	2	Ì		: :	-	1::4:	!
PPAPE FOWTV	POLV(A) POLYMERASE REGIN A LORY SIBILAIT	IOWLPOX VIRUS				1		;		-	;
PPAPE MYXVA	POLYLAI POLYNEDASE REGULATORY SIMUNIT	MYXOMA VIRUS (ISOLATE AUSTAINTARRANT RC: 1101)	• • • •			1					
PAPE VACCE	POLYTAL POLYMENASE REGIL ATORY STAUNIT	VACCINIA VIAUS (STRAIN COPE MIACITIN)	101-116								
VACCO	POLYALPOLYNGRASE REGILATORY SCRUMIT	VACCINIA VIRUS (STRAIN WR)	917-00	i		-					
7477	POR VAN POR VACEDACE BECAM A LOBY CITRIDAIT	VARIOUS VIELS	977		:	 -				İ	
R		PARTY PROPERTY AND A MINE ARE POLICE AND POL		227.766	:	İ				İ	1
אריא איי	CALL CALLING LELL POLLICAR AND DELL					İ			İ		
MAN COM	IND PROTEIN IN PR. S PL COON	DACTIA PARCIATIONALA MINLIR AFSIO PULTIN URUSIS VIAIN	_			-			İ	-	
PPEJS HOVAC		AUTOCAZIA CALIFORNIA MIALEAN IN THEIMONS VINIS	-	-	; ;	j				1111	1
	MAJOR DOFEDIATE EARLY PROJEIN	AUTOGRAPHA CALIFORNICA MINTERAL VIII VIII DIRINSIS VIRIUS	=:		:					İ	į
PPENS ADEOS		INDIAN ADENOVIBUS TYPE 1	=:	j				-		1	!
PPENI ADEOS		HUBLAN ADENOVIRUS TIPE S	_		1				į		
PPENI ADEGX	PENTON PROTEIN	AVIAN ADEMOVIRIIS GALIO (SIRAIN SATI	194-214	101.124							
PPIVI ADEDI	200	INDIAN ADEMOVIRUS TYPE ?	10.41							İ	
		WORKE ANGMOVIETE TYPE I	100		i	:	!	i	:	i	•
	MALON TOP TROUGHT	DAME OF VEHICLE CONTRACTOR AND ADDRESS AND	11.11	816.046	1011.1004						
TOTAL BANKS		İ					1		: : :	1	:
- 1	- 2										
PROLI COAV	ANA! POLYPROJEIM	HUNGARIAN GRAPEVINE CHRONE NIOSAIC VIRUS	1	040		·	į		:		
		GRAPEVINE FAM. EAF VIAUS	180.196	431.501	303.564	1076	1100	3	1761.178	1021-1040	2070-704
		TOMATO BLACK AING VIRUS (STRAIN S)	1137-1159			~					
PPOL ABAN		ARABIS MOSAIC VIRUS	13:150	12.00	13		:	:	:		
		BABLEY YELLOW MUSAIC VIRIIS (CHANIAN ISIN, ATL)		463.485	:			:			
TANK I TOR		MARIE Y VELLOW MICKAIT VIRIES LIAFANI S. STRAIN II. D.	115.350	463.485	!			!		İ	!
		COASSALINE SANDERS VIBILE	Ī	101			İ			İ	!
		CALLA TO A A CHE DELIC COMPANIES						!			i
CAR THE		IOMAJO BLACK MING VIRGS (STRAIN 3)		1				i			
אאו נומי	RNAJ POLYPROTED	IOMATO MINISTROT VIRUS (1501. ATE MASTORIREY)	200								
PPOLO BOVEV		BOVING ENTEROVINGS (STRAIN VC-3-27)					-÷	İ			
POLO BVOVE	GENOME POLYTROTEIN	BOVINE VIKAL DIARRILLA VIRUS (ISULATE MADE)	677-633	8		121		701	1400 7481	107-101	
			101:310	3330.334	2	1967 1980	∹				
Proto Byoys	GENOMOR POLYPROTEIN	HOVINE VIKAL DIAMBIEA VIRUS (STRAIN SULT)	67/70				1180-1203	1303-1301	1101.1101	116-1602	A P
			23.6-23.0	276	279).280	100			İ		
Proto COXA	GENOME POLYPROTEIN	COASACKIE WIRLIS AJI (STRAIN COE)	130-067		į		ļ				
POLO COXAS		COASACRIEVIRUS AZI (ECMO V VIRUS)			1						
PPOLO COXA9		COXSACRIEVIRUS AV (STRAIN GAUGGS)		200							
Proto coxal	GENOME POLYPROTEIN	COXSACKIE VIRUS BI	1433-1496	1582-1607							į
PPOLO COXB)	GENOME POLYPROTEIN	COXSACKIEVINIS B)	331-355	1475-1501	1315 1610						
POLO COXII	GENOME POLYTROTEIN	COXSACK (E VINITS B4	331.146	103.169	1303.1601						
POLO COXOS	GENOME POLYTROTED	COXSACKIE VIRUS BS	1475.130	1585-8610							
PHOLO DENIS	GENOME POLYPROTEIN	DENGIE VIRUS 11PE I (STRAIN SINGAPORE S275/90)	611.96)		1211.1336	021.1521	1612-1678	1111.114	2100.2164	2401.2476	1010 106
PROLO DENIE	GENOME POLYPROTERY	DENGITE VIRIS TYPE I (STRAIN WESTERN PACIFIC)	919.914				_	_			!
CONTRACTOR OF THE PARTY	GENOME POLYPROTEIN	DENGUE VIRUS TYPE TUSON ATE MALAYSIA MIN	136.350								
FFOLO DENZE	GENOME POLYPROTEIN	DEMOUE VIRUS 1YPE 2 (STRAIN 19481)	191	. 176 616	113:113	194-1761	1011111	0791-1191	300.2018	1347.7364	2401.2425
			2700-2726					_	_	_	
PPOLO DENT	GENOME POLYPROTEIN	DENGLE VIRUS TYPE 2(SIRAID IGAIL-PDKS))		919.044	113.1130	1344 1361	101.101	1116-1196	100	200 2110	2307.1364
			2	1100.1736		-		_			
PPOLO DENID	PPOLO DENID GFNOAGE POLYPROTEIN	DENGUE VIRUS TYPI 2 (STRAIN D2:04)		910.044							

PCCTNE	1011/21/21/2															
FILE NAME	PROTTIN			i	1.	1										
PPULO DENZI	CANCINE POLYPROTEIN	DENGLIF, VIRIS TYPE J (STRAIN JANIAICA)	32	7	3	3		200	AMI A	PRCA B	A 5					
			1 Part. 272s.			-					-					
POLO DENIN	GENOME POLYPROTEIN	DENGLIE VIRUS TYPE 3 (STRAIN IN CHIPA A C.)	180 130	8	100.20	-				İ						
POLG DENZE	_	DENCITE VIRUS 19FE 2 (STRAINFRISO SI)	919.011	13:13	1347.1361	100	136.1194	1611.1620	1100.11	100.7161	60.7631					
1	1		2697.3331				_		İ		!					
		DENGLIF VERIS LATE, DIVINARIO (CONC. A 1974)	99 609	113.639	_	- Sel - Sel] . !					
į			24. CI.	6.C) at C)	F. 12:22	=======================================	- C- II-	- THE SEC	117. 1111	- 11 C 11 1	1.1					
	CENCRAGE POLYPROTEIN	* 34X 5 3 4 4 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5 7 5	77.18				_	!								
01044	STATE OF STA	DENOCE VIEWS 1 115 V	8	-	1011-11-27	220.2346	2342-2159	2400-3420	1045-1064		į					
1	CENOR FOLISCHE	ECIDADOS II (SIKAIM LIKISIADA)	000	72.74												
	CENTRAL POLITICAL	EMCEPHAL UNITOCARTHITIS VIRIUS	_	550.578	2	1610.1767					į					
	OL VENOTE IN	ENCETIAL DMYCCARDITIS VIRUS (STRAIN THE IS NOWINAND TOCKING	260.580	130.11	14.12			 i		_	_					
	GENOME FOR VIROTEIN	ENCEPTIAL CMAYOCARDITIS VIRUS (VIRAIN DATE DE DINAME TINE)	240.580	- E - S - E - E - E - E - E - E - E - E	11% 1317	, .				_						
POLO ENAIGO	GENOMIE POLYPROTEIN	MENGO ENCEMIAI OMYCICARINI IS VIRUS (STRAIN 17A)	\$60.580	:	!	!	!	:	:	:	:					
	GENOME POLYPROTEIN	MENGO ENCEMIAL ONIVOCARDITIS VIRUS	115:10			1				Ì	İ					
POLO FADVI	OLYPROJEIN	FOOT AND MOUTH DISEASE VIRIES IS TRAIN A 10 A 11		18	100				Ì							
POLO FLOVS	GENOME POLYPROTEIN	SOOT AND ABOUT DISEASE VIBIG ASIDATED AS				9	_	100-1101			!					
	CENOME FOR VPROTEDY	TOTAL AND LOCATION DATE AND LOCATION AND LOC					İ		-							
ON COLOR	MINISTER POLICE PROPERTY AND APPROPE	TOUR MOUNT MAIL AND A PRANTIN ALL	2	_	1010 101	96	_	261-170	:							
2000	CENOMA POLITICISM	POOT AND MOUTH DISEASE VIRUS (STRAINS OF AND OLDES)	=	916-1001	301	9.51	1665.1483	161.170	:	:	 					
	CENTRAL FOR LANDIE IN	PUDI-AND-MUDINI DISEASE VIRITS (STRAIN CI-SANTA PAU (C. SB))	301.330								į					
_!		FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1)	131-141				_	_								
1	CENONE FOLITACIEN	INPATITIS CVIRUS (INDICATE I)	2		619.640	693.699	_		200.200	2011.1019						
1	OCHORE FOLITACIEM	IND CHOLERA VIRUS (STRAIN ALTORT)	102-126	143-1161		1770-1402	2370-3367	3518-2538		11.11	1167.1782					
01001	144.000		3077-3893		_	_	_									
ī	CHEMOME FULTERN	HOG CHOLERA VIRUS (STRAIN BRESCIA)	101-178	1143-1161	10(1:41)	230-97	110.210	1510-2530	2011111	111.111	187.1787					
THE PERSON NAMED IN			3177-3103	_		-	_	_	_	İ						
	GENOME FOLVETONED	IEPATITIS C VIRUS (150LATE BK)	113.03	101.169	619 640	601.60	1117.2147	2441.2016	2016-2050	1988. 100)						
TO SECUL	UEMONE FOLYPROJEIN	IEPATITIS C VIDUS (ISOLATE ECT)	17.53		,	•	Ī	_	_	i	İ					
	CENTRE FOLTER	IEPATITIS C VIRUS (ISOLATE II)	113:133	_	019.010	PA9-109	39.63	143.680	2002-2005	2837.7850						
	CENCINE FOR VITIOIEDA	HEPATIFIS C VIRUS (ISOCATE INCV.476)	112.133	143.660		•	ī	ī	_		İ					
100		PREPAREIS C VIREIS (150), ATE (ICT27)	17-5				İ			Ī						
		HE PATITIS C VIRITS (1501 ATE ILCT16)	11.53					ĺ			İ					
		IRPATITIS C VIRUS (150LATE LICV.RF)	113-113	143-160					i	-						
		HEPATHIS CVIRIS (ISOLATE HC.11)	13.13	43.164			İ	İ			1					
PACTOR AND	CENTRAL FOLVERON	JEPATITIS C VIALIS (ISCA ATE INC. 13)	112.133	i i		101.100	ī	÷		İ						
		TELATITIS CVIRIS (ISOLATE IIC.16)	112-133	i	i		191.60	1887-1881	111.111	100.500	0101.101					
The Contract of the Contract o		ILEPATITIS C VIRUS (150) A 1E IIC. 11)	103.109	. :	_	ī	ī	_	_	÷						
VIA DI DO	TO THE PARTY OF TH	INCALLIST VIRUS (1501 A 1E PIC. 10)	3		101.100	193-11	Ī				010(-110					
TAND DIVIN	Control of Control of		13:13			1	ī				1001 1001					
PHOTO HEVER	CENTRE POLITICAL	TECATION CONTRACTOR	=======================================	14).169	619.640	1	111.13	-	777.177	3116.3156	!					
PROLEG HEVEN	THE POST AND THE PROPERTY.	THE PARTY OF THE P	2.53	_			_		_	i						
PPOLO IPAVI	GENDAGE FOR VPROTEIN	THE PARTY A VIBIG SEPANSION OF THE PARTY OF		9	419 640 4	483 496		1117 2343	******	38 tA. 28 cm	1001					
	GENOME POLYPROTED		Ī		j											
	GENOME POLYPROTEIN	A VIEW A	77.0		2		-	100E 2012								
	GENONG FOL YPROTEDY	DEPATRIS A VALUE (STRAIN 18)	Т		1001	1008 3001	1064-1062	<u> </u>								
	GENOME FOLYPROTED				8		2001									
POLO IDAVG	GENOME POLYPROTED						-			-						
PPOLO IOAVH	GENOME POLYPROTEIN	URPATITIES A VIBUS STRAIN IN 1711	1			i	i	-	:	1						
	GENONG POLYPROTEIN	IGPATITIS A VINUS (STRAIN (A)	ī		_		8	-		:	;					
PPOLO IDANI	GENOME POLYPROTEIN	ICEPATITIS A VIRUS (STRAMPARIN)	Т			ě	D	-	:	:						
	GENCHAL POLYPROTEIN	SDAIAN HEPATITIS A VIRUS ISTRAIN ACALTI			-		100	!	j	:	:					
	CENONE POLYPROTEIN	HE MAN REUNOVINUS IN FIRM IN		_	_	W. 1. 1.01	i	į	!	· :						
POLO IGIVIA	CENTIAE POLYPROTEIN	HUNOVIRUS IA HIRV IA)	2		-	Ī	-		-	<u>:</u>	:					
	CENONE POLYPROTEIN	US IB (III V IB)	Τ	ſ	- N. F. S.	GENOME POLYPROTE IN	HIPMOVIRUS 2 (HEN 2)	Т	i			_	_	_	9	i
╗	GENOME POLYPROTEIN	150 VEST CO VI	\$76.595	12	1300				╌	100	!					
				7		7	-	_	-		7					

1	PUCTUZIP	All Virtues (Ne Datterlaghaars)			Г						
CILE HABIL	CADILLE	STRIK	A TA	AIN.A 2	JHCA 2	AIIC H	A10.7.5	MILA	AWA?	3411.3.1	VIII.A Y
TO DUIN	INSTRUMENTAL AND A PARTITION	THE WAY IN THE WAY IN	11.1.1.1	:	:	-:					
PKK 0 LEDVO	STRUCTURAL FOLYPROTLIN	AVIAN INIPERIORS FURSAL INSTANT VINUS (STRAIN CIT)	Ī			-	-			į	- !
POLO IAEVI	SENONG POLYPROTEIN	TAPANESE FACEPHALING VIRUS (STRAIN SALLA)		200	1042-1658	2345.2370	2326-2161	2462-7481			
PIOLO IAEVS	SENONG POLYPROTEIN	INDANESE EN EPHALITIS CIRUS (SIRAIN SA(V))	3	108-133	1643-1658	2145 22 70	1134.3151	3463-7481			
PPOLO IAEVI	ZENOME POLYPROTEIN	JAPANT SE EM EPITAL HIS VIPTIS (STRAIN JADARSON)	1	200	B(4) (44)	23.65.22.20	1124. 2151	146. 5.48.	•	:	
PIOLO JAEVN	SENONE POLYPROTEIN	JAPANI CE IM FEILAL JIIS VIRIIS (SIR AIN NAKA) ANIA)	168 A18	111111111	:						
PPOLO RUMIN	LENOME POLYPROTEIN	KUNIN VIRUS ISTIBAN KIRKISTO	361.576	1144.160	1307-1126	10.41.16.19	2346-2271	2327.2352	2440 2400	246.1 218.70	1000
			3398.3814				Ī				
POLO LANVI	CENOME POLYPROTEIN	ANGAL VICE STATE OF THE PROPERTY OF THE PROPER			1	100	1011	100	100,017		
T											: 1 : i
7 774									:		:
7	LEAGUE FOLTFILLE	LANGAT VIRUS (SIRAIN 1) I AMISEV)		22.22		- !		٠			
POLO LIV	GENOME POLYPROTEIN	LOUPING ILL VIAUS (LI)	61.69	117.451	115.00.2	!					
PPOLO LIVS	ENONE POLYPROJEIN	LOUPING ILL VIRUS (STRAIN SD 526)	167.591	İ	!	ĺ.			1	İ	
A POST IN THE	SAMAR BALL VERNISHE	ANDROGEN COLUMN ACCUMA COL AVIORALICA	111	100		100					: 1
	ACTION OF THE PROPERTY	אינים אינים וויים אינים וויים אינים וויים אינים						707-7107			;
	DENOME FOR 19801EAN	MAKE DWALD MUSAIL, VIRUS				·					-
PPOLO MOREV	ACHOME POLYPROTEIN	MURITAY VALLEY ENCEPHALITIS VIRUS	331.347	\$63.378	937.862	1305 1924	50.034	1585-1602	1641-1647		
740 0 DAY	CHONE POLYPROJEN	DAYITHOGALUM MOSAIC VIRUS	80.10	111.136	678-696	191.914				ĺ	
PROLID PEAVE	CENOME POLYPROTEDY	PEPPER MOTETI E VIRGIS (CALIFORNIA 190) ATE)	68.717	134.046	1009.1014	101.101	1411.1483	1414.150	1474.1461	1001	1101 1001
	CHAIN AND AND AND AND AND AND AND AND AND AN	The state of the s									1000
	ACROME FOLITA STATE	POLIDAROS I ITE I (SIRAIM PUBLUME I)	5			j					1
MOLEO POLIS	GENTRE POLYPROTEIN	POLIOVIRUS TYPE I (STRAIN SABIN)	1410-1433			••					
POLO POLIL	EDNOWE POLYPROJEIN	POLICYTHUS TYPE 2 (STRAIN LANGING)	= -								
PROLO POLIVE	JENONE POLYPROTEIN	POLIOVINUS TYPE 2 (STRAIN W.1)	1696-1631						İ	! !	
PROLO POLIS	GENOME FOL YPROTEIN	POLIOVIRUS TYPE 3 (STRAIN 2) 1273	177.5M	1407.1410					-		!
_	CANANA BOL VOID ISIN	Selection of the select			: !	-		-			i
	The second secon							titi			
	UCACHE FOLITAGE	PLUM POLITICIS (STRAIN D.)	2	31.37		3	1441.1495	1407.151)	26/16 2624	1014-1106	
-	EDICAME POLYPROTEDI	PLEM POR POTYVIRUS (STRAIN EL AMAR)	# · #	141-141							
_	ж		37.13	113.740	907-1816	407.		2605-2623	3066 3090		į
PPOLO PPVRA C	CENONE POLYPROTEIN	PLUM PUX POLYVIRUS (STRAIN RANKOVIC)	20.00	111 340	1001	1467.1494	446 1513	2601.2621	1011 1101	İ	İ
_	114	PADAYA ENGSPOT VIBIR SCIBAIN PALMITANT IIA	1	:	:	!		:		:	
CASTO CITAT	ENOVE BOL VPBOTEDA	PARAMA BRANCADO VIDIA COLO ALLO PARAMA DA VALORA DE LA CALIFORNIA DE LA CA		i				-		;	:
ь	THE PARTY OF THE P			}	i				-		į
- 1	SCHOOL PARTIES AND SELECTION OF THE PARTIES A	A TACK MANASON VINIS (SIRAIN W)		-		•	i				
s١	ENOME FOR YPROTEIN	PEA SEED BORNE MOSAIC VIRITS (STRAIN CPLN)	19.03	251.260	10.01	110.010	1001-130	1011-1438	1505-1592	3708 3736	
	CENONE POLYPROTEIN	POTATO VIRIIS Y (STRAIN C)	155.176				_		_		i !
PPOLO PYYILU G	ENONE POLYPROTEIN	POTATO VIRUS Y (STRAIN INDICARIAN)	185.776	964.982	9101 0101	100	1436-1481	1481.1501	1617.1678	1922 1946	2011
							-		•		
	GENOME POLYPROTEIN	POTATO VIBUS Y (SIBAIN N)	155.776	10.194	1010.1016	100	156.1483	1485.1501	1677.1691	1922.1946	1120.3400
ľ	LENOME POLYPROTEIN	POTATO VIDUS Y (STRAIN O)	Т							-	
PPOLO PYTVI G	EMONE POLYPROTEIN	PARSNIP YELLOW IL ECK VIRUS (1501.ATE P.121)	593.616	1376.1144	1636.1651	1901.1074	1631.3643	201 1011	1000	Ī	
PPOLO STEVA	ENOME POLYPROTEDY	ST LOUIS ENCEPHALITIS VIRUS (STRAIN MC). 11	101.1174							-	
PPOLO SIEAVS	SACAS HOLYPROTEIN	CUCABCAND MOCALT VIBILS OF BADE CO.									Ì
DAMA O MAG	CENOME BOL VEROTERY	COUNTY VEGICIES AND SIGNATURE AND SINGLES SAND		-				-			į
TO THE PERSON NAMED IN	ELICAMENTO VALUE OF THE PARTY O	The state of the Asset of the state of the s	R	200	1						
27.24				22.	-	-					
	STATE OF THE STATE	Ī		327.55	= :	200		1740-1761	1310 2353	_	1765-2781
	ALICA TANDER	HILA-BURNE EMERICALITIS VIALIS (M.) SILINIS SELLICIS (M.)	-	337-551	_	210	-		=======================================	766.2784	
ALC ILV	PENONE POLYPROTEIN	TOBACCO ETCH VIRUS (TEV	827.853	951.980		114.1130	107.4124	100 1 506			
PPOLO THEVE C	ENONE POLYPROTEIN	THE BLEAS MURUNE ENCEPHAI ONIVELITIS VIRUS (STRAIN BEAN 0)164	924.941	1014-1095	0116	1320-1346	658-1677				
PHOLO THEYO G	ENOME POLYPROTEIN	THE LLEA'S MONUME ENCEPHIAI DAIYELIIIS VIRUS (STRAIN DA)	1072.1093	1117.1111		646.1635	Ī			Ī	
PPOLO TAGENO G	GENOME POLYPROTEIN	THE BLEAS MODINE EN FILIAL DATY ELLISS VIRUS (STRAIN GOVID	645.670	24.04			411.00	1440.1441			
Prot 0 TUNY	ENOME POLYPROTEIN		11.10	1 100 00	-	٠.	÷		Ī		İ
PHOLO TYNKY	ENDAME POLYPROTEIN	TOBACCO VERNIMOTH ING VIBILIE	Ī,			_					
PROLO WARY	ENONG POLYPROTEIN	WATERKE ON MISSAIC VIRIS IS	Ŧ		:	:	ī		2	j	:
PPOLO WAY	KINDAG POLYPROJEN	WEST MILE VIEWS	T			_					
PPOLO YEUVI	ENOME POLYPROTEIN	VELLOW FEVER VIRILS (STRAIN)	ī	12					_	2010-101	703.70
TO VEIVE	ENGINE POLYPROTEIN	YELLOW REVER VIRILE COMMANDA COLOR TO DAY	Ī								
PROLO YEFVE	GENOME POL VPROTEIN				_						!
MI NO M NOGO	JANOAG HOI VPROTEIN	POR INCIDENT AND A SECTION AND				Ì			j	Ī	
100	TOTAL STATE OF THE PARTY OF THE	POLICY LAND 1 TPE 1 (3) HAVING 1 (1)	1410-1433	٠.	1						
7	WOSINIA, IURAL FIN. ICRUITIN	VERFAUELAND STORE FROM FILLS VINITALIS (STRAIN TRINIDAD INDI	W. 107	111.14	411 414	1001-1001	1111111111	1971 1914	1177	1755 1755	
											1

PCCENE	PINCTLEIP	All Virgaes (No Betteriophoges)	П	П	П		П	П	П	П	
THERM	PADITIN	WRUS	1	7	3	7		3	1	CENT !	AMILA Z.
WOLN JOYC	NON-STRUCTURAL POLYPROTEIN	PERSON CALIFORNIA (STRAIN CALIFORNIA)	Ī	!	ī		İ	1		:	
POLK PCVF	MON-STRUCTURAL POLYPROTEIN	TELINE LALMINITIES (STRAIN JAPANIS), 14)			1000		_	200	i	: !	İ
NO.	NON-STRIKETIONAL POLYPROTEIN	FELIME LALICIVITY (SIRAIN FO)	1	7.70	7				- 11		!
DEVEN IS VOICE	NON-STRUCTURAL POLYPROTEIN	HEPARITISE VIRUS ISTRAIN HURKIA)	٦		Ī			1	:	-	:
PPOLN IE VACE	MON.STRUCTIONAL POLYPROTEIN	IGPAINISE VINUS (SIRAIN MEXICO)	2000		!	1			İ	-	1
	NON-STRUCTURAL FOLYPROTEIN	HE PATITIS E VIRUS (STRAIN MY AMPIAR)	١	2	; ;	:		;	: : :	!	:
PPOLN IR VPA	NON-STRUCTURAL POLYPROTEIN	IEPATITIS E VINUS (BIRAIN PARISTAN)	249 265	1333-13-0						_	
PPOLN MIDDOV	NONSTRUCTURAL PALYFROTEIN	MIDDELBURG VIRUS	115.213	628.643							
10	MONSTAUCTURAL POLYPROTEIN	ONYOND-NYONG VIRUS (STRAIN GULU)	\$0.103		-	1170-7240	_				
PROLE BLOV	NOW STRIKETURAL POLYPROTEIN	RADDIT HENORAHAGIC INSEASE VIRES	9	10.75	277.170	13.00	110.011	1100 6.0	#11:00 H	:	:
PPOCH RUDY!	NON-STRUCTURAL POLYPROTEIN	AABBIT IBANIANIACIC DISEASE VIRUS (STRAIN V. 151)	:_	:			<u>-</u>		:	:	:
POR IN BRAN	MISICAL PAR VALUE IN	ROSS BLVER VIRUS (STRAIN NIN 1092)	ī	- 219-119	1111.1111	3161.1204		Ī	i i		j j
TO BE A LOSS	MONOTOR AL POS CAROLINIA	POCCEIVE VIEWS (STRAIN 141)	L	34.17	_	-	i		!	:	
	MANAGEMENT TOT IT TO THE	AUSS MIVES VINIS (4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ï			107.01		100.000	1011	!	-
POLY RUBY	NOWSTRUCTURAL POLYPROTEIN	KAIN HIGHIN)	ī			_;;	i	1		1	-
POLY ST	NOWSTRUCTURAL POLYPROTEIN	:	:	17.5	790		_				
PPOLN SDADO	MONSTRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTATION KITTED / KITTAIN I INTERNATION	!	2		32 000		: : :	1	:	i
PPOLIN SONDV	NOWSTRUCTURAL POLYPROTEIN	SINDBIS VIRUS (STRAIM HRSP)		91	3	8	9			:	
PPOLIT EPINV	ANA REPLICASE POLYPROTEIN	ECGPLANT MOSAIC VIRUS	E08-833			1					
PPOLIL OYNV	ANA REPLICASE POLYPROTEIN	ONOMIS YELLOW MOSAIC VINIS	101.111	941.963		1					
PPOLR TYMY	ANA REPLICASE FOL YPROTEIN	TURNIP YELLOW MOSAIC VIRUS		36 53	1133-1102						ļ
PICE TYNYA	_	TURNIP YELLOW MOSAIC VIRIS (AUSTRALIAM ISON ATL)		134 451		:			:		
PPOLE TYMVC	_	TURNOP YELLOW MOSAIC VIRUS (ISOLATE: TYNIT)	113-113	15 43	1113.1193						
PPOLS EEEV	STRUCTURAL POLYPROTEIN	EASTEAN EQUINE ENCEPHALITIS VIRUS	33.50	213.23	105-105						
PPOL S EEEVI	STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS	3.30	114-230	193.508						
mous Elwi	STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-03)	10.4	336.243	20.53	١.			ļ !		
PROLS EEVY	STRUCTURAL POLYPROTEIN	VENEZUELAN EQUINE ENCEPHALITIS VIAUS (STRAIN TRINIDAD DON	7	336.345	20.50			1			
PPORT INDV	STAIRCHMAL POLYPAGIEIM	AVIAN INFECTIOUS BURSAL DISEASE VIRIS (STRAIN 1771)	3	!						_	
PPOLS USDVA	STAUCTURAL POLYPROJETY	AVIAN INTECTIOUS BUILDISAL DISEASE VIRUS (STRAIN AUSTRALIAN O	110.00	i i			İ		! ! !	:	
PPOLS INDVC	STRUCTURAL POLYPROJECT	AVIAN INSECTIOUS BLISSAL DISEASE VIRUS (STRAIN CU.1)	170.00			Ī		i		i	
PROLE MOVE	STAIRCHURAL POLYPROTEIN	AVIAN INFECTIOUS BURSAL DISEASE VIBUS (STRAIN PIG. 90)			İ		- i				
POOL S MOVE	CINICHINAL POLYPROFFIN	AVIAN DEFCTIONS BURSAL DISEASE VIRIS (STRAIN STC)				Ī	Ī		-		1
PPOLS DIMING	STRUCTURAL POLYPROJETY	ONYONG-WYONG VIAUS (STRAIN GULU)			İ				: !	 	i
PPOLS BAVT	7	ROSS MIVER VIRIUS (STRAIN T40)	1316-1343		l i		Ī		į	!	
PPOLS RUBVI		BIDELLA VIRUS (VACCINE STRAIN HPV77)	101.102		ł						۱ ا
PPOLS RUBYA	: "	AUBELLA VIRUS (STRAIN MI))	100 001	! !	i !				i i	:	•
1.1	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIM RAIT.)	731 303				!		 - -		
5	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN THERIEM	181-303	2							
	STRUCTURAL POLYPROFEIN	SEMLIKI FOREST VIRUS	5.5	<u>ء</u>	2 2		Ì				
200	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKILL BO / STRAIN EDSBYN 11-1)	2		-		j				
	STRUCTURAL POLITICION	MINISTER CHILD ENGENERAL TIC VIEW		1	1					-	
TO TOP	POL BOX VERO 16 DA	AVIAN BETICIT OFNO DICTIONS VIBILS	101.18				Ì		İ	1	
POST PARTY	POS POS CARDON COMPANY	BANCON EMPOSEMENT VIBER (CTBAN LC)		- 1997	1010	100	Ì				
PPOL BIVOS	POL POLYPROTEIN	BOVDYE DOADNODES ICIENCY VIRUS (ISOLATE 106)		70.74	3		Ī				
POL BIVT	POL POLYPROTEDY	BOYDRE DANDACH FICIENCY VIRUS (ISOLATE 127)		103.768	1		Ī				
PPOL BLVAU	POL POLYPROTEIN	BOVINE LEUKELDA VIRUS (AUSTRALIAN ISOLATE)	487.504	1		T	Ì	Ī			
PPOL BLVI	POL POLYPROTEIN (REVEASE TRANSCRIPTASE	BOYINE LEUKEAGA VIAUS (IAPANESE ISULATE BLV-1)	<u> </u>				Ī				
PPOL CAEVO	POL POLYPROTECN	CAPADE ANTHRITIS ENCEPILALITIS VIRUS (STRAIN CORK)	1914110	536-671		ļ	Ī				
PTOL CAMVC	ENZYMATIC POLYPROTEIN	CALL DLOWER MOSAIC VIRIS (STRAIN CM 1841)	184.704	100-401	111 494						
	ENZYMATIC POLYPROTEIN	CALA GLOWER MOSAIC VIRUS (STRAIN ON!)	73.17	175.402	1						
	ENZYMATIC FOLYPROTEIN	CALL IT LOWER MOSAIC VIRUS (STRAIN BBC)	¥.70	100.001	3						
POL CAMON	ENZYMA IN POLYPROJEIN	CAULIFLOWER MOSAIC VIRIS (STRAIN MYBIS)	70.07	107.50	5	411-403	Ī		$ \overline{ }$		
	ENZYMATIC POLYPROTEIN	CAULD LOWER MOSAIC VIRUS (STRAIN STRASBOURG)		100-401		Ī	Ī		Ī		
	BITT TAVE BY YEARTEN	COMMETCRED FURNISHING			1		Ť	1	Ī	Ī	
TOTAL STATE	POLATIVE FOLLTROIFIN	FOURSE DE PUTICINA ANGRALA VIBILA CLIONE 17401	1	100		8	1	Ī	Ī	Ī	
TAN ELAN	POLITICAL TROLLEIN	COUNTY THE CHAINS ARE MIN VIPOS (CLONE 1997)		1	Ī	T			Ī		
200	CALL CALL DESCRIPTION	The state of the s				1	1	1		1	

Tributarion on Control wy										
		1		7757	ī	T	- 9	Ī	- 497	241.0
POL POLYPEGIEN					-	1	!	i ::	:	
		ī		1		:	:	:		٠
	İ	ī		!	-	1::1		i	:	
FOL POLYMOLEIN				į					. !	-
		T	200	61.61	30					
		ī	101-101							
POL POLYPROTEIN		_[Ī	j
CIBDON APELFUXENIA VIRUS			18.				i		i	
POLYTROIEIN	TE ISTANTANTA						1	: :	:	
IN THE PROPERTY OF THE PROPERT	TOWNS OF THE PROPERTY OF THE PA		-	-	+		j			!
	1101 100			1	1	Ī	Ī			
	TYPE I (ARVZ/SFZ ISOLATE)	Τ	900							
	TYPE I (BHID ISOLATE)				1				-	
FOL PROJECT THE STATE OF THE ST	TYPE I (BITS INC. ATE)				-	Ī	1		:	:
	TOTAL STATE OF THE PARTY OF THE	ī		!	1			; ;	:	:
		Ī		-	j			İ		!
SOOMING WATER				1	-					
SICHE THE STREET	TYPE I CALL TOOL ATEX			-	1					
SOCIAL PARTICULAR PROPERTY AND ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE	CONTRACTOR AND A CONTRA				Ĭ					
THE PARTY OF THE P	SOL APEN		1119		1					
STATE OF THE PROPERTY OF THE P	CHARLE TOTAL TOTAL TOTAL TOTAL	Т	100	İ						
AND THE PROPERTY OF THE PROPER	TABLE OVER 1001 ATEN	ī		-				Ì	!	-
STORY IN THE STORY	Ī	7	929		j.					-
NAME OF TAXABLE PARTICULAR OF TAXABLE PARTIC	-				1		j		1	İ
2 ACMINISTRATION OF TAXABLE	CONTRACTOR OF THE PROPERTY OF THE PERTY OF T	ī			j		-	1	!	!
	14	T	200 000		ŀ				!	Ì
POL POLYPROTEIN	TYPE LIZAIRE A PON A TEL	Ī		İ	1				i	
	TYPE 1 (ISOLATE BEN)	ī	100				-		!	-
<u> </u>	i	100					-	i	İ	ļ
	TYPE 1 (ISOLATE DI94)	39.421	216-526	i !	-				i ! :	:
POL POL YPROTEIN INSOLATE DIOL	TYPE 1 (1501.ATE D205.7)	903.934								
	TYPE 2 (1501.ATE CHANA.1)	٦	=						ļ	
	TYPE 1 (1501.A TE WITH 2)	ī	79.78						į	
IN INCHES OF THE PROPERTY OF T	TYPE 2 (1SOLATE ROD)			!						
POLYPROJETY FOLYP	TYPE 3 (150LATE SELIST)	10.00	010	-						
	<u> </u>	ī	10.33	460 417		Ī		Ī		
		Γ	96736	200	ī	36.789				
LYPROTEIN	si si	103-130	20.00	100	475.042					
POL POL VRAGTERN SIZEEP PULMONARY ADERIOANTOSIS VILUS (IAAGSEKTE SIZEP ALT (164.21)	VIRUS (JAAGSIEKTE SJEEFPRET	3	2	ş						
POLYOLYROTEIN MAN TO THE POLOS FOR MINE AND THE POLOS FOR THE POLOS FOR THE POLICY POL	LEURENIA VIRUS (ISOLATE CI	2			ļ					
				4401 4041	190	İ	1	;	: !!	1
DA CAS BR E MUNDIE LEINENIA VIPUS		ī	9	101.101		i	Ī		- - - -	:
POL POLYPROTEDI	SOLATE 57)	١	1001.00	1009-1029	1036-1102					
	COLATE F024)	Γ	1001	1009-1029	1006-1102					
	SOLATE PVC. 211)	П	100	000 1030	1014-1102					
		3.	10.00					į		
FOL POLYPROTEIN RADIA HANDELLE KIR VIRUS		=	2	700	100				i	
	IS (STRAIN KAPLAN)		60						-	-
TOU POLYPROTEIN	TANIN BRO		۶i اع					-	;	
			469 411	137	2				:	!
	GUE CI	ī			3					!
	RIBV	ī	1038-1063			Ī				
	ISOLATE PHILIPPINES	T	100	Ī		Ī			Ī	
POLYPROTED RECE TANGRO BACILLI FORM VIALIS (R'BV) POLYPROTED RECE TANGRO BACILLI FORM VIALIS (RSOLATE PHILIPPINES)	NTBV) ISOLATE PHILIPP	INE S)	80 - 64 S		P1-815	\$10.00 \$10.00	\$10.00 \$10.00	\$10.00 \$10.00	\$10.00 \$10.00	80 - 64 S

PCCENE	100000										
THY HAME	PROTEIN	VIRUS			Т						
20.	POL POLYPROTEIN	SOUTH FORMY VIRUS (TYPE 1)	207		3		3	1	AMA	ANTAL	ARS-
25.7	POL POLYPROTEIN	SOUTH FORMY VIRUS (TYPE 1/ STRAIN LK1)	114.204	1	┰						
NA.	POL POLYPROJEIN	SUMIAM DAMINODEFICIENCY VIAUS (AGMISS ISON, ATE)	10.00		ī						
TO SIVA	POL POLYPRUTEIN	SIMIAM MAMINIONE IT LENCY VIRIS (ACM) ISOLATE)	311.336	026-006		1		-			:
TANK TO THE PARTY OF THE PARTY	FOL FOL YPROJEIN	SIMIAN INDITINODE ICIENCY VIRIS (ISOLATE AGM / CLONE GRI 1)	826.650		Ī					1	
1	PUL PUL VPIDIEIN	SIMILAM INDACTION OF TICHERCY VIRIS (TYO.) IN ATE)	1 2 2	\$19.915							+
	FOL FOLLYPROTEIN	CHROANZEE INIAH MUINEFICIENCY VIRUS	10.00		1						-
İ	TOL TOL TROUGH		640.00	91.0	!	į	!		!	::	:
TAN SINK	POLYPROTEIN	SIMIAN IMMUNCHE I FCIENCY VINITS (MINI (2.11) SULATE)	180 407	116.804	:	:					
1	POL POLEN	STATIAN INDITINGUEFICIENCY VIRIS (KAW ISOLATE)	180-403	111111	100	!	ļ	1	İ	į	į
	TOUR TOUR TYPIOLEGY	SIMILAN INDAMPODE FILTENCY VIRUS (F216/SAGIM ISOLATE)	143.370	100 140	Ī	1				-	
1	PUL POLYMOTERN	SIMIAN DARMODE ICHNCY VIRIS (PRIMCI) ISOLATE)	146.373	18:51	İ						
E SEC	FOL POLYMOTERA	SQUIMEL MONKEY METROVIRUS	748.360	1		-				1	!
- 1	POL POLYPROTEIN	SIMIAM SARCIMIA VIRTIS	5	100		. !	:				
POL SOCIA	ENZYMATIC FOLYPROTEIN	ARDITION VINITS	116.15			~					
POL SAVI	POL POLYPROTEIN	SIMON RETROVIXIES	176	1		İ				ļ	
PPOL VILV	POL POLYPROTEIN	VISNA I ENTIVELIE ACTUALITY									
PPOL VILVI	POL POLYPROTEIN	VISNA LEMINIBLY CONTRACTOR CONTRACTOR CONTRACTOR	0	9	8	•					İ
PPOL VILV3	POL POLYPROTEIN	VISNA FEMTIVISIS (CTO AIN 1917) PLONE IN 1917	0	3		-					
PPIS IICAVA	LANGE STRUCTURAL PROSPRIOPROTEIN PRISO	HINAM CYTOMICS IN CHAIR STATE COLUMN COLUMN CANADAM CA	201	99	31.93	1					-
PPPI HCMVA		HIGHER CYTOMEGA DEPARTMENT AND		2		. !			!	i !	:
PPP4 HSV60	PHOSPHOPROTEIN PAI	INCRESS OF THE STATE OF THE STA	=								Ī
PPRS HOUVA	65 KD LOWER MATRIX PROCEROUS TEN	HEALES SWOLER VIRUS (1776 6/ STACINGS)	131.175	186.4							İ
PR. 100 V	A KD LOWER MATRIX BLOCKHOOP CO.	INTERNATION OF THE POINT	11.33							İ	ļ
AVACH 15999	THE PER MATERIA MICENSON	MINISTER CT TONE GALOVINIS (STRAIN TOWNE)	101.123			!• •		:			-
PPE 3 LOATVE	PROTEIN PERI	ILLALAN CYTOMEGALOVIRUS (SIRAIN AD169)	79.102		!	-	İ	<u> </u>	<u> </u>		!
Party Marry		FIGURE MANDHARY TIPIOR VIRUS (STRAIN BR6)	19.00				İ			İ	
PPB N LANTVO		MICHOLSE MANGRARY TIRIOR VIPLIS (STRAIN CR.)	40.41			F					i
PPR.78 NG/TVO		PHOUSE PLANDARY TIMOR VINUS (STRAIN GR)	44.63								1
PRASH LISTRIA		MUUSE MANOKALIY TIMOR VIRLIS ISTRAIN CR)	60.61		i i	-		İ			
PRASH BRASV	TRANSFORMING PROTEINS FLI AND PLY	HARVET MUTUNE SARCONIA VIRUS	69.35	 	 						
PREEP CSV		KASIRED RAT SAICOMA VIRUS	35		!	-	İ			-	
L	DIFAMPICAN DECISTANCE PROTEIN	LAMOUL IIS SONORE MSIS VIRIUS	14.16		<u>.</u>	-		-		:	
ī	RISANDICIDE COLONIA PROTEIN	VALCIMIA VIRUS (STRAIN WR), AND (STRAIN COFFINIAGEN)	274-796	111	517.515		ĺ			i	ļ
i	MEN PROTEIN	A ALOUE A VIRUS	114.198	316 335	513.416					Ī	1
Т	REVENTEN	SIMUAN MONDAUDE I ICIENCY VIRUS (AGAI) ISOLATE)	3-13							Ī	
Т	RIBONACLEOSIDE DIPHOSPITATE REDICTASE	SOUTH PRODUCE FELT VINOS (ISOLATE CB.)	П								
PRIR! EDV	RIBONUCLEOTIDE REDUCTASE	PROTECT MADE VINITE AND	٦	180.310	015-507				I	Ī	Ī
PRICE HOUVA	AIBONUCLEOTIDE REDUCTASE	INDIAN CYTINGON ON DESCRIPTION	٦						ĺ	İ	Ī
PRINT MSVII	AIBONUCLEOTIDE REDUCTASE	PERPER CHAME EN VIETE CAME LA PER LA PER LA PER LA PERFECTION DE LA PERFEC	Ī	Š						Ī	Ī
PRIN HSVED	AIBONUCLEOTODE REDUCTASE	EOUDIE HERPESYMENS I VPE I VATER IN A PASSA	اء	2						İ	
PROFILES HSVSA	AIBONUCLEOTIDE REDUCTASE	SERPESVIRUS SAIMINI (STRAIM 11)		2	PAL 604						ĺ
PACE VACCC	RIBORACLEOTIDE REDIXCTASE	VACCOMA VIBUS (STRAIN COPENIACENI			:						1
کرا الا	RIBONUCI ED IDE REINICIASE	VACCINIA VIRUS (STRAIN WR)		1	1 :::						1
PRIR! VARV	RIBOMICLEOTUSE REDIXCTASE	VARIOLA VIRUS				-					
200	RIBONUNI EOTIDE REDUCTASE	VARICELLA-ZOSTER VIRUS (STRAJN ININIAS)	Ī	177	200	Ì					
Ī.	AIBOMUCLE OF THE AFEDUCTASE	EPSTEIN-BARA VIRUS (STRAIN 895.0)		İ	-						İ
ī	RIPOWING EUTIDE REDIKCTASE	INCRPES SUCCLEX VIRUS (TYPE I / STRAIN 17)	Ī	135.202	İ		1		Ì	-	i
1000	AND THE PROPERTY OF THE PROPER	IERPES SDAPLEX VIRIS (1 VPE 1 / SIRAIN KOS)	Ī	192.50	174.301	İ			1		
Ŧ	BIROWINI COSING RECORDS AS	IREWES SOULEX VINUS (1 VF. 2 / STRAIN 111)	1	33.20		Ì	Ī	Ī	İ	Ī	
ī	RIBORICI EGILDE RELIGIASE	POVINE IRRESVIRUS 1YPE I (STRAIN 34)	366.266		<u>-</u> !	Ī	Ī		Ī	İ	1
PRIRE HSVSA	RIBONACL EOTIDE BEDIECTAGE		1	31.31	-	İ				i	
PRILL SPVKA	RIBOMICL EDITOE REDUCTASE									-	İ
PRING VACCE	AIBONUCLEOTIDE REDUCTASE	VACCING VIRIS (STRAIN COEMINGER)	1	=						İ	
П	RIBORUCL EOTIDE REDUCTASE	VACCENTA VIRUS (STRAIN L.IVP	2								
PRINJ VACCV	AURONIACLEO TIDE REDIACTASE										İ
				1	1	1					

Percent	416.11.74.19		П		\Box		Γi		$\overline{}$	_						
PILE HAME			AREA L AB	ABCAJ OF	BREAL BREE	APICO OFFICE	17 APT 45 - 1	- VIII 4	TA NA	A	_					
PRIR1 VARV	INIBONALCLEOTIDE REDUCTASE		ì		:	1	•	•	_		_					
100		VANCELLA-20STER VIRUS (STRAIN DUNIAS)	13.38	_	;						_					
	4 DNIMED ISSUED TO STATE OF ST	AVIAN BOILS, ASSOCIATION VINITS TVPI	160 405	_	_				_		_					
AVBVA	MAIL SEVIEW FROIGH RINASE INVESTIGATION	The state of the s	265	100	261.53	-	•	-		-	_					
PRIM VACCV	RNA-POL-ASSOCIATED TRANSCRIPTION SPECTAC	CLINIA VIETO CONTRACTOR CONTRACTO	ī	18	201.131	<u> </u>	<u> </u>	<u>i</u> 		<u>-</u>						
THE VAIV	RNA.POLASSOCIATED TRAMSCRIPTION SPEC FACT	MOCA VIRIIS	Ī			1:00	<u> </u>	<u> </u> 		<u> </u>	Ī					
PIPOL VACCC	DHA-DOLECTED KNA POL. 147 KD POL YPEPTIDE	CCINIA VINIS (STRAIN COPEMIACEN)	Ī	-			<u> </u>	1	<u> </u>	<u> </u>	<u> </u>					
PRPO! VACCV	V DNA DOLECTED ANA POL THERASE 147 KD POL YPE VA	CCIMIA VIRUS (STRAIN WR)	1	•	1		1	:	!	=	:					
PEPOI VARV	DNA DIRECTED INA POLYNGRASE 147 KD POLYPE	MICHA VIRUS		1		7	_									
PRIOT CAPUT	THAT DIES CHED AND POLYMERASE 112 KO POLYPE	PRIPOXVIAUS (STRAIN KS-1)	Ť		;	-					_					
	SAY IN CASE SAN SAN IN AN AND AND AND AND	WPOR VIRIE	ī	31 37	200	١.										
7	DAY-DIRECTED BANK TOLINGENSE STEELS	COMPANY COMPANY OF AND COMPANY CONTRACTOR	91.9	140.374	19	<u> </u> -	:	:	:	_	<u>-</u>					
A NOT A VACE	DRA-DIRECTED AND THERASE 11/ RUPOLITE		4	71.6	15	<u> </u>	i	:	<u>i</u>	:	_					
PAPO2 VARV	DNA DIRECTED RNA POLYNERASE 111 KI) POLYPE	VARUE VIRIS		<u> </u>	-	1	-	:		_	:					
PRINCH VACCC	DNA. DIRECTED RNA POLYNGRASE 15 KU POLYPEP	VACCINIA VIBUS (STRAIN COPT MILAGE PO	-	:	-	-	:	_	-							
PER VACTV	THA DIRECTED BNA MY YAFBASE 15 KD POLYFLY	VACCINIA VIRUS (STRAIN NR)	=		_	_				_	_					
1	THE THE PARTY AND AND AND AND AND AND AND	VARIOU A VINIS			_			_			_					
		AND COMMENTS AND AND COMMENTS OF STREET		<u> </u>		-	-	_	-	_						
A ACC	DAY DIRECTED HAY POLITICANS IN ALL POLITIC			•		.:		_			_					
PRINCI VACEV	DNA DIRECTED RNA POLYNERASE 19 KO POLYTEP	ACCINIA VINUS (STRAIN WE) AND (STRAIN CONTINUES)			_	· ·	_	_								
PRPO) VARV	DNA DIRECTED BNA POLYMERASE 19 KD POLYFEP	VALUE A VIRUS		:	•		1	i		į	:					
PRINCE FORDS	DNA DIRECTED ANA POLYMERASE IS NO POLYPEP	DWILDOX VIRUS (STRAIN FP. 1)	=======================================	_		_		-		_	_					
	BULA NOBELLEN BULA BOL VALEBACE	LYSTAD VIDIS	19:191	107.17	1101 11111 1211	100	111 mm 111	1111 IVE PAY-1933	<u> </u>		<u>.</u>					
			31.11	:	-	:					_					
	÷		7			;	1111	!		_						
THE EX	=	EQUINE ARTHRUIS VIRUS	200				_	-		_	-					
Secretary Control	=	DRIORI VIRING ASTRAIN PAINANCING	247.764 274	= 22	13.14	F. 69.53	- F			_						
	÷	ŀ	1 33		-			_	_	_	_					
PRUPI LADON	AMA DIRECTED RUNA POLYMERASE SUBUNIT PI			-	-	1	1	<u> </u>	i		ı					
PLUP! LABEL	RMA DIRECTED RNA POLYMERASE SUBUNIT PI	VINUS (STRA		- i	-	-1	<u>i</u>			!	-					
MANAL 1888	THE STREET THE THE POLYMERASE SUBUNIT PI	TOLUENZA A VIRUS (STRAIN ACTUAL DINIATI)	344-363			_										
				<u>:</u> :	:	-	<u> </u>	<u>:</u>	<u> </u>	:	i					
TAN TAN	ENA DUECTED KINA POLYNERANE SUBURILLY		<u> </u>	: 1	<u>:</u> !					:	;					
PREDI LAIGO	ANA DIRECTED ANA POLYMERASE SCIBLINI PI		707	:	-		1	:		_						
PEN MIT	ANA DIRECTED ANA POLYMERASE SUBUMIT PI	INTELENZA A VIRUS (SIRAIN AEQUINETI: NNESSEEVIGI	244-262					-	-	1						
	;	MILLENZA A VIRUS (STRAIN A/KIEV/19/19)	244-262				_			-						
A 10 10 10 10 10 10 10 10 10 10 10 10 10	÷	MATTERIZA A VIRIUS ASTRAIN A/RORE A/426/611	14:36	İ				<u> </u>	· -	_						
	÷	10	244.343	<u>:</u> 	<u> </u>		<u> </u>		<u>:</u> -	<u>:</u>	•					
7 W	MAN DIRECTED MAY POLYNE MASE SHIBLING PA			1	1	<u> </u>			!	<u> </u>	:					
	ANA DIRECTED RINA POL THERASE SUBLINIT PI	CHANA		!	-		 -	!	1	:	1					
THUS WED	AMA DIRECTED RIMA FOR YMERASE STIDITULE PL	╼,	797.707	į	<u> </u>	1	-			-	:					
PRINCIPAL SALAN	ANA DIRECTED ANA POLYMERASE SIBUNIT PI	VARUS	244-262	_ <u> </u>	_	<u> </u>	-	<u> </u>	i	-	1					
PRESIDENCE IN COLUMN	ANA DIRECTED BINA POLYNGRASE SUBLINIT PI	NULUENZA A VIRUS (STRAIN ANCIAPHIS/1/11)	244.262							_	-					
PARSI IAMTA	MAA. DIRECTED RIVA POLI YAGEASE SUBURIT PI	MILUENZA A VIRUS (STRAIN ANTMOND)	344.363													
MAY 104 PE	BMA. DIBECTED BMA POI VACERASE SUBINCIPE	NEL LENZA A VIRUS (STRAIN APUERTO RUCOAVIA)	346.363		<u> </u> -	<u> </u>		-		 - !	<u> </u>					
	÷	MATHEMPA A VIBIL (CIBARIA A/CINCAP/DE/1/47)	246.363	<u> </u>				<u> </u>	<u> </u> - 	<u> </u> -						
	-	VIEW ACTOR AND	36.36	<u> </u>	<u> </u> 	<u> </u>	<u> </u> 	<u> </u>		!	i					
1	+		Ī	1 1 25 77	1	1	<u> </u>	 -		 	1					
	Ŧ		Ť	1		<u> </u>			1	1	1	1		<u> </u>	1 -	;
THE LAWS	7	A CHILD				!		1		-	<u> </u>					
PARTI LAZIU	=	INTELLEGE A VIRUS (STRAIN ASSAUNTATION CAUCATORIS)	707		: :	<u>i</u> 	1	<u> </u>	-	:	:					
PRINT LAZON	ANA DIRECTED ANA POLYMERASE SUBLINIT PL	INTLUENZA A VIRUS (STRAIN A/SWINE/ONTARIOVAL)	244.262	-	 	-	<u> </u>	<u> </u>	-		Ī					
PRUS WATE	RINA DIRECTED RNA POLYNGRASE SUBINITY	VIRUS (STRAIN ASWINF/TENNESSEE/26/72)	244-362	-	!	_			<u> </u>	; 	:					
PREPI DOM	AMA. DURECTED RNA POLYNGRASE STRUNIT PI	I VIRUS (STRAIN BANN ARBONING (COLD ADAPTED))	201-122													
DEN DEAD	RNA DORF CTED RNA POLYMERASE SUBINIT PI	DATLIENZA B VIRIIS (STRAIN B/ANN ARBORING WILD: TYPE)	208-222		<u> </u>		<u> </u> 	<u> </u> 	 -	_	ļ.					
100	ANA HIRECTED BNA POLYNGRASE SUBINIT PI	LVALUS (STRAIN BALFE/40)	705.333	<u> </u> 			<u> </u> 	<u> </u> -	<u> </u>	<u> </u>	Ī					
	SALA MARCHES BALL BOX VICEBACE COMPANY PI	VIBILE (S.IB ATA CAUSE)	ï	101.171		<u> </u>			<u> </u> -	!	į					
- 1	THE CONTRACTOR OF THE PARTY OF	A VIDELS AND ALK AND ADDITIONAL	1	1	!	<u> </u>	!	: :	:	_	•					
	MAN WALL IEU ANA TOLITHERASE STILLING	Control of the second s		1	•	:	:				_					
	THE CARE CAN AND THE RASE SAME AND THE	A VIETE AND AND AND THE COMPANY OF T		· 	:	:	1	:		•	,					
TREES LANK	STAN CHECKED HAN TOLITHERASE SUSPENIES	A CIBIN SCHOOL SCHOOL STANDS		-	i !	!	:		<u> </u>	!	i					
	AND DESCRIPTION OF THE PASS OF STREET	A VIETO A MINISTER AND MINISTER	100	<u> </u>	<u> </u>	<u> </u>	1	l	<u> </u>	! !	:					
	MAN DUELLED MAN FOL PRENASE SUBLIMITY	A VIDEO SERVICE AND POST OF THE PARTY OF THE		1	1	<u> </u>	<u> </u>		<u> </u>	<u> </u>	Ī					
TAMES INTO	MAN DURE LED MAN TOL I MERASE SUBJECT I			!	-		1	<u> </u> 	<u> </u>	1	1					
PREMIALES			314.337			$\frac{1}{1}$		$\left {} \right $	1		7					

1	PRICTIZIP	All Viruge (No Batteraphages)				г		ſ			
LITERAKE	LAGICIA	VARUS	CATES J	1 V 100	A C. L.	121	A 11.4	ABI A.	411.1	MIN	ALC: N
PARCE LAPINE	THAN DIRECTED AND POLYMERASE SUBJECT FOR	INCLUENZA A VIRUS (STRAIN AFTINITALIZATION OF TAXIONS)]	·			-	!	:	
PRIPE IARUD	ANA DIRECTED ANA POL THERASE SUBINIT PT	LUENZA A VIRUS ISTRAIN	_		:	-1-		:	1	: !	-
PRRF IASON	ANA DIRECTED RNA POR TAGE RASE SUBINIT P.	A A VIRIJS (SINA	534-557	; 						ĺ.	İ
PRRF2 LATEGE	MAN DIRECTED RIMA POLITICERASE STRINIT PT	A A VIRUS (SI	334-553	-							
PRED INCH	ENALDIRECTED BAY POLYMERASE STRING TO	INCLUENCE A VIEWS (STRAIN AND LOOK SAITTUIN)		3	!			!		:	!
PRILITY LAZERU	AMA DIRECTED HAP DUNIERASE SIBILINIT PI	A A VIRUS IS	100	1		i	; !	:	:	=	
31	AMA DIRECTED RMA POLYNIERASE STIBLINIT PT	VIRUS (STRAIN	134.557	İ	:		!	; 	!	:	:
	RMA DIRECTED RNA POLYMERASE SUBUMIT PT	Z	\$10.519]]	i
	RMA DIRECTED RMA POL YMERASE SUBINIT PI	5	**								-
ZEL DEAD	MA DIRECTED ANA POLYMENASE SUBINIT PI	2	<u>ج</u>								
•	TWA DRIECTED TWA POLYMERASE SUBLINIT P.	INGLUENZA B VIRUS (STRAIN BISINGAFORE/2717/9)	25.52			i		:	:	!	
12	DAY DURECLED RIA POLYMETASE SUBUNIT P	INFLUENCA C VIRUS (STRAIN CANS)	406-435			١					
	WAS CRIECTED TWA POLYMERASE SUBURITY	IMPLUENZA A VIRUS (STRAIN A/ANN AMBORUSOS)	19.34	25.00							
NAC CAR	MAN DIRECTED AND FOLTMENASE SUBJECT FOR	INCLUENCE A VINCE (STRAIN AND COCKTOANDER AND STATE INCLUENCE A CHIEF AND A CH	Z			_ :					
MW (SH	MA DIRECTED RNA POL VACRASE SUBLINIT PI					•		İ		İ	
PRUS LAW	NAM-DIRECTED RIVA POL VACERASE SUBJUNIT PI	DELIENZA A VIBUS ISTRACK ASOWI 91 ACUE VIBUSANT VIBUSANT	716.916		İ	1				į	
PARPI TAGUS	ANA DIRECTED ANA POLYMERASE SUBUMIT PI	INTEUENZA A VINUS (STRAIN ACULLANARYLAND/104/17)	2	38		T		!	:		
PREP INCUA	ANA-DIRECTED ANA POLYNGRASE SUBUNIT PI	Z	119.234	36.56							
PRINT MICKS	-	INTLUENZA A VIRUS (SIRAIN AEQUINEMENTUCKY 7/26)	19:33	943.50							!
PRRT MEO	RMA DIRECTED RMA POLYNGRASE SUBUNIT PI		110-334	342.540	İ	İ	İ			!	-
PRATE WOR	RNA DIRECTED RNA POLYNERASE SUBLINIT PI	INTLUENZA A VIRUS (STRAIN ARQUINE/FRACTIT/1/16)	18.33	3						İ	-
PLACE AKE	RMA-DIRECTED RNA POLYNERASE SUBUNIT PJ		547-360								İ
THE PARCE	RMA-DIRECTED RMA POL YMERASE SUBLINIT P)	(STRAIN AROREA/SE/EI)	119.234	35.58							
_1.	MAY DIRECTED RAY POLYAGEASE SUBLIMIT P)	RAIN AR ENINGRADVIJ493)	119.334	3							
_L	BAN DIRECTED AND PAR TAKE BASE SUBLIMITED	INCLUENCA A VIRUS (STRAIN ALE MINGRATATOTATA)	10.00	3	Ì			Ī		İ	
. 12	ANA DIRECTED BAY NO WIGHAGE STRING FO	DATIFIED A VISUS (STRAIN ALENINGAND) SOUTH		3		•			Ī		
	RNA-DIRECTED RNA POLYNGRASE SUBLINIT PJ				-	Γ		Ī		i	-
	ANA DIRECTED ANA POLYMERASE SUBURIT PI	AUS STRA		9	Ī	1	Ī				!
1 1	ANA DIRECTED ANA POL YMERASE SIJBITALE PI	INFLIENZA A VIALIS (STRAIN APUERTO RICOVIA)	18.31		62.50	İ	Ì	Ī		İ	i
اه	ANA-DIRECTED RNA POLYNGRASE STRIPLITY	(SIRATH AMUDOY TURNSTONEMEW JERSEYATI		100 100	1	İ	Ī	Ī	-		-
CALL LASE	RMA DIRECTED ANA POLYMORASE SUBINITY	A VIRUS (STRAM ASEALAIASSAC)IUSE TTS/11/47)	33.5	3						İ	:
ı۱۹	DAY CHIECTED MAY FOLT FEE KASE SUBJECT TO	INTUENZA A VINUS (STRAIN ASINGAPORE/1/17)	20.55	35.56							İ
Т	RNA-DURECTED BNA POLYNGRASE SURINIT PI	A VIRGO (STRAIN		2	Ī		Ì				
	-	NY IS			İ		Ì		Ī		
П	RMA-DIRECTED RNA POLYNGRASE SUBLINIT P)	(STRAIN ASWINE TOWALISTO)	316.214	35.56	İ	Ī			Ī	Ī	
	RMA-DIRECTED RMA FOL YNGRASE SUBURIT PT	ASWINETENNESSEEDAMI)	118.314	30.50		Ī	Ī	Ī	Ī	Ī	
PARTY BRACE	<u> </u>	TRAIN BIANN ARBORING ICOLD ADAPTION	2	19.761			İ	Ī		!	
The second second		TAKIN BANN ABBONING [WILD: TYPE]	2	22.50	 						İ
PRESI DICIS	1	Carlotte Carlotte	2 12			1					
PREPI THOGY			T		İ	Ī	İ	Ì	Ì		
PREA CYES	RNA-DOLECTED RNA POLYNGRASE	HUMAN CORONAVRUS (STRAIN 27ºE)	8	410.436	13.00	1001	133.130	1541.1568	25.3160	2014.3003	111.111
PRRFA CYMID	RNA-DIRECTED RNA POLYMERASE	MIJITURE HEPATITIS VIRUS (STRAIN DEFECTIVE HIM)	Π	Т	i	-	÷	-			
MAY CANOIS	MANDIMECTED NAM POLYNGRASE			1100-1235	-	433 1649	Ť	-	1783-1806	1165.3192	117.2354
VARIABLE NEV	STABLE BANK BOAT AND USE OF THE	21 GEV, 24 GEV	2	7640.7676	-	1	405-1475	1011.1014		İ	
PRAPS CYLAS	ANA DIRECTED BNA POLYNGRASE		Ī	2	_	111.118				i	
	RWA-DIRECTED RWA POLYAGERASE	MURINE CORONA VIETO COLONA DIES			_	200	-	Ī	İ	į	
PRUPE CVPES	NNA-DIRECTED ANA POLYNGRASE	IS COMONAVIRUS (STRA)	ī		ž į	_	100		Ì	:	
_!	RWA-DIRECTED RWA POLYMERASE	1118111	Ī	,	İ	Ì		Ī		Ī	
FREE DVS	ANA-DIRECTED RNA POLYNERASE	AVIAN INFECTIOUS NAOMCHITIS VIRUS (STRAIN BEAUDETTE)	310	316.365	110:41	1115-1115	674.167e		Ì	Ī	Ī
200	MACHINET ED MAN MACHINES AND	BL. DE TOWARE VIRITS (SERIETETE 107 ISOLATE USA)	17-1	146-161							

PCGUME	וויכונזוי	All Vicesco (No Barteriophoges)									
FILEMANE	PROTEIN	VIRUS	45561	AHTS J	CV.HQ	2	ANICA	4 1 1 4 E	A10.17	A 1. 1 a	- V III
PRAM BUNYW	ANA POLYMERASE	BUNYAMWERA VIRIIS	20.5	2.5	440.44.9	10%-1116	=======================================	141.1%	1110.111	Man. ton.	200 July
PRINT EBOY	RNA DIRECTED RNA POLYNIFRASE	('BO). A VIRUS	= = = = = = = = = = = = = = = = = = =								!
PREPL HANNY	RNA POLYNGRASE	ILANGAAN VIRUS (SCRAIN 16 111)	151.168	10:00	10 46	361.1383	1081.2105		i		! :
PRUL IGSV	ANA POLYNGRASE BETA SIBINIT	INDIAN RESPIRATORY SYNCYTIAL VIRUS	===		! !					r. -	-
PRINT HOUSEA	RNA POLYNGRASE BETA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	=	100	_	19:19	1039.101	100.00			
PREPL MABYN	RNA DIRECTED ANA POLYNIFASE	MARBURG VIRUS (SIRAIN NUSOKE)	8.5	3	33.34	1		206.30	936-116	1007.1001	1410.1436
			111-121	1030-3013		_	_		İ	-	
PRPL MABVE	RMA-DIRECTED INABOLVAIERASE	MARRURG VIRUS (SIKAIN FUFF)	13-10	51.15	-	_	\$46.165	₹. =	1017.101		1677.16%
			1313-1331	100	1940-2017	_	3333.3346	!		•	:
	RMA POLYNGBASE BETA SIBIRUIT	MEASILES VIRIIS (STRATH ETMENNSTON)	111.78	13.63	1201.004	100	1376-1304	1930-1940	1038-7061		
Į	ANA POLYNGRASE BETA SUBIRGE	MAN SVINIS (STRAIN MIYAJIARA VACCIME)	27	200	-		100	3		131.313	
<u>.</u>	RNA POLYMERASE BETA SIBUNIT	MEWCASTLE DISEASE VIPUS (STRAIN BEALIDETTE CAS)	104.124	121.13	_	12		-	ĺ	!	i
!	KNA POLYNGRASE BETA SIRIMIT	INDIAN PARAINTI UENZA 2 VIRTIS (STRAIN TOSHIBA)	2 2	20.20	÷		1562-1588	1983 2010	2015.22		İ
PRIN MILL	ANA POLYMERASE BETA SUBUNIT	HUBAAN PARAINTLIFERTA S VIRUS (STRAIN MII 47895)	100	9	191.00	200	1911	2068 2084			
PRINT PURDO	RMA DIRECTED RNA POLYMERASE	PUDDALLA VIRUS (STRAIN IIA) LNAS his	201.12	7	1561.1165	16.73	2016.3110				İ
PARM ANDW	RNA POLYNERASE BETA SUBUNIT	RABIES VIXUS (STRADA PV)	344.384	13	121.12					İ	
PHUN MABYS	RWA POLYMERASE BETA SUBUNIT	RABIES VIEUS (STRAIN SAU DIO)	346.346					144 1 741			
PRINT ROV	RNA DIRECTED BNA POL YMFBASE	BACK DUABLE VIELS									
PREP EVEVE	BHA DIRECTED BHA POLVAGRACE	BOR VALUE VIBILIE AND MAINTAINS			_			-		1	
HEN CENTS	BHA POLYNOBALF BETA SIRIDUIT	CONDAI VIBILE (CIBAN 9 / 0.000 ACTIVATO)				+	13				
PART TO PE	BMA POLYNORACE BETA CITATOR	CENTRAL VIBILITY CONTRACTOR						-	-	101.70	
TO THE PERSON	BLA BOLVANDA CE BETA COBINET	SERVA VIKUS (STRAIN ENTITES)			101.10			=::			
1000	BUT THEFT BUT BY WATER TO	SENUAL VINOS (STRAIN Z.)		2	104-21	_	8	2	791	2	
	ANA DIAKE I KA ANA POL TRERASE	SCOUL VIAUS (STANIN DO: JV)			100	2		201.3105			
FREE SVOWA	MA POLITICIA SE BETA SUBURIT	SUICAN VINUS S (STRAIN 21000-WR)	*	200	263.789	1004-1718		1556-1580	3113.2137		
PRECE STRV	MAA POLYMEMASE BETA SUBUROT	SOMERUS YELLOW NET VIRUS	26-146	8	-	704-73(5		116-911	1484-1510	1176-1792	
T T T	ANA DURECTED RINA POLYNIERASE	TOMATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPMILIBA OI)	958-976	1383-1410	-	2609-7627					
PRRM. USA	RWA POLYNGBASE	LUCKUNGENG VIRUS	691.714	13 64	1404-1411	1870.181	2046-2043				
PREM. VSVA	ANA POLYMERASE BETA SIBINIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW IERSEY / STRAIN IIA	154-113	111	903.938	1656-1917			i 	į	į
TIME VIVO	KNA POLYNGJASE BETA SLBUNIT	VESICILLAL STOMATITIS VIRUS (SEAOTYPE NEW JERSEY / STRAIN OF	156-113	112.339	1936-1982	2080-2101					
FRAM. VSVS!	RNA POLYMERASE BETA SUBLINIT	VESICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)			_	_					
PRAPO ACLSV	ANA-DIRECTED RNA POLYMERASE	APPLE CILLOROTIC LEAF SPOT VIRUS	326.247	1036-1054	133.115	175.121					
PRING BWYYF	PUTA IIVE RNA DIRECTED RNA POL	BEET WESTEAN YELLOWS VIRUS (ISOLATE FL.I)	299.336		!					Ì	
FEETO BYTON	PUTATIVE RNA DIRECTED RNA POL	BARLEY YELLOW DWARF VIRUS (ISOLATE MAV.PSI)	150.886	17	\$05.533						
PREMO BYDY	PUTATIVE ANA DEPECTED ANA POL	BARLEY YELLOW DWARF VIRUS (ISOLATE PAV)	359-386	277	505-512						
PILLO BYDYR	PUTATIVE IMA DIRECTED IMA POL	BARLEY YELOW DWAST VIRUS (ISOLATE P.PAV)	139-116	101-416	505-512						
2	PROBABLE MA-DUCECTED HAN FOL		6.3 0	a	127.150						
VILLO COMPA	PUTATIVE INVA-DIMECTED WAS FOL	MARIE WATERMELON STRAIN	40)-466	376-591	1017.1032	1323-1539					
	PRUBABLE RIVA DIRECTED RIVA FUL	CUCUMBER PECKUSIS VIRUS	8	5	170.494						
2	PRUMABLE INTA-LUCEL LED INTA PUL	CYMBILIANIA MINGSPATI VIRUS	= -	<u>=</u>	470-444						
	PUTATIVE MAN-DUELTED MAN FOL	INFECTIOUS PANCILEATIC NECROSIS VIRUS (SEROTYPE JASPER)	21.23								
2	ANA POLIMENASE	L'INCHESCY IN CHUMICHE MINGIFIS VINUS (STRAIN AUXISTRONG)	35-55	197.613	650 682	988-1006	1334-1358	1370-1795	1011.2096		
200	NAME AND THE PASS.	LINCTICL THE CHINCHENINGHTS VINUS (STRAIN WE)	23:52								
WILL SELECT	BULL OFFICER BULL BY VICEASE		Ī	ء اع	3						
	Several and your grant was		-	3	95	28.22					
WALL OF SAVE	PITATIVE BIA DEFETTO BIA POL	TO TOTAL STATE OF THE STATE OF	2	8				İ	İ		
NAME OF THE	MITATION PARTIES NAMED IN	PERSON LAND TO LINE STATE AND THE STATE OF T		8	Ì						
WALL OF THE	PITATION BUY DOSETTED BUY ACT	DED CLOSE MEDICE VICTOR STAIN	20.00	200	1069.1086	100.100					
PER BEAU	BNA. MIRCHEN BNA POL VACEACE	PEDVIDIR STORE STEED AND MINUS	8	!				į			
н.	ANA DIRECTED BAY NO VAGE AND	ACCURAGE CAVES AND ACCURAGES	20								
	THE THEORY OF SHIPING OF		91:136			i					
•-	ANA DIRECTED RIVE FOR SCHOOL VE		2	20.70	3	Ī	l I	1077.1046			
	PAN DAR CHES BAN FOL BURGHT VE	BOVING RUINVINUS ISTRAIN UR)	3	2	=) (1027.1046			
	THAT DUE CITED BYA POR SUBIDITY VE	PORCING BOTACIBLE ACTION CONDICTOR		20.72		ī					
	ANA DARFOTED ANA POR SIGNALI VP.			27.75		ī	- 1		18.	1017.101A	
PRESO SEACY	PROBABLE RNA-DIRECTED RNA POL					T	-	91		-	!
PRING TACY	RWA POLYMERASE	TAT APINE VIPE	Ī		8		9		اءً	-	!
			٦	100		16 16. 1402	2014-7048		1	1	

POCENE	1011/11/21									•	
FILENANT	PEDITIES	VIETIGE CONTINUES (NO DOCUMENTS)		7	7	7	П	П		Г	
PALEO TREVC		TOWATO BUSSINY STIDIT VIBILS IS THAN CHEER VI	4	ℷ	J	1	ARIAN	155	ANIA	TVIEV	ARIAS
PRING TCV	PUTATIVE RNA-DURECTED RNA POL	TURNO CRIMA E VIRIS	3			1					
PREPO THEMY		TOBACCO MILD CREEN MOSAIC VIRUS (TALV STRAM LT)	206.311	3	Ī	1		-			
PRING THY	PUTATIVE ANA DIRECTED BNA POL	TOBACCO MOSAIC VIRUS (VIR GARE)	711			-					
PRILIO THYKE		TOBACCO MOSAIC VIBUS IS IRAIN KOREAN	700.134	1		T				Ī	
0	PUTATIVE RMA-DIRECTED RNA POL	TOBACCO MOSAIC VIBUS (STRAIN TONIATOR)	700.774	é	2	417.11					·
PARPO THYA	RNA-DIRECTED RNA POLYMERASE	TODACCO MECROSIS VIRUS (STRAIN A)	13:13						:		
PREMO TRVO	ANA-DIRECTED RNA FOL YMERASE	TODACCO NECROSIS VIRIES (STRAIN I)	12.5	:	:	:	· · · · · · · · · · · · · · · · · · ·			=	
PREST CAV	RNA POLYMERASE ALPIIA SUBUNIT	CHAMDIPURA VIRUS (STRAIN ISSISTA)	176.106	İ	!		Ī	-			1
PRET LEBEL	RNA POLYMERASE ALPHA SUBITME	MUMOS VIRUS (STRAIN SOL-1)	111.316			1			Ì	Ì	
PREP MADE	ANA POLYNERASE ALMIA SUBURIT	MUNOS VIRUS (STRAIN ENDERS)	213.330		Ī	1	Ī	Î		Ī	Ī
PRRP MACH	ANA POLYNERASE ALPIA SUBUNIT	MAMPS VIBIUS ISTRAIN MIYALIARA VACCINES	212.216				Ī			Ì	
PALLY NOVA	RNA POLYNERASE ALPHA SUBUNIT	MEWCASTLE DISEASE VIRUS ISTRAIN AUSTRALIA, VICTORIAAN	1		j	T			ĺ		-
MULTI HOW	RNA POLYMERASE ALMIA SUBLIMIT	MEWCASTLE DISEASE VIRING ACTION AND ALLEGAN		İ	1	-	:::	•	:		
Γ	ANA POLYMERASE ALPHA SUBLINIT	HERAN PARAINELIENZA 3 VIBIN				1					
Г	RAY POLYNERASE ALPHA SUBURIT	MAKAN PARAING LES NZA I VIRUS STRATIVITOS INTAL								Ì	İ
Г	RUM POLYNGAASE ALMIA SUBLIMIT	HEBLAN PARADOLISMS AT COMISSIONAL TOSHINA				.					
Т	RUA POLYMERASE ALPHA SUBLINIT	HEBLAN PARADYT LIENZA AB VIBILE (CTBAILLE)									
ī	RUA POLYMERASE ALPHA SUBLINIT	PREV VIEW									
•	RNA POLYMERASE AL PARA CIPELDAIT	DADIE VIBILE AND A LOSS				1					
_	DNA POLYMORAST ALPIGA STRUMOT	BABITE WELL TO BE AND THE TO	7		j						
PLUP LABOR	RAW POLYNERASE ALPRA SUBLINIT	BARIES VILLE (CTRAIN FRANCE AND COURTED BASIS			Ì						
7	ANA POLYNGRASE ALPHA SUBURAT	BARES VILLE (STRAIN P.V.		10.00	1	1		Ì			
_	ANA POLYMERASE ALPHA SUBINGT	BABIF VIETIC STRAIN CAN BIS.		110-111	İ						
Г	RINA POL YNCEASE ALPIN SUBLINET	SIMILAN VIETES SASTEAN WITH	7	110-21		·					
Γ	RAY POLYNERASE ALMIA SUBURIT	VESICION AND STOMATITIES UMBIT (GENOTUME NEW PERSTEX 1878 - 112 PM	27.2	01.10		•					
	S271R PROFESS	APINCAN SWING PRIVE VIBIRE ACTORNIC BASIN	-			4					
L	SUPEROXIDE DISPAUTASE LIKE PROTEIN	VACCINE VIBILITY OF THE CENTRAL CENTRAL	7.4		j	-					
г	SUPEROXIDE DISMOTASE LIKE PROTEIN	VACCIDED VIBILITY OF A DATE WELL			1	Ì					
	SUPEROXIDE DISMUTASE LIKE PROTEIN	VARIOLA VIBLIS				Ì					
	SPIEROUDIN	AMSACTA MOORE! ENTOMOPOXVIRUS	T	***	†	1		Ì	İ		
_	SPHERODON PRECURSOR	CHORLSTONEURA BIENNIS ENTOMOPOXVIBUS	ļ			7-	1		Ì		
			T		+				j		
			T			Ì					
		VINUS		İ			1				
MALA POVBA		POLYOMAVINUS BK (STRAIN AS)	Т	177.007							
TALA POVEK		POLYOMA VIRUS BK	Т	29.044	+	1	1	Ì	Ì	İ	
		BOVING POLYOMA VIRUS	Т	Ì		Ì	T	1	1	İ	
		AVIRUS	99-69	20.364			Ī	İ	Ì	İ	
	LANCE I AFFICE	POLYOMA VIRUS AC	667-102	438-443	Ì	Ī		Ī		İ	ĺ
	LANCE TANTOCK		П	\$16.543	-			Ī		T	
T	I ABOR T ANTICEN	MOUSE FOL TORIA VIRUS (STRAIN 3)	165-965							İ	Ī
	LANGE T ANTIGEN	MODES FOR VOLVENING (5 to AND CO. T. C. C. C. C. C. C. C. C. C. C. C. C. C.	374.500								Ī
PTALA POWER	LAKGE T ANTIGEN	MOUSE POLYONA VIRILE CERAIN FINANCE	Ī	┪							Ī
-	LARCE T ANTIGEN	SUGAN VIRUS 40 (5 V 40)		200	46.472	Ì					
TAME POWA	MIDDLE ! ANTIGEN		T		Ì	1					
	SHALL I AMIGEN				†						
TASH PONY	SHALL I ANTIGEN			İ	-	1		Ì			
	SMALL I ANTIGEN	Ī	T	-			1				-
TATE POVAC	TRANS.ACTIVATING TRANS REG PROTEIN	PROSIS VIRUS			\dagger	T	1	1	\dagger	1	1
-	TIANS ACTIVATING TRANS REG PROTEIN	Ī	97-117	İ	+	1		1	1		
-	HAMS ACTIVATION TRANS BEG PROTEIN	AOSIS VIAUS	300-414	T		T	T	\dagger		1	
T	TRANCACTIVATION TRANSPECTOR PROTECT	П	66.30		<u> </u>	T	T	T	$\frac{1}{1}$	\dagger	1
Ī	TRAME ACTIVATION TRAME BEO DESCRIPTION	BOVING PRODUCTION Y VIRUS (150LATE 121)	66.59						T	\dagger	Ī
T	TRANS.ACTIVATING TRANS BEG PROTEIN		162-310						T	T	
1			102.216		H	$\ $		H	H	H	Π

PCCENE	Pucture	All Viruse (No Batteriaphages)							П		
FULHAME	PROTEIN	VIRUS	AREAL	LAMA	ANTAL	OREA	AMEAS	LAMA	7 7787	3860	14.16
PTAT HVICE	TAT PROTEIN	HIDMAN INDADNODEFICIENCY VIRUS TYPE I (STRAIN UGANDAN/ISO	3			1			1	j	
710 114	-	I EL DAE L'EUKEANA VIBUS	111			-				1	
PIECP MINTE	_	EQUINE HEADES WIRUS TYPE I (STRAIN ABAP)	101-101						j		
THE MYEK		EQUINE HEAVESVIAUS TYPE I (STRAIN KENTUCKY A)							т		
TEOU EDV		EPSTEIN-BARK VIRUS (STRAIN B93-0)	3	767.788		1032-1075			т		20.0
TEQUINONA	PROBABLE LARGE TECHNENT PROTEIN	(INDICAM CYTOMEGAL DVINUS (STRAIN ADION)			100	1707-1011	223-1163	2	303		1
PTEGU MSVII	LARGE TECHNOST PROTEIN	HERPES SOCIETY VIIIUS (TYPE 1/ STRAIN 17)				****	****			Ī	Ī
TEGU HSVAO	LANCE TECHNOMY MOTETY	INCINES SUPELEX VIRUS (1772 67 STRAIN GS)	76	30.00	919-610	107	3761-1378	_		Ī	
THEOU HIS VES	LARGE TECUNEDIT PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN ARAP)	***	22.363	1073-1099	107.1133	91.1		-	÷	
PTECU HSVSA	PROBABLE LARGE TECHNENT PROTEIN	NEXPESVIRUS SALMIN (STRAIN 11)	163-491	716-737	119.1000	- F	35.174	<u> </u>	1501-1323	2 2 2 3	694.1915
			361.703			~				_	
MEGU VZVO	LARGE TECUMENT PROTEIN	VAUCELLA ZOSTER VIRUS (STRAIN DUMAS)	27			679-108	274-648	1017:107	┰	60.77	189
			1707-1007								
PTERM ADEON	DNA TERLADNAL PROTEIN	INDIAN ADEMOVIAUS TYPE 1	8 6	39.616		•					
PTERM ADEM	DNA TERMINAL PROTEIN	INDIAN ADENOVIRUS TYPE S	8	1							
PITERIA ADEBI	DWA TEMMENAL PROTEIN	INDIAN ADENOVIBUS TYPE ?	63-60	\$10.60)		-					
PRESSA ASSETS	DNA TELLABRAL PROTEIN	HUBLAN ADENOVIRUS TYPE 12	•	334-330	\$46.369	•					
PTOP1 ASSES	ı	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	19:14	606.707		•					
PIOP ASM	_	AFRICAN SWINE FEVER VIAUS (ISOLATE MALAW! LIL 10/1)	119-148	e#5:706							
PTRIN HOWA	KYPOTHETICAL PROTEIN TAL 14	HORLAN CYTOME GALOVIAUS (STRAIN ADIAS)	139-165								
PTREE AVOLE	-	AVIAN RETICUL DENDOTIGIOSIS VIAUS	26.74								
PTYSY VZVD	THYMEDYLATE SYMHASE	VARICELLA ZOSTER VIRUS (STAATH DUMAS)	11.39								
PUSE MEVEL	POSSIBILE GANCIEL DVIR KINASE	HELPES SOCIETY VINUS 17 YPE 47 STRAIN UCANDA - 1102)	400-413								
PUZI. HSV&U	PROTEIN 2.	HERPES SUPLEX VIRUS (TYPE 6 / STRATH UGANDA-1102)	6.3								
PLEDPE NOVAC	LIDE CLUCOS YL TRANSFERASE PRECURSOR	AUTOGRAPIA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	465.650			-			Ī		İ
AVA 01 10 14V	MANAGEMENT AT PROTEST IS 2	HENNAM CYTOMOGRAL OVINING STRAIN ADIAS.							!	::	:::::
AVAILABLE AVAILABLE	LAVEGREEN AL PROTECT IN 1	HODAAN CYTOMEGAL OVINING STRAIN AD1091	1			-		:		:	
PLE OF EBV	VINION PROTEIN BERS!	EPSTEM-BALA VIRUS (STRAIN 895-0)	153.266			-				Ī	
PULDE MONVA	INVIOUSE TICAL PROTEDI U. 6	HODAN CYTOMEGAL DVIRUS (STRAIN AD 166)	101.70			-				Ì	
MI OF MIVIE	VIBION PROTEIN IN A	SCREET SEACH BY VIRING ITYPE 17 STRAIN 175	604.429							Ī	Ī
HI OF HIVE	WARCH CENT AS PROTEON	FOUNDE MEMPERVIRUS TYPE I (STRAIN ABAP)	17.44			7			Ī	Ť	Ī
PLES HSVSA	VIRION GENE 41 PROTEDY	HEAPESVINUS SAIDARD (STRAIN II)	97.72			+				İ	
PUL 67 EBV	BEAUS PROTEIN	EPSTERY-BARK VIRUS (STRAIN BP)-8)	37.149							T	
PULLEY MOLVVA	INVESTIGAL PROTEIN U.	HOMAN CYTONGGAL OVIRUS (STRAIN AD169)	101.00	186-309							
PULAT HEVIL	PROTEDVIA.1	HEAPES SMOLEX VIAUS (1 YPE 1 / STRAIN 17)	177.200								
PULLET HEVED	CEME 55 PROTEIN	EQUING HEAVESVIRUS TYPE I (STRAIN ABAP)	11.33							Ī	
PULLET HEVEA	CEME 42 PROTEIN	HEAPES VIXUS SAINURE (STRAIN !!)	77								
HULD VZVO	GENE SI PROTEIN	VALICELLA-ZOSTER VIXUS (STRAIN DUMAS)	138-138	102-124							
PULSE HEVII	PROTESM ULI	HELVES SDAPLEX VINUS (TYPE I / STRAIN I?)	114-518	97.6-600							
PULM VZVD	GENE SI PROTEIN	VARICELLA-ZOSTER VIRUS (STEAM DOMAS)	226-255	39).416							
PLACE HEVIL	ORIGIN OF REPLICATION BINDING PROTEIN	HEADES SOULEX VINUS (TYPE 1/STRAIN 17)	564-554								
PLEAS HIS VES	ORICHA OF REFLICATION BENDONG PROTEDI	EQUING HEAPESVIRUS TYPE I (STRAIN ABAP)	131-144	113-431							
710	ORIGINAL REPLECATION INDIDING PROTEIN	VARICELLA-POSTER YIRUS (STRAIN DURAS)	66-03	8	414.500						
ME BONA	KYPOTHETICAL PROTEIN US.11	HEMAN CYTONE GALOVINUS (STIAIN AD169)	2								
A NOW	MTPOTHETICAL PROTEIN ULTS	HEBITAN CT CONDUCTOR (STILATE AD 189)	469-467							Ì	
MALIA MONYA	NYTOTAL INCAL PROTEIN UL 14	HUMAN C T LANGUAL DVIKUS (STILATIN ADTOR)	100						j		
TALK BOVE	HYPOTHETICAL ULIA PROTEIN	HELVES SUPPLEX VOIUS (TYPE 1/STRAIN 17)	74-116 74-116								
PLE 18 HSVEB	HYPOTHETICAL GENE 48 PROTEIN	EQUIDE HEAVESVIRUS TYPE I (STRAIN ABAP)	100-137								
PARIS HSVII	PROTEEN U. 14	HEAPES SOUPLEX VIRUS (TYPE 1/STRAIN 17)	11-49								
PARIS HIS VED	CENE 44 PROTEIN	EQUING HELVESVINUS TYPE I (STILARY ABAP)	26-4)	=	34.110						
PULIS HEVEA	CENE 11 PROTEIN	HERPESVINUS SADAIRI (STRAIN !!)	11:5	ž							
74.16 7270	CENE 4 PROTEIN	VANCELLA-20STER VIRUS (STRAIN DURIAS)	65.80	<u>:</u>							
ME 19	PROTEIN BOLD I	EPSTEIN BARR VIRUS (STRADY 899-8)	11:10								
PULIT HOLVA	INTOTAL PROTEIN UL. 17	HOUNAN CYTOMEGALOVIRUS (STRAIN AD169)	2								
TO THE	FRUEN WIT	MEMORE SECTION (177E) / SINGIN IT)									
MEN BONA	COME 33 PROTEIN	MEANISTY WILLS SAIDADD (STRAIN !!)		5.370	1				1	1	1
100 mm	MINUTE INC. TRUISIT OLIV	מחשמי בנוסיינטיוט וויטיוט וויטיוע אחומי		bracket	bracket				1	1	7

502	Puchar	All Visions (No Besteates)									
DILEBAME	PROTEM	Value of the control						L			
TOTAL PRIVATO	ULJO MEJANIKANI PROTEIN HOMOLOG	PSEUDORABLES VIRUS (STRAIN MA. 1)	1	3	3	4854	ABCAI	AREA	AREAS	485.5	AREAS
24.70	_	VANCELLA ZOSTER VIRUS (STRAIN DUNAS)	76.	\downarrow		-				Т	
¥	_	INDIAN CYTOMEGALOVINIS COTTAIN ABILES		\downarrow		-					
MAN HEALT		DELPES SECTION FX VIRING TIVE LA CHALANTA								-	
NEW PROPERTY.	PROTEIN ULS!	HEAPES STADIES VIBING CIVER LA CORRECTION	20.00	8							Ī
ALC: NO.	GENE 40 PROTEIN	EQUINE HEAPESYBUS TYPE I ATTACA A BASE		8							Ī
24.24	GENE 18 PROTE DI	VANCELLA-ZOSTERIVELIS (STRAIN INDIAS)		2	79.40)	412-427					1
Y THE	HYPOTHETICAL PROFEIN UL 23	HUMAN CYTOMEGAL OVIETIC STEAM A DIEGO	167 077	ŝ						Ī	
2	PROTECT EXOF.	EPSTEN BARR VISIN 1678 AND BOS D.	4								
A PO	HYPOTHETICAL PROTEIN ULZA	PRINCH CYTOME CAR OLIGING COT AND	2						İ		
M. 24 HSVII	PROTEIN UL24	MERDER CINCHES VIETE 1 200 ALC	706-722						İ	Ì	
Tune arm	PROTEIN ULZ4 HOMOLOG	INTERNATION CONTRACTOR CONTRACTOR	147.166							Ì	
PULIS HOMYA	INTOTIGETICAL PROTEIN UL 25	INDIAN COOKE AND MACHETIES VIRUS (STRAIN TIONNE VEEZ)	130-179						Ì	Ì	
PLE 25 28V11	WALON PROTEON IN 35	THE PARTY OF THE PARTY STRAIN AD I 69)	484.500						İ	Ì	
PUL 23 HEVED	VIBION PROTEIN IN ST	PUBLICES STURIES VIRUS (TYPE 1 / STRAIN 1)	101-91		i 			;	:		
NI SCHOOL	WEIGHT OF THE WAY	EQUAME IN AMIS VINUS I YPT. I CLIMAIN ALIGE		:		~			_		
	VICON CERE IN PROTEIN	HERPESVIRUS SAIMIN ISTRAIN III							_		
	MI KD VIJON PROTEIN	DOBECTIONS AN VACOUR ACTION CONTINUES OF THE SAME		744-36					İ	ĺ	
PULLY HOWA	HYPOTHETICAL PROTEIN UL 22	MELLIN POST OF THE PROPERTY OF STRAIN THORNE VERY	36.23	316.336		ŀ		Ī	Ì	Ì	
PULTO HOUVA	HYPOTHE TICAL PROFESSION IN 34	MANAGE CYTOME CAL OVINUS (STRAIN AD149)	307.324	486.307		ŀ		T	1		
PULTO HONVA	HYPOTHETICAL PROPERTY IN 12	HUMAN CYTOME GALOVIALIS (STRAIN AD169)	230.264								
	MINORAL PROJECT UZ 30	HUMAN CYTOMEGAL OVIRUS ISTRAIN ADIAN				1			-	İ	
	PROJECT BFLF?	EPSTEIN-DARR VIBILS (CTRAIN 1101 a)							İ	İ	
	HYPOTHETICAL PROTECN UL 11	MANAY CVTONES AND DESCRIPTION OF THE PERSON	273-246					i	-	-	
PLE JI HSVII	PROTECN ULJ!	SCHOOL CONTROL OF THE CALL OF THE AD 169)	410-437	503-602				Ī	1		
PULLI HIS VED	CENE 29 PROFEIN	COLORS SHOULE VIRUS (TYPE I / STRAIN 17)	93-116			1	T				
PLC: HEVEL	Care at the second	EQUITE NEWESTATUS TYPE I (STILAIN ABAP)	104.134	368.300							
ML3 VZVD	National Control	HEAVES VIRUS SADIGIU (STRAIN II)	145.161	4		•			-		
PRE 39 LAVIE	APPROVE TO THE PROPERTY OF THE	VALUCELLA-ZOSTEA VIRUS (STRAIN DURLAS)									
10000	PROPERTY PROCESS ENV OF YCOPROTEIN UL.)	MEANES SIMOLEX VIRUS (TYPE 1/STRAIN 13)				1					Ī
200	MANOR ENVELOPE OF YCOPROTEIN 300	EQUING ACAPESVIRING TYPE 1 /878 AND ABAR.		384-385		_				l	Ī
2020	PROBABLE MAJOR ENY GLYCOPROTEIN 26	VAUCELLA ZOSTER VIBIN (CTA AND IN ALLA)	80							\dagger	Ī
VAN COM	GATEOTED COUPLED REC HOMOLOG (IL))	MAKAN CYTOLEGA! BUT IN A TO	332-374				ľ				Ī
TO HOW	HYPOTHETICAL PROTEIN UL 34	ILBAAN CYTOLOGOS OVER 12 TANKS AD 189)	76-162			-	T	İ		+	Ī
Man Havin	VIDUON PROTEIN ULDA	HEAPES SUMPLEX VISING IT VPG 1 / 64% AND 13	36.23	207-321		-		<u> </u>	\mid		
7	VICTOR OENE 26 PROTEIN	EQUING NERPESVIRING TYPE I ATTENDATED ANALY	231-233				İ	İ	-	ł	
J	GENE 47 PROTEIN	HEADESVALIS SAMILI ISTA AND ILL	200.364					T		\dagger	Ī
┑	VIDION GENE 24 PROTEIN	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	203-226			Ī	İ		T	1	
	HYPOTHETICAL PROTEDVIEWS		244-366				\dagger	Ì	1	1	1
ž	HYPOTHER TICAL PROTEIN ULSS		П	316-339	100	T	İ	1		1	
	PROTEGNIOUS	FORTER BARE THE COLLOWING STRAND AD 1889)	143-168	367-410		Ť		1	1		
	PROTECTIVIES	LESTERATOR VIACO (STILLING BASES)	Г	135-133	201.130	984.1004				1	
	CENE 23 PROTEIN	ECHAPTER TO THE PRINCIPLE OF THE PRINCIP	255.05	۲	Т	т		Ť			
L	GENE 4) PROTEIN	LYCLUS PERCENTINGS 1 TPE I (STRAIN ABAP)	41440	91.310	Ī	T	T	23-67A	1201-000		
1	GENE 31 PROTEIN	HEAVES VINUS SALBORI (STRAIN 11)	Ť	Ŧ	Ť	T	MI-NIA				
		TOWELLA COSTER VIRUS (STRAIN DUNIAS)	•	04.124	140.161		ī	7	ī		
_	INPOTICAL PROTERTIES		26.95	ī	Ť	T	717-81	22.02	248-269	670-694 77	176.603
PULAD HOUVA	Profile IICAL PROTEIN IN AN		97.34	Ī	İ		j				Ī
Т	HYPOTHERITAL SPOTENCIA AL	PROMOCE CALOVINUS (STRADY AD169)	1	Ī		1				_	<u> </u>
T	MENCRANG PROTECTION AS		T	114.11		1					ĺ
PULAJ HSVED	GENE 17 MG LANG AND DECISION		T	T						\vdash	
۲	CANE IN LICENSES AND DESCRIPTION OF THE PROPERTY.		T	Т	7	14421					Ī
Т	PROTEIN IN AL		T		7					<u> </u>	Ī
Ī.	PROTECULA		T		2	277.296	174.400	-		 	Ī
Τ	10 12 10 10 10 10 10 10 10 10 10 10 10 10 10	15		Ì				<u> </u> 		<u> </u>	Ī
_	PROTEINING			İ	1			-	<u> </u> 	ļ	Ī
TIAM AVE	CORPOR BEOTHERS AS		Ī.	╗	7			-		<u> </u> 	Ī
-	VISION PROTEIN A		T	3	32.58	614-640 74	741.766			<u> </u>	Ī
L	OTED AT MA TO ANY BANK MINE			İ	j			_	_	<u> </u>	Ī
Т	97 KD AI PILA THANK DINI CINC PROTEIN	(STAAM PG.3)	197	1	1				_	\mid	1
	7		100.001	\dagger						-	Ī
				1	1	1			-	ŀ	Ī
											7

PCCENE	PHOTEM	All Virones (No Becteriophages)		П	П	П	П	П	П	П	
THE HAME	PROTECT	VINS	3	4	কু কুমুক	4 24 3		PER	3	PER	AREAL
PULS HISVE	AT IN ALPHA TRANS-DEDUCING PROTEIN	EQUINE REJUSTS VINUS 1 VPE 1 (31 NAIR ADAP)		408.633	+	†	T				
PIE ZO ERV	HAVOUR TICAL BIRES PROTECT	FOSTERN. BARE VIETS (STEAD BOS.D)	114.334		t	F	İ	Ī		Ť	Ì
PUL OF HOAVA	HYPOTHETICAL PROTEIN 12 49	HUMAN CYTOMEGALOVIRUS (STRAIN ADIO)	10.05	138.543	T	t	Ť			Ť.	Ī
PUL 49 HSVII	TEGUNGANT PROTEIN ULAP	HEAPES SIADLEX VIRUS (TYPE 1/STRAIN 17)	36.35		İ		İ			Ī	
PULAS HISVEA	HYPOTHETICAL GENE ON FRUTEIN	IERPES VIRUS SAIMINI (STRAIN II)	133-353		<u> </u> 						
PLESS HICKYA	PROTEIN ULSO	HUNGAN CYTOMEGALDVIRUS (STRAIN AD189)	61196								
PULIT HSVII	PROTEIN ULS!	IEADES SINOLEX VIÁUS (TYPE 1/STRAIN 17)	3								
	GENE & PROTCIN	EQUINE INSPESSVEIS TYPE 4 (STRAIN 1942)	16-0-130								
PARSI ISMBI	(BINE BIRGHEIN	HURBE HEFFEVERS IVE: I (STRAM ARCT)	<u>2</u>		<u>:</u>				į	-	į
MLJI VZVO	GENE 7 PROTEIN	VAUCELLA.ZOSTER VIRUS (STRAIN UIMIAS)	10.49		-		Ì				
PULSS EDV	PROBABLE DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIAUS (STRAIN B95-8)	5			İ				j	
74.53 HSVII	DNA REPLICATION PROTEIN ULS	PENES SIMPLEX VIRUS (TYPE I / STRAIN IT)	25.			1					
PLS BY	DNA REPLICATION PROTEIN U.S.	EQUINE HEADES VIRUS TYPE 4 (STRAIN 1942)		_	-				į		
2 EVE	DNA REPLICATION PROTEIN ULS	EQUINE (IERPESVIRIES TYPE I (STRAIN ABLE)	<u>:</u>		115-117						
PLS ISVSA		HERMESVIRUS SAIMINI (SURAIN II)	10. VE	500.00	-	1					
74.53 7270	PROBABLE DNA REPLICATION CENE & PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	100.000	65.670							
PLE SI HONA	PROTEIN ULS)	HEBICAN CYTOME GALOVIRUS (STRAM AD169)	173-188		-	1					
PLE 33 HS V6U	ULSS PROTEIN HOMOLOG	ieapes sdælek virus (type 6/strain uganda.1102)	2.2			-					
PLES HOWA	HYPOTHETICAL PROTEIN UL 60	HEREAN CYTOREGALOVIRUS (STRAIN AD169)	20.14			-					
PULES HOUVA	HYPOTHETICAL PROTEIN ULAS	IGAKAN CYTOMEGALOVIRUS (STRAIN AD169)	3	178-205							
ME HOW	HYPOTHETICAL PROTEIN ULAS	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	103	Ţ	╗	7		٦			-
PLE NO HOLVA	PROBABLE DNA REPLICATION PROTEIN LL 10	ITBAAN CYTOMEDALOVIRUS (STRADI AD169)	200	608-430	679.516	626-645	170.71				
ML71 HOWA	HYPOTHETICAL PROTEIN UL71	HOMAN CYTOMEGALOVIRUS (STRAIN AD169)	214-250		┪	1	İ				
PULTY EBV	HYPOTHETICAL BLADI PROTEIN	EPSTEIN-BARK VIRUS (STRAIN B95-8)	2		1	- 	j				
PLE 23 HSVSA	HYPOTHETICAL GENE SI PROTEIN	GENESYRUS SAMIRI (STRAIN !!)	21:33		-		أ				
MEN HOWA	HYPORETICAL PROTEIN ULTA	INDIAN CYTOMEGALOVINUS (STRAIN AD169)	=			- -	İ			Ī	
	VICTOR PROTECT OF THE TENTON	INDIAN CYTOMEGALOVINOS (STRAIN ADTO)	70	77	+	İ	1			Ì	
TAL IN HOUSE	MYPOTHE TRAL PROTEIN UL. / I	RANCA CYTCHECALOVIEUS (STRAIN ADIOV)	2	602.04	1	<u>-</u>	Ì			Ì	
10000	A POLINE I CAL PROTEIN OCA	TOWARD CONTROL OF THE AND ADDRESS OF THE AND ADDRESS OF THE ADDRES			1	Ť	Ì			İ	Ī
	ACT END TO INTERCEDIATION AND PROTECTION	CONTRACTOR CONTRACTOR AND TOWNS			t	7	Ť			İ	
Variable in the	HYPOTHETICAL PROTECT BUCKS	POTENCIAL VALIS (STRANDING)		110.619	l	1	Ť		1	Ì	Ī
HELL PROVIN	HYPOTHETICAL PROTEIN LG 83	MAKAN CYTOME GAL OVINIS (STRAD) AD149)	116.79	Т	19 117	117117	18.75	1		1	
HULST HEWELD	MYPOTHETICAL PROTEIN SR	HERPES SECTEX VIXUS (TYPE 6/STRAIN UGANDA-1102)	22.10	Т	Т	Ť		Ī	T	T	Ī
PULIT BYEA	HYPOTHETICAL GIDE 24 PROTEIN	IEDZES VINUS SAIDANI (STRÁNH II)	11111	T	\$10-505	T	Ī	Ī			T
PLE HOWA	INVOINERICAL PROTEIN U. 11	ILDALAM CYTOMEGALOVIRUS (STRAIN AD169)	132-101	151.579				Ī			
PER HISVED	INTOTHETICAL PROTEDIAK	HERPES SINGH EX VIXUS (TYPE 4 / STRAIN UCANDA-1102)	190-173								
PLE IN HOLVA	HYPOTHETICAL PROTEDY UL 90	HIMAN CYTOMEOAL OVEN'S (STIADA ADIAN)	3.5								
	HATOITE IRAL TRUILLY BA	HEAVES SOUTHER VERUS (1775 67 STRAIN UCANDA-1102)			1						
HA OF HEVEL	INVESTIGATION OF	HERBES SEARCE X VIRIES (1 VIDE A / CTD AND INTANNA . 1 (67)		911	+	Ì	1			1	
PULSH HOMYA	PROTED ULA	HERMAN CYTOMEGAL OVERUS (STRAIN AD169)	2		\dagger	\dagger	Ì	Ī		İ	Ī
PLEN EDV	HYPOTHETICAL PROTEIN BOLL!	EPSTEDI-BALL VIEUS (STRADH BPS-1)	201-223		+	T	T	Ī	Ì	Ì	
PULBS HONA	HYPOTHETICAL PROTEIN UL93	HEMAN CYTOMEDAL OVIRUS (STRAIN AD149)	206-526		+	T	T	Ī	Ī	ĺ	
PULES HIS VALU	HYPOTHETICAL PROTED/11R	HERPES SOMLEX VIDUS (TYPE 6 / STILAIN UGANDA-1102)	2	128-344	-	T		Ī		Ī	Ì
ME 65 HSVSA	HYPOTHETICAL GENE 14 PROTEIN	HERPESVIRUS SAIDAUN (STRAIN II)	113-309								
PLESS HOLVA	GANCICLOVIX KIRLASE	INDIAN CYTOMEGALOVIRUS (STRAIN AD169)	206-328	341.567						İ	
MEAN HOPA	HYPOTHETICAL PROTEIN ULIO	HUMAN CYTOMEGALOVIRUS (STRAIN AD164)	186-193								
MAN HOWA	PROTEIN ULID	HUMAN CYTOMEGALOVIRUS (STRAIN AD166)	2								
M.A. HOWA	VILLON PROTEIN UT. 104	HUNGAN CYTONE GALOVINUS (STRAIN AD169)	32.33	433-450							
A POST	HATCHIE II. AL PROTEIN UL 100	MANAGE CATOMEDIAL OVINCE (STRADY AD169)			+						
HILLI HOLVA	INPOTRETICAL PROFENIALIS	RUMAN CYTOMEGALOVING STRAIN AD IAN	7		1			Ì		1	
PULBY HOWA	HYPOTHETICAL PROTEIN UL 117	HRACAN CYTONEGALOVIRUS (STRAIN AD169)	176.101		<u> </u>	1	İ	1			
PULBS HOAVA	HYPOTHETICAL PROTECN ULTIB	HANAN CYTONEGALOVIRUS (STRAIN ADISM)	81.60	_	+	t	Ť	T	T	T	T
PULCI HONVA	HYPOTHETICAL PROTEIN UL 121	HUBLAN CYTOMEGALOWING (STRAIN AD 140)	1		t	t	T	T	T	T	T
					1	1	1	1		1	7

PCGENE	Pitcher	All Virust (Ne Betterlephene)									
THEMAIL	PROTEIN	VIRUS	APEAL	AREAL	AREAL	ANEAS	AREAS	AREAS	AREAL	AMEA	AREAS
A POR	HYPOTHETICAL PROTEIN ULIS	INTERAN CYTOREGALOVIRUS (STRAIN AD169)	4-23			-			Γ	7-	
LAND FOWL	URACEL-DWA GLYCOSYLASE	FOWLLOX VIRUS (STRAIN FP.1)	11:33							T	
PUNC HSVE	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP)	274-350			-			ľ	Ì	
PUPO VACCC	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN COPENHIAGEM)	101.10							į.	Ī
A A C	ULACEL DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN WR.)	(0)-(0)							Ī	
200	UNACEL-DINA GLYCOSYLASE	VAUCOLA VIRUS	23-163								ŀ
OAZA CHAR	DEACEL DRA CE YOUR WASE	VAUCELLA ZOSTER PIRUS (STRAIN DUMAS)	22.23	Ì						-	
	DENE OF PROTEIN	PULLING HEILDES VIRUS TYPE I (STRAIN ABAP)	49.63								
AND PORT	USI PROTEIN	EQUINE HERPESVINUS TYPE I (STRAIN KENTIJCKY A)	[7-]							:	:
TOTAL PROPERTY.	PROTEIN UST HOMOLOG	PSEUDORABLES VIRUS (STRAIM MIA-J)	20136	_ 		 			i i	-	İ
TUSS HOUVE	MOLE PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	£	Ī		-				†	
PUSOS HISVIII	PUTATIVE GLYCOPROTEIN USS	HERPES SINGLEX VIRUS (TYPE 1 / STRAIN 17)	5:8	Ī						Ì	Ī
PUSOS HIS V2	PUTATIVE CLYCOPROTEIN USS	HERPES SIMPLEX VIRUS (TYPE 2)	8.5		Ť					Ì	
PUSO HOAVA	HYPOTHETICAL PROTEIN HID FO	INDIAM CYTOMBOAT OVIBING (STRAIN ADJAN)	3		Ť						
MUSII HOWA	HYPOTHETICAL PROTECNIAND BY	Manual Control College And Applications				+					
MAIN MONA	HYPOTHETICAL PROTECTING IA	THE PLANT COLORED STREET STREET	٦	┪		·					
	HISTORY OF THE PROPERTY AND ADDRESS OF THE PARTY OF THE P	PLANTA CT 1 CPC CALUVACO (STRAIR ADIES)			35.222						
	HATFORE IR AL PROFESS HVL/)	HUMAN CYTCHEGAL OVINUS (STRAIN AD169)	11.33	331							
MONTH HONA	HYPOTHETICAL PROTEIN HYLF4	INDIAN CYTOMEGALOVIRUS (STRAIN ADIAS)	316-366			-				İ	
PUSIS HOUVA	INPOTHETICAL PROTEIN (INL)	INDIAM CYTOMEGAL DVIRUS (STRAIN ADIGS)	Ī	461.66	Ī					İ	Ī
PUSIG HOMVA	_	PUMAN CYTOMEGALOVIRUS (STRAIN AD162)	Π	240.367	:	<u>.</u>	1	:		i	:
PUSIT HOWA	_	HUMAN CYTOMEGALOVINUS (STRAIN ADISS)	Τ		Ì					Ì	
PLS19 HOLVA	1	PRINAM CYTOMEGALOVIRUS (STRAIN AD149)	Τ	131.303	314.315					Ì	
PUBBI HOWA	HYPOTHETICAL PROTEIN HWLF1	INDIAN CYTOAGGAL OVINIES (STRAIN ADIAN)	1	Т						1	
PUSES HOWA	EARLY MICE FAR PROTEIN INN. 51	HOMEN CATOLOGIC STRAIN AD ACT	Ī,			-					
PURIT HOLVA	ACCEPTATION OF THE PASSAGE OF	THE PART OF THE PA		Ì	Ì	-					
HRIT LINA	INVESTIGATION IN THE INCIDENT IN THE	CALLAN POSTOR CALLONING (STRAIN AD 187)	292-310		Ì						
MIKIN NO.	Checking Come and are consisted to	THE STATE OF CALCULATION (SERVICE SERVICE)				1					
A PARTY OF THE PAR	A MOTERN COURSE PARC HOMOLOU USAI	HUMANIC TIME CALLOVINOS (STRAIN AD169)		3							
100	INCOMPLETATION CONTROL REPORTED USE	INCHAMICY I CHECALOVINUS (STRAIN TOWNE)	٦	90-160							
1000	INTRODUCE IN THE SECOND STATES	HUMANIC TICING GALOVIAUS (STRAIN AD169)								İ	
A PROPERTY OF THE PERTY OF THE	INTRODUCAL PROJESS NOUS	HUMAN CYTOMEGAL DVINUS (SYNAIN AD149)	2	206.233							
	NITOINE INCL. TRUIEM MILES	HUMAN CTIONS (STRAIN ADIAS)	41-39								
	I TO PROTEIN	LELY STACTON ESS VIRUS	27-46								
A MANAGEMENT	LE TABLE IN	POTATO VIRUS S (STRAIN PERUNTAN)	20-49								
١	TALD PROJECT	MINIST (PVX)	7								Ī
ļ	/ KD FROILEM	POTATO VIDUS X (STRAIN XX)	7							l	Ī
-1	/ K.D. PROTEIN	POTATO VIRUS X (STRAIN XC) (STRAIN CP)	31-46							İ	Ī
	LIST THOUGHT	AFRICAN SWINE FEVER VIRUS (STRAIN LISS)	7.2								Ī
2014	IS AD TACKER	ALFALFA MUSAUL VIRUS (STRAIN 429 / ISOLATE LEIDEN)	19.70							-	
	IN THE PROPERTY	POTATO VIRUS M (STILADA PLUSSIAN)	79-96								
A INVE	IN NO PROJECT	TOBACCO RATTLE VIRUS (STRAIN PLB)	14.51								
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TOTAL AND	AUTOGRAPHA CALIFORNICA MUCLEAR POLYNEDROSIS VIRUS		146-463	1013.1037					t	
	I C TO PROTED	BARLEY STRIPE MOSAIC VIAUS (BSAV)	14-29	8					Ī	T	Ī
	IN THE PROTEIN	AREL SON MURDIE LEUKENZA VIRUS	П	138-154						T	
2010	TRUISIN BIY	VACCINGA VIDUS (STRAIN WR)		183-173					Ī		
	AMOUE	BROAD BEAN MOTTLE VOLUS		152.771						İ	
TAIL CAN	IAFOIEIN	BRONG MOSAUC VIRUS	343.363	l						T	Ī
	INTROIGIN	COWPEA CHLOROTIC MOTTLE YIRUS	344-363								Ī
A CHAPA	IA PROTEIN	CUCUMDEA MOSALC VIRUS (STRAIN PNY)	115.800					Ī		I	Ī
IVIA CAVO	IA PROTECT	CUCLABER MOSAIC YIRUS (STRAIN O)	113.000				Ī		Ť	T	
A CANO	IAPROTEIN	CUCLIMIER MOSALC VIRUS (STICKIN Q)	114.75		İ		Ī		1	T	
NEW YEAR	IA PROTEIN	PEANUT STUMT VIDUS (STRAIM I)	672-493	783-608	İ				İ	T	
PVILE HSVIN	23 STO PROTEIN	TURKEY HERPESVIRUS (STRAIN HZ)	136-191		İ	Ī		Ī	Ì	\dagger	Ī
WIR MAN	20 KD MOTEIN	POTATO LEASTICLL VIRUS (STRAIN 1) (Γ	107.00	İ		Ī		İ	\dagger	
	IN IND PROTEDS	POTATO LEASTACLL VIRUS (STRAIN WAGENBACIEN)	7.3	193.203	T			Ī	T	T	
TATE BANK	IN KID PROTEIN	BEET WESTERN YELLOWS VINUS (ISOLATE FL.1)	13-43	134-157				Ī		T	
200	Selection of the select	PILA EALLY BROWNING VIRUS							T	l	Ī
**************************************	IA FRUIEIN	BROME MOSAIC VIRUS	1115-300	141.054				Ī			
]

		2		-	-	-				Γ
PCCENE Pri E HAND	F13C 112.17		AREAL	AREA! AREA?	1.2 AREAM	A AREAS	ABEAS	AREA?	AREAL	AHEAS
V.X 60-7	3	EA CHO.OROTIC MOTILE VIRUS	100-762			į				
PVIA TAV	24 PROTEIN	OMATO ASPERMY VINIS	314.311							
PV JOK TRYTC	29 I KU PROTEIN	INBACCO RATTI E VINIS (SIRAIN TCM)	11:11	:	:					
PVIIK TOBSV	11 PKD PROTEIN	OBACCO STREAK VIRUS (STRAIN WC)	226-250							
PVIG ASIBI	K'362 PROTEIN	GRICAN SWINE FEVER VIRUS (STRAIN BATIV)	<u></u>		<u> </u> 					
PV175 ASPLJ	LIS 375 PROTEIN	AFRICAN SWINE 1EVER VIRUS (STRAIN LISTY)	2		<u> </u>		1	 		•
PVJ81 ASPLS	LIS 101 PROTEIN	URICAN SWINE FEVER VIRUS (STRAIN LISSY)		1	<u> </u>	<u> </u>	:			
- 1	ORDING MOTTLE VIAUS			1	<u> </u> 	1	<u> </u>			
	JA PROTEIN	UCUMBER MOSAIC VIAUS (STRAIN PHY)		1	1		 			Ī
PVJA CAPAR		UCLAGER MOSAIC VIRUS (STRAIM M)			<u> </u> 	<u> </u>	 		Ì	
77A CA70		CICUMBER MOSAIC VIRUS (STRAIN U)	6	1	1	1				Ī
PVIA CAMO		UCUMBER MOSAIC VIRUS (STRAIN Q)	£	1	<u> </u> 	1				Ī
PVIA CHIN	MOSAJC VIRUS (STRATH Y)		314.335					1		
PV3A IBVB		I VIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE)	ž.		<u> </u> 	-				
PVJA IBVM		AVIAN DIFECTIOUS BRONCHITIS VIRUS (STRAIN MAS)	27.5							
PVIA IBVP3		VIAN DEECTIOUS BRONCIUTIS VIRUS (STRAIN PORTUGAL) 112/12]								
PVIA BINUS		A VIAN DIFECTIOUS BRONCHITIS VIRUS (STRAIN UTURING)	15.21							
PV5A TAV	1A MOTEIN	TOMATO ASPENAY VIRUS	147.166			-				
PVSEK BEACY	18 KD PROTEIN	BARLEY STRIPE MOSAIC VIRUS	30.00		<u> </u> 	<u> </u>				
	PROTEIN 68	CANINE ENTERIC CORONAVIRUS (STRAIN K178)	917.6		_	<u> </u>	<u> </u> -			
	69 KD PROTEDY	TURMIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)	5.5	<u> </u>			<u> </u> -	_		
	NO KED PROTEIN	ALFALFA MOSAIC VIBUS (STRATM 425 / ISOLATE LEIDEN)	\$5.5		<u> </u> 	<u> </u> -				
PVADI VACCE	PROTEIN A4	VACCINIA VIRUS (STRAIN COPEMIAGEN)	217.344		<u> </u>	<u> </u>				
PVADA VACCV	PROTEINA	VACCINIA VIRUS (STRAIN WR)	317.344		 -	 	<u> </u>			
PVAM VARV	PROTEDIAL	VANOLAVIRUS	307.334		<u> </u> 	<u> </u> -	<u> </u> -			
PVAM VACCC	PROTEDN A9	VACCINIA VIRUS (STRAIN COPENHAGEN)	3							
PVAM VARV	PROTEIN AP	VARIOLA VIRUS	3				 -			1
Ł	PROTEINAIL	VACCINIA VIRUS (STRAIN COPENHAGEN)	Π	100 110	<u> </u>	_	 -			
1	PROTECUALI	VALIGIA VIRUS	1	11.00	=	<u> </u>				
PVAIS VACCE	PROTEINAIG	VACCINIA VIAUS (STRAIN COPENITAGEN)	39.65			 -				
	PROTEIN A 14	VARIOLA VRUS	19-61			7	L			
PVAIS VACCC	PROTEINAIS	VACCINIA VIRUS (STRAIM COPEMIAGEM)	341-363							
PVAIS VARV	PROTEDIALS	VARIOLA VIRUS	340.361							
PVAIL VACCE	M KD ABORTIVE LATE PROTEIN	VACCIMA WILLS (STRAIN COPEMIAGEM)	429.443		1	<u> </u>		$\frac{1}{4}$		
TVA IS VACEV	MACO ABOUTING LATE PROTEIN	VACLINIA VICES (STRAIN WR)		<u> </u>	1	<u> </u> 	1	1		Ī
20010	STATE OF THE PARTY	ANCIDER ABILITY CONTRACTOR	T	1	<u> </u>		 -			Ì
PVAN VARV	PROTEDIAZO	VALIDIA VIRUS	Τ	907:161		<u> </u>	+	-		Ī
PVALL VARV	PROTECNAL	VANOLA VIRUS	31.63			-	L	-		
PVASI VACCV	PROFEIN ALI	VACCIMIA VIRUS (STRAIN WR), AND (STRAIN COPEMIAGEN)	2:3		<u> </u> 	<u> </u> -				
PVALI VARV	PROTEIN A19	VARIOLA VIRUS	57.78							[
PVAJE VAČEV	PROTEIN AJS	VACCIMIA VIAÚS (STRAIN WR), AND (STRAIN COPEMIAGEN)	265-228							
PVAJI VARV	PROTEIN AJI	VARIOLA VIRUS	175-190							
PVAS VACCC	PROTEIN ALL PRECURSOR	VACCINIA VINUS (SITIAIN COPEMIAGEN)								
VAUS VACEV	PROTEIN AJS PRECURSOR	VACCIMIA VIRUS (STRAIM WA)	1	3	1	1				
TVAU VACE	PROJEM AJ	VACCURA VIEUS (STICAIN CUTEMIACEN)	8							
7 V	PROJECT CO.	ACCIMINA VINCIO (3) RAIN WAY	2	1	1					
TVAN VACCE	FIGURE AND THE PARTY AND THE P	VACCINIA VINUS (STRAIN CUPEROIACEN)	R	1	1	1	1			1
PVA VALLE	PROTEIN AND PARE UNDOR	VALLINIA VIRUS (SURAID COT MINUCA)			+	1				
PVACE VACEV	PROTEIN AND PRECUENCE	VALLING THUS (STRAIN WA)		1	+	+	+	+		Ī
A 44	TRUEIN AN PRECURSOR	VACCOUNT WHITE GOVERNMENT PROPERTY OF THE			1					
	TOTAL AND	VACCIONA VINITA (CTA IN WE)	1		+	1	$\frac{1}{1}$	+	1	
VAC VALV	PEOTEDIA A 13	VALICIA VIRUS	T	301.336	+	1	-			
PVAJS VACCE	PROTEIN ASS	VACCIMIA VIRUS (STRAIN COPEMIAGEN)	Ļ	14.404	<u> </u>	<u> </u>	<u> </u>		Ì	
PVASS VACEV	PROTEIN ASS	VACCINIA VIRUS (STRAIN WR)		184.404	-	+	-			
VAL: BCIV	AL! PROTEIN	BEET CURLY TOP VIRUS	П				-			

1000	111111111111111111111111111111111111111	All Varters (No Batteriophages)					Г	l			ſ
300	A CONTROL		141	PREAL	AREAL	VICE	ABEA ?	ABLAS	ABIA	AREAT	ANTA 9
1 V	ALL PROTEIN	CASSAVA LAIENT VIIIIS (STRAIN WEST RENYAN 844)	2.74		;	1		_		_	
	ALI PROJEIN	CASSAVA LATENT VINITS (NIRATE NICE RIAN)	2.5		:	<u>-</u>					
	ALJ PROTUIN	DEET CONLY TOP VINUS	8	:	:	<u>:</u>				•	
אארו	AL) PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST RENYAN 144)	100		İ	İ		Ť	Ī	7	Ī
TAY DA	AL) PROTED	CASSAVA LAIEMT VIRUS (STRAIN NIGERIAM)	18:21		İ	İ	Ì	Ì		Ī	
	ALJ PROTEIN	TOMATO YELLOW LEAS CURL VIRUS (STRAIN MARMANDE)	2	İ	-		Ī	T	Ì		
WE THE	AL) PROTEIN	TOMATO YELLOW I GAP CURL VIRUS	11.00	İ	1	Ť	İ	Ī		İ	
PVAT CAMVC	APHID TRANSMISSICIN PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CM-1841)	1	İ	<u>:</u>	Ī	1	! i	:	- : :	
PVAT CAMVD	APHID TRANSMISSION PROTEIN	CALL ISLOWER MOSAIC VIPUS (STRAIN DA)		İ	Ì	ŀ	Ì	Ì	Ì	1	
PVATCUM	APKED TRANSMESSION PROTEIN	CALL DUNER MOSANC VIRING ISTRACH BRICK		İ	+	1	Ì		Ì		
PVAT CALVNI	APHID TRANSMISSION PROTEIN	CAULIFIC OVER MOSAIC VIBILS (STRAPS NVB 131)		Ì	1	+					
DVAT CARP	APHID THANSLERGEN PROTEIN	A10 ECI CARCO DAGGA CO LABORA CONTRACTOR CON				4					
PVAT PALEVE	A TAKING THE LANGING THE COLUMN	AUTHORITION OF MINISTER PRINTING	134-037								
	ATTEND FRANCISCO FAULEIN	CAUCALOWER MOSAIC VIRUS (STRAIN STRASBOURG)	134-153							Ī	
TAT CANN	APHED TRANSMESSION PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN W260)	14.46		t	†		Ť			
PVAT CERV	APILID TRANSPASSION PROTEIN	CARNATION ETCHED BING VIPIN			Ì	1					
PVAT PAND	APPED TRANSLOSSION PROTEIN	TOWNS TANK IN COME SEE SEE SEE SEE SEE SEE SEE SEE SEE S									
PVBOS VAPAP		Const month, vaca (strong DAs)	132-139			-					Ī
	7. FOIEW 86	VALLEMA VEIUS (STRAIN COPENIAGEN)	22:55:		r			İ			
AND AVEC	FROTEIN BY	VACCINIA VIRUS (STRAIN WR)	20135	-	İ			Ì			
PVB64 VACCC	PROTEIN BA	VACCINGA VIDUS (STRAIN COPENDIAGEN)			1	†	1	1			
PUBOR VACCV	PROTECU BA	AACCINA WRITE AND WAL				1					
PVROV VARV	PROTEIN	WALLES A MAIN	40.3	_				-			
I.	A PARTY NAME AND DESCRIPTIONS OF THE PARTY NAME AND	AMALA VIRUS	49.55							Ť	Ì
7	PLAQUE-MEN HOST MANGE PROTEIN PRECURSOR	VACCINITA VIRUS (STRAIN LC 14440)	131.331				İ	Ť	Ì	1	
_	PLAQUE SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINGA VIRUS (STRAIN COPENIAGEN)	36.331				1	†		Ì	ĺ
	PLAQUE-SIZE / HOST ILANGE PROTEDN PRECURSOR	VACCINEA VIBILIS (STRAIN) ISTERS				1					
PVBOS VACEV	PLACOUR SIZE / HOST BANGE PROTEIN PRECITATOR	VACCINA UPSIG (679 A.P.) US.			-	-					
Т	PECTED IN	ACCING VINO (3) RAIN WILL)	231-271			i				İ	
200		ALCEMIA VILLES (STRAIN WR), AND (STRAIN COPENHAGEN)	59-63			İ	İ			İ	Ī
	PROTEIN	VACCEMA VILLE (STRAD) COPERINGEN)	100			+		Ì	1	Ì	Ī
A A A CC	PROTEIN BIS	ACCINIA VIDIUS (STRAIN WA)	131-143			+	1	1	Ì		
VARY	PROTEIN BIS	VARIOLA VIRUS	131.161	1		ŀ	t	1		1	
PVBIT VACCE	PROTEIN BIT	VACCIDIA VIDUS (STILAIN COPENILAGEN)		l	T	1	1				
WIII VACEV	PROTEDUBLY	VACCINIA VIRUS (STRAIN WR)			+	+	1				
אמן כיא	BLI PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENVAN BAN)		1	1	-			İ	1	
WILL CLAN	DL! PROTEIN	CASSAVA LATENT VIBILS (STRAIN MICERIAL)		1		·		1			
PVBL1 SLCV	BLI PROTEDI	OUASH LEAF CIRE VARIN									
PVBE ABLOW	PRI PROTECT	ABITTE ON MORAL VINE LIES AND WELL LAND									
PVBA! BOAV		MEAN OF THE MANAGE WAS INCIDENTED TO THE ANGLE OF OF THE ANGLE OF THE A							İ	<u> </u>	
PVBR PYNVV		Comment with the second	2					ľ			Ī
72 18 18		TOTALO TELLUM MUSAIC VIRUS (ISOLATE VENEZUELA)	101-101		<u> </u>			l	Ì		Ī
PVOBI VACTOR		MUNICIPAL CUM, VICES	193-218						Ì	t	
740 1000		ACCUMA VIEW (STEAM COPEMPACEN)	76.90 06.90		-	-		l	İ	ļ	Ī
		ACCIDIA VIDUS (STRAIN WR)	13.01	-				Ì	İ		Ī
		VAUGLA VIRUS	100	-		İ	ļ	t	1	j	
7		SHOPE FIRMALA VIRUS (STRAIN RASZA)	-			1	1			1	
┪	COUPLED RECEPTOR HOMOLOGICS	SHOPE FUNDALA VIDUS (STRAIN RASZA)	2	101 95	ļ	1	+	+	1	1	
LACH AVOID		VACCIDITA VIBLUS (STILADIN COPENILAGEN)	Ī		+	1	1	1		1	
ACK ACK		VACCORIA VIBUS (STRATH WR)	10.10		+	\dagger	+	1		1	
PVCB SVKA		SHOPE FIBROMA VIRUS (STRAIN KASZA)	Ş		$\frac{1}{1}$	1	1	1		İ	
VVCB SVRA	CAL PROTEIN CI	SHOPE FIBROALA VIRUS (STRAIN RASZA)	9.5		+	†		1	İ	Ì	
TVCD VACCC			1	1							
PYCOS VACCV					1	1					
PVC10 SPVKA	AL PROTEIN CIO	DI KASZAI			+			1			
PVCI9 VACCC				$\frac{1}{1}$	1	1					
PVCIO VACCY					1						
PVCIO VARV					1	1					
ī		(STRAIN COPENIAGEM)			1	1	1				
					1						
8			200			1					
PVCAP EBV	NOTER								H		
			1	7	1077-1093	1					
											1

PCCENT	PRICTUZIP	All Virgos (No National Ages)									
TREBATE		YIMUS	4	VAILA	-	SAIA.	S CANO	AREA	SHEAL	A ATTAC	AHI.A 9
LACAL IICAVA		HUMAN CYTOMEGALOVINUS (STRAIN ADIO)		1		: :		1	!	1	
I ACA		HEAVES SIMPLEX VIRUS (1 YPE I / STRAIN 17)	263-302	-	1137.1153						
PVCAP HSVEB	MAJOR CAPSID PROTEIN	EQUINE HERPCSVIRUS TYPE I (STRAIN ANAT)	31.30	П		-				j	
PVCAP HSVSA	MAJOR CAPSID PROTEIN	ICENTES VIRUS SAIMINI (STRAIN 11)	104-168	369.287	Z	063.1019					
PVCAP PRVIS	MAJOR CAPSID PROTEIN	PSEUDORABIFS VIRTIS (STRAIN INDIANA S)	115.362								.
2022	MAJOR CAPED PROTEIN	VARICEL LA-2015TER VIRUS (STRATH DUNIAS)	381.401	010-100	1156.1176						
PVCU) MVAC	DAY-BROOKS FOLEN	AUTOCRAPHA CALIFDRINEA MUCLEAR POL VIIFDROSIS VIRUS	3								
1	PROJECT I	VACCINIA VILUS (STRAIN COPEMIAGEN)	2								
VODE VACCV	PLOTEIN 03	VACCINIA VIRUS (STRAIN WR)	17.30							İ	!
WEST VARV	PROTEIN D3	VARIOLA VIRUS	17.38		!					i	
PVD05 FOWPE	91 6 KD PROTEIN	FOWLPOX VIRIS (STRAIN #P.1)	344.365	113.31		I					Ī
PVD05 SFVKA	PROTECN DS	SHOPE FIBROALA VIRUS (STRAIN KASZA)	34.78	31:15			Ī				
PVD05 VACCC	PROTEIN DS	VACCINIA VINUS (STRAIN COPENIAGEN)	130.340	T	110311					Ī	
PVD05 VACCV	PROTEIN DS	VACCOUS VIBUS (STRAIN IVE)		Т							
PVD05 VARV	PROTEIN DS	VARIOUS AVELIC				1				Ì	
PVDBP CAMVC	DNA-BOODNO PROTEDA	CAIR IS! OWER MOCAIC VIBILS ACTOR IN 19411		Ť		-					
PVDBP CALVO		CALL ISLOUGE APPARE VISING STRAIN DAIL				.					-
PUTAL CALVE	DAL BINDING PROTECT	CALD IN CALCULATION OF THE PROPERTY OF THE PRO									
Puller Californ	Plus Englished September	CALL LOWER MOSAR, VINCS (3) RAIN DILL)				- }					
2 10 10 10 10 10 10 10 10 10 10 10 10 10	CHANGE AND THE COMMENT	LAULIFLUWER MOSAIC VIRUS (STRAIN MYBIS)	31.38		j						
2000	_	CAULIF COWER MOSAIC VIRUS (STRAIN STRASBOURG)	3.5	٦		••					
אבסו אשררר	-	VACCIMIA VIJIUS (STIKAIN COPEMIAGEN)	70.07		\$40.538						
PVEGI VACCV	PROTEIN E.	VACCIMIA VIRUS (STRAIN WR)	70.67	335-380	540-558						
VVEG VARV	PLOTEEN EZ	VALIDLA VIRUS	70.01		100.558	Ī					
VVEDS VACCE	PROTEINES	VACCINIA VIBUS (STRAIN COPENHAGEN)	314.379			-					
PVE03 VACCO	PROTEDIES	EM 1)	114-319			F	Ī				
PVEOS VACCV	PROTECT ES	VACCINIA VIRUS (STRAIN WR)	114.939			-		Ì			
7	PROTEIN ES		124.339		İ	-		Γ			
PVEOR VACCC	PROTEINE	EMIAGEN	10.45							Ī	
	PROTEIN EG	S (STRAIN WR)	430-451								Ī
_	FROIEN		251.265	15-011		-					
т	74 CM CM	EMILIGEM)	254.270								ĺ
200	TRUILURE EN EN	S (STRAIN WR)	354.370								
7	PACIFICATION EN		254.276							Ì	Ī
	FACEAGLE BY PROTEIN 2		163.183							İ	Ī
7	SALV IN SALV FROIEIN	ADIOMACNA CALIFORNIA MUCLEAR POLYIEDROSIS VIRUS	3								
T			265-282	\$17.533							
	EI PROTEDA	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		<u> </u>	1	j					
i	MOTOR IS	┱					Ì			1	
L	EI PROTEIN		Т		+					j	
L	Et PROTEIN					1	Ī			1	
	EI PROTEIN		2	Ŧ		Ì	Ī			İ	
	EI PROTEIN		218.266		T	Ì	Ī	Ī		İ	
	EI PROTEIN	HUMAN PAPELOMAVIRUS TYPE 19	20.5		Ť	Ì	Ì	T	Ì	Ť	
	EI PROTEIN		163.100	İ	†	T	Ī	Ì	Ť	+	
	ei photein		20.30			T	Ì		Ť	İ	
200	EI PROTEIN		92.05		T	Ť	Ì	Ì	Ť	Ì	
	EI PROTEIN		318-315	76:11		T	Ī	Ì	Ì	İ	Ī
	EL PROTEDA	VIRUS TYPE 1	31.314	110.176		Ī	Ī			İ	
	STATE OF THE PROPERTY OF THE P	Ī	286.300							<u>-</u>	!
T	ES PROTEIN	TOTAL PARTY CALL (SHOPE) PAPILL CALAVIRUS (STRAIN KANKAK)	2							İ	-
L	E) PAOTEDO	7	2	-							
Γ	EFROTEIN		RISE	1							
	EJ PROTEIN		1	†	İ	1	j	İ	Ì	-	
	E2 PROTEIN				Ì	T		Ì	1	İ	Ī
PVEJ IBVII	EJ PROFILM		200.113			T	1	1	Ì		
						1	1	1	1	1	7

1000	PAIN HAIP	All Viruses (No Bacteriaphages)			_			Г		Γ
1000		VIEW	AREAL AREAL	AL ASSEAL	LAREAL	AREA 2	7	ABCA? A	ARLAI	AREA
TO STATE	E PROTEIN	MUNICIPAL CHANGES 17 PE 33	23.73		1				Т	
PVE 3 (BV16	Es partient	HIGHEN SAME CALLES 177E 15	289-107							Ī
1000	C. PROTEIN	PICHARA FACIL LONA VIRUS 1 VPE 10	37.710		-					İ
PVET LOVE	E SECTION	TARREST DESSE PARTERIES SOFT TO THE ST		_ - 						
PVEJ HOVED	F2 PE016 N.	HE PARK PARK CALLANDERS CONT.			<u> </u>				<u>-</u>	
DVEL PAPVO	PECHAEIRESPECTEN	OKEN PART ON THE PART OF THE P							<u></u>	
PVEJ MOVI	E3 PEO 15 PE	TOTAL CHICAGO AND	=	-	_	:		!	_	
PVES BIRDY			2					-	•	
7.00			1							
	TRUBABLE ENTRUIEM		7.14		-			•		
	PROBABLE E+ PROFESS	HEDRAM PAPILLONIA VIRUS TYPE 41	2.3	<u> </u> -	<u> </u>					
	PROBABLE EAPROTEIN	HEMAND PAPEL COLIA VIRUS TYPE SI	3.5					İ		Ī
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PROBABLE EN PROTEIN	IN ESUS PAPEL CONTAVINUS 117PE 1	1	<u> </u>			Ì	İ	İ	
PVESA HPVII	PROBABLE ESA PROTEIN	SUBJAN PAPEL DALA VIBLIS TYPE II	176	<u>i</u> :	1	1				•
PYESA LIPVIC	PECMANGE STATES TO STATES THE STA	MANA PAPELLINIA VIBIN INT.		_	•					
1469 6344	ES PROTEIN	MOVING PARTY CIRCLE VIEWS TANK IN THE CO.								_
PVESTIGIVES	Photograph & Change Ba	I THE PARTY OF THE		i	-					_
100	PROBABLE RESPECTATION		2							
1000		HOWAN PARLOMAVIRUS 17FE JI	25.11						<u>-</u> -	-
	FRUIT ES FRUIEIN	HUMAN PAPALONAVIRUS TYPE 43	\$9.50	<u> </u>					<u> </u>	
	FROMALEESFROTEN	HEMAN PAPEL COMAVINIS INFE SI	===	<u> </u>	<u> </u>			:		•
WE INVEN	PROBABLE ES PROTEIN	9		· ·	•	_				_
PVES RUDVI	PROBABLE ES PROTEIN	MIESUS PAPELONIAVINUS IVPL I	10110	:	<u> </u>	::::	:		:	:
PVEG BOVE	EAPROTEIN	BOYDAE PAPIL CALAVIRUS TYPE I		1			İ	j		
MES CELVE	EA PROTEIN	COTTON ALL BABBIT (SUIDPE) PAPIE I DALA VIBILE (STRAIN PANCAC)			1		Ì	-	-	
PVES INVE	Es PROFERI	SORAN PAPEL CALAVIETE TVEE					j			
PVEJ IPVIA	EA PROTECT	MALAN BANK CALL CONTRACTOR								
PVEA 18VII	64 PECTEN	MARKET AND							<u> </u>	
1200	7	HUMAN FAPILLUMIA VIRLYS 1971; 33	2				<u> </u>	<u>:</u> :		i :
	TA THOUSEN	INMAN PARLICHAVIRUS TYPE 35	9.36	_	<u> </u>				<u>:</u> :	: : !
775	STEEN STEEN	HUNCAM PAPIL LONG VIRUS 1 YPE SI	9.26	<u> </u>	-					-
1000	C. DECAMENT	PRINCAM PAPEL COMA VIBLOS 1 YPE 57	18.0							Ī
727	1, 14, 10, 10, 10, 10, 10, 10, 10, 10, 10, 10	FUNDAM PAPILLOMAVIRUS TYPE SO	7.	<u> </u> -			Ť	<u> </u>	<u> </u>	Ī
1000	TO PROTEIN	MACROMYS MINUTUS PAPILLONIAVIRUS	3.5	 	-		İ	1	<u> </u>	ĺ
	L'ARGIEN.	COTTONTAL RABBIT (SHOPE) PAPILL CHÍA VIAUS (STRAIN KANSAS)	3:5	<u> </u>	-		Ì	<u> </u>	-	İ
100	47 PRO1806	HIDGAN PAPILIONAVIRUS TYPE 13	10.1				İ	-	1	-
IVE! IOV!	EVROTEIN	PROMAN PAPILICALA VIRUS TYPE SI	10.5	<u> </u>			İ	-	†	İ
YET HOVE	ET PROTEIN	HOGGEN PAPILLOMA VIAUS 17PE 4B	160			Ī	\dagger		1	
	E7 PROTECT	APESUS PAPELOMA VIRUS TYPE I	79.00	<u> </u>	-		Ì	1	1	
TALE NAVAC	EALT WILD PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	78-99 203-223				ĺ	1		
LAS CALK	VIDAL ENGANCING FACTOR	TRICHOPLUSIA MI GRANULOSIS VIRUS	154.195	100		Ì			1	Ì
VENV BLV	ENVELORE PROTEIN	BEINE VILUS	63.16	Ť			Ì		İ	Ī
PVENT DATA	ENVELOPE GLYCOPROTEDY PRECUASOR	DHOOL VIRUS (STRAIN INDIANI) () (A)	47.57				ļ	1	1	Ī
V	PROBABLE ENVELOPE PROTEIN	EQUINE ALTERITIS VIRUS	340		-			1	1	
	-	LELYSTAD VIRUS	11-11					\dagger	-	Ī
	-	MOLLUSCIM CONTAGOSUM VIRUS SUBTYPE I	8-10		-		\mid		1	Ī
	_	MOLITUSCUM CONTAGIOSUM VIRUS SUBTYPE 2	T	_				+	+	Ī
ASA INCO	-	THOOOTO VIRUS	194-221	1	-			1	1	
TVE IM MOVAC	ECOLL I SITE PROTEIN ETM	AUTOGRAPHA CALIFORNICA PUCLEAR POL'PIEDROSIS VIRUS	12:103	Т			İ	Ī	\dagger	_
AVE VACCE	14 KD MAJOR MEMBRANE PROTEIN PRECURSOR	VACCOUR VIRUS (STRAIN COPENHAGEN)	180.303				ł		t	
LAND AWC	IN R.D. MAJOR MEMBRANE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN L.IVP)	200-305				t		$\frac{1}{1}$	Ī
A A A A A A A A A A A A A A A A A A A	N KID MAJOR MEMBRANE PROTEIN PRECURSOR	VACCIMIA VIRUS (STRAIN WR)	201-106					+	1	Ī
A 10 10 10 10 10 10 10 10 10 10 10 10 10	16 KD MAJOR MEMBRANE PROTEIN PRECURSOR	VARIOLA VIRUS	200,002					1	1	1
TALL CALL	FROTEINT	VACCINIA VIBUS (STRAIN COPENHAGEN), AND (STRAIN L.IVP)	175.700			İ	\dagger	l	<u>+</u> 	Ī
VALUE VARV	PENTENTE	VACCINIA VIDUS (STRAIN WR)	136.300			İ	1		$\frac{1}{1}$	Ī
PARIS VACOR		VAUCLA VINUS	176-708				-		<u>!</u>	Ī
VALUE VALV	PROTEIN	VACUALLY VIEWS (STRAIN COPEMIAGEN)	161-184						<u> </u>	Ī
PWHIS VACCE	PROTECULAL	14 1 P A 14 P C C P 1 1 P P 1 P	161-114					-		Ī
-			13-50	Н			T		+	Ī
								1]

							ľ	ŀ	-	-	Γ
	VIII. ILAN	V10.15	AREAL	AREAZ	AREAJ	AREAS	AREAL	AREA CHEAT AFEAT	IV TY	ī,	OF CHY
	Penting	VACCINIA VIAUS (STRAIN L.IVP)	Γ				_				
VALVA VALVA	PRO1619	VARIOLA VIRUS	25.5	!						-	-
Verel 10mbv	14 X131004	JOWLPOX VIRUS	107.333								
Anna Idea	PACIETY FP.	FOWL FOX VIRUS	\$8·104								
Very Cove	PROTERY	CAPRIDOXYIAUS (STRAIN KS.1)	111 68								1
VANDE TOWNS	7	FOWLPOX VIAUS	63-80							j	-
WH COW	1	CAPAUPOXVIRUS (STĮLAIN XS-1)	21.76					_		=	
PVFUS OUTHZ	+	ORF VIALIS (STRAIM MZ.)	39.48								
PWFUS VACES	+	VACCINIA VIRUS (STRAIN WR 65-16)	73.44				- 1			- <u> </u>	Ī
PVCel MAYER	т	EQUINE HEAPES VIRUS TYPE I (STRAIN ABAP)									
PACE LITTLE	۰	CTALURID HERPES WAUS I		317.339	389-416	1					
SUPERIOR DE	4	VACCINGA VIRUS (STRAIN COPENIAGEN)	3115.842	376-795							
A WIA IRON	4	VACCINGA VIRUS (STRAIN WR)	137.357	115.534						-	
Value Value	┰	VARIOLA VIEUS	30.00	136.395					<u>-</u> 	<u>.</u> !	:
The state of	UNPOSTUCIONE CENT PROTECTA	VARICELL A. POSTER VIRUS (STRAIN DUMAS)	20-02					i i	<u>. </u>	!	!
	PROTEIN CI	VACCIDAL VIBIN (STRAIN COPENHACEN)	20.23			-				-	
	The state of the s	VARIATA VIBIA	200					-		İ	
	PROPERTY.	VACCORIA VIRUS (STRAIN COPENIAGEN)	=			•					
TOTAL VALUE	PACHENIA ZI	VARIOLA VIBLIS	E:E			•				<u>!</u>	
PVD-L VLD	PROTEGICAL	VACCINIA VIALIS (STRAIN COPENHAGEN)	17:15					-		İ	
ANYA PANA	PROTEGNICA	VALIDILA VIILIS	15:16					-		Ĺ	
PVON HEVI	MYPOTHETICAL ODD & MENDEAND PROTEIN	ICTALIAND IGRAESVINUS I	134-160	199.185				-	-		
1	DATE OF THE PROPERTY	K-TATIRED IS BECAME IN	\$ 55					-			
AUNIT THEFT	т	HE SPECKISH CALLIED ACTE AND 111	100-120	155.170						İ	
	т	PER LESS CONTRACTOR OF THE PER CONTRACTOR OF	101-133	10.136		-				l	
	MINORESPECTOR OF THE PROPERTY	CTALLED GENERALIS	T	376.786					T		Ī
	THE STATE OF THE PROPERTY OF T	REDECTION CANADA AND III	Τ			-				t	Ī
	CONTROLL CONTROLLOR	ICTAL IN THE LEGISLAND IN	11.113								
SCALL STATE	MINUTE INC. COLOR IN PROPERTY AND	ALVEACE A LIBERTAIN MACHINETIS	11.11			F		\mid		I	-
1000	-	SPIROPLA CALLA WALLE COVI. REAL! B.	Т	459.478		Ī			l	İ	
1000	-	KTALIED JERPESVRIK	L		Ī	7	Ī	T	T		Ī
The state of	MANAGEMENT OF THE STREET	FTALLIBED (GIPE SVIRUS 1	114.115			1		Ì		l	Ī
The state of	TAYAD THE TAYAN OF THE ST PROTEIN	ICTALINED USE EDES VIBILS I	1	Ī			Ī	l		İ	
The Property	MAYOR THE THE AT CARREST PROPERTY.	HEAPESVIRE SABAIRLISTRAIN (1)	109.336			Ī		İ			Ī
AVAIL HEVE	INVOINE TICAL CENE 28 PROTEIN	ICTALIND HEAVES WALLS I	Τ	401.516	T	Ī		T	t	T	Ī
PWG28 HSWLA	HYPOTHETICAL CENE 28 PROTEIN	HEAPES VINUS SABAINJ (STRAIN 11)	10.00						-		
PVOM HEVE	HYPOTHETICAL GENE TO PROTEIN	ICTALURID HEAPESVIRUS I	1791						_		
PVOIS HEW!	HYPOTHETICAL GENE SOPROTEIN	ICTALUMO HERPESVIRUS I	164-191					-			
PWOM VZVD	_	VARICELLA-ZOSTER VIRUS (STRAM DURIAS)	90-109								
PVOM HSVSA		HELDESVIRUS SADARA (STRAIN II)	100-123	144-362							
PVG35 HSVII	HYPOTHETICAL CENE 37 PROTEIN	ICTALUMO HERPESVIAUS I	╗				1				1
PVOTE MSVII	ANYOTHETICAL GENE 19 PROTEIN	ICTALIBAD MERPESVIRUS I	اء	8	90.00			1	1	1	
PVOse HIVI	HYPOTHE FICAL GENE 40 PROTEIN	ICTALIAND MEANES VALUE (2					1	1	1	
PVOIL ISTAIL	HYPOTHETICAL CENT 41 PROTEIN	ETALUACO PERPESANUS I	T		П			1	1	1	
PVG45 HSVE	HYPOTHETICAL GENE 4) PROTEIN	ICTALUMID HERPESVIRUS I	П	33.178		321-538					
PVOM HSVII	PROBABLE MAJOR CLYCOPROTEIN	ICTALUNUD HERPESYINUS I	24-136	180-607	937-963	1244-1370					
PVG48 MSVI)	HYPOTHETICAL CENT 48 PROTEIN	ICTALUMO HEAPESVIRUS I	71.63								
PV056 HSVSA	PROB TRANSCRUPTION ACTIVATOR EDAF!	NEXPESVIRUS SABIIRI (STRAFILI)	5.30	31.13							
PVOSI HSVII	KYP CENE SI NESGRANE PROTEIN	ICTALUMD HEINESVIRUS I	į	20.103				1			
PVGS2 HSVII	. JIYPOTIETICAL CENE 13 PROTEIN	ICTALUADO MERAES VIRUS I	279-252				1	+	1	1	Ī
PVOSS HEVEL	HYPOTHETHEAL GENE 35 PROTEIN	ICTALUMD AG IPESVIAUS I	2	19:158	119.300	1	1			1	1
PVOSS HEVEA		HEAPESVINUS SABARN (STRAIN 11)	2								
PYON HISMI	7	ICTALUND NEWESVIRUS I	23.138		┪			1	1	1	Ī
PVOSE HSVSA	Ť	IERPES VOUS SAIMIRI (STRAIN 11)	3	2	30.35	30.34			1	1	1
PVGM MSVII	CATE CENE SE MEMBER CATE TROUBLE	CORONA SCALA VARIES A		111.11	Ì				1	1	Ī
TO COLUMN	MANAGEMENT COME TO PROPER		10.00	1			1	+	t	1	Ī
100 P	HIVING INCHES]	1	1	1	1]

VARIA PROTECT GENE & PROTEIN CTAL VARIA VARIA PROTEIN VARIA PROTEIN VARIA PROTEIN VARIA PROTEIN PROTEIN VARIA PROTEIN PROTEIN VARIA PROTEIN PROTEIN PROTEIN PROTEIN VARIA PROTEIN PROTEIN PROTEIN VARIA PROTEIN PROT	VIRUS]		2	10 ·	20100		1000	
HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 12 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN PRECINGOR HYPOTHETICAL GENE 13 GALYOPHOTHEN			Т	-			_	_	_
HYPOTHETICAL GENE B) PROTEIN HYPOTHETICAL HYPOT		70-101	2 2 2 2 2	+	+	t	+		+
HYPOTHETICAL GLAE 44 PROTEIN HYPOTHETICAL GLAE 41 PROTEIN HYPOTHETICAL GLAE 41 PROTEIN GLAE 0 PROTEIN GLAE 0 PROTEIN HYPOTHETICAL GLAE 11 HYPOTHETICAL H		T		+	+	1			
HYPOTHETICAL GENE 61 PROTEIN GENE O PROTEIN HYPOTHETICAL GENE 61 PROTEIN HYPOTHETICAL GENE 19 THETICAL GENE HYPOTHETICAL GENE			161 391	101	100	1107.1174	1347.1360		ļ.
HYPOTHETICAL GENG 19 MOTERN GENG 3 PROPERTY HYPOTHETICAL LENG 19 PROTEIN HYPOTHETICAL LENG 19 PROTEIN HYPOTHETICAL LENG 19 PROTEIN HYPOTHETICAL LENG 19 PROTEIN GENG 3 PROTEIN GENG 3 PROTEIN GENG 3 PROTEIN HYPOTHETICAL LENG 19 HYPOTHETICAL HYPOTH		T	7	Т	Т	+	-	1315-1341	<u> </u> T
HYPOTHETICAL TEME TO PROTEIN HYPOTHETICAL TEME TO THE TOWARD TO THE TOWARD THE HYPOTHETICAL TEME TO THE TOWARD TO THE TOWARD THE HYPOTHETICAL TEME TOWARD TOWARD THE HYPOTHETICAL TEME TOWARD TOWARD THE HYPOTHETICAL TEME TOWARD THE HYPOTHETICAL TEME TOWARD TOWARD THE HYPOTHETICAL TEME TOWARD THE HYPOTHETICA	ICTALUMD REACTES VIRUS I	Т	Τ	Т	T	1-			
HYPOTESTICAL PERE SI PROTEIN HYPOTESTICAL PERE SI PROTEIN GENE OFFICIENT GENE OFFICIENT HYPOTESTICAL CENT OF PROTEIN GENE OFFICIENT HYPOTESTICAL CENT OF PROTEIN GENE OFFICIENT HYPOTESTICAL CENT OFFICIAL ESTICAL HYPOT		184.209	T	\mid	-				-
ITTOPINATE SECTION OF CONTROL INTOPINATION CONTROL INTORNOTION OF CONTROL INTORNOT	AMILI	84-105		Г					
GHOTEN COUNTED RECURSOR GENE 9 PROTEIN (GENE ENE 9 CHOOPERINE (GENE 9 CHOOPERINE		485-471 5	115-561 77	730-744 (12)	1352-1269				
GENE O PROTEIN I I PROTEIN II GLYCOPROTEIN HOLINGOR EI GLYCOPROTEIN PRECINSOR EIN PRECINSOR GLYCOPROTEIN PRECINS	KIN II)	124-151							$\frac{1}{1}$
H PROTEIN I GLYCOMOTEIN NOI PRECINSOR III GLYCOMOTEIN NEICUSOR III GLYCOMOTEIN PRECINSOR III GLYCO		57.72					_	7	
16 G. VCOPROTEIN NO! PAECUASOR 16 G. VCOPROTEIN NO! PAECUASOR 18 G. VCOPROTEIN PAECUASOR 10 G. VCOPROT	URUS (STRAIN BEAUDETTE)	П	1856-1877 31	3100-2127 22	2210-3226 27	N 9097-9847	2973.2989 30	1073-3090 3120-3145	145 1174.1199
16 GLYCOMOTEN NON PRECINSOR 16 GLYCOMOTEN PRECINSOR 18 GLYCOMOTEN PRECINSOR 19 GLYCOMOTEN PRECINSOR 10	1601-3625							•	
III GAYCOMOTENI PLECATION III GAYCOMOTENI PLECA		157.178			7				_
ES CLYCOMOTERS PLECURSOR CURSOR CLYCOMOTERS PLECURSOR CLYC	IN BUI STOOMBALTINI IS	(34-19)							-
EI GLYCOMOTEIN PLECINSON MOTEIN PLECINSON GLYCOMOTEIN PLECINSON		П		П		٦	1259-1260		1
ES GLYCOMOTEIN PLECUASOR ECUASOR GLYCOMOTEIN PLECUASOR		123-130	174-190 20	П	7	┪	1259-1260	$\frac{1}{1}$	+
ESTATION OF THE MECHASOR ESTATION OF THE ME		10-33	133-139		П	7	1259-1280		+
EI GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR GLYCOMOTEIN PRECUISOR		133-139	134-190 30				1		1
E GLYCOMOTEIN PRECINSOR ES LYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR GLYCOMOTEIN PRECINSOR		П	133-139			┪	1259-1280		4
E GLYCOMOTER FECURIOR OR GLYCOMOTER FINE FECURIOR GLYCOMOTER FINE FINE FINE FINE FINE FINE FINE FINE		123-139	174-190 21	_	591-1017 12	1259-1280			-
ES GLYCOMOTEM MECHASON COMOTEM MECHASON GLYCOMOTEM GLY		766-794	1053-1071	11151134	_				
ESTATOPHOTER MECINSON MECINSON GAYCOMOTER MECINSON GA	WILD TYPE 4)	6 1111-56	1 5201-666	1167-1290 11	1317-1330				
ES GLYCOPROTEIN PRECINSOR GLYCOPROT		95-111	947-973	21 8(21-212)	1265-1286				
15 GLYCOMOTERN PRECINSOR PRECINSOR 18 GLYCOMOTERN PRECINSOR	MEDIE CHEDNA VIEUS MAY (STRAD) DOWN VALIANT CL-2)	Γ	L	1267-1290 13	1317-1334				-
E GLYCOMOTERN PRECINSOR EL GLYCOMOTERN PRECINSOR G		111.56	t	1136-1149 11	1176-1197		H		
15 GLYCOPROTEIN PRECINSOR PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 17 COPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PROTEIN PROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PROTEIN PROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PRECINSOR 18 CLYCOPROTEIN PROTEIN PROTEIN	(STRAI	Γ	Ť	₽	1038-1054 12	1374-1397			
EL GLYCOPROTEIN PECINSON	PORCEOU TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAI)	Γ	Г	П	П	П	1374-1297		
ELGLYCOMOTERI PRECINSOR	PORCHAE TRANSMISSIBLE DASTROENTERITIS CORONAVIRUS (STRAI)	17-19	555-099	504-519	198-814	1036-1062	1372-1395		
ES CALVOMOTERIN MECUNSON ES CALVOMOTERIN MECUNSON ES CALVOMOTERIN MECHSON CALVOMOTERIN ENECH		64-43			01 718-804	1036-1062	1272-1295		
ES GLYCOPHOTEIN MECHNSOR GLYCOPHOTEIN B PRECINSOR GLYCOPHOTEIN B PRE		218-233 5	Ĩ	814-840 10	50-1603				-
ES GLYCOPAGREN PRECINSOR GLYCOPAGREN PRECIN	j	33				_			+
ES CA YOOFFOTEN PRECINSOR PRECINSOR CA YOOFFOTEN B PRECINSOR CA YOFFOTEN B PRECINSOR CA YOFFOTE	PORCING TRANSMISSINGE GASTROENTENTIS CORONAVIRUS (STRAI)	٦	_	-	708-814	036-1062	1272-1295		+
13 CLYCOPACTEN PRECISSOR 13 CLYCOPACTEN PRECISSOR 13 CLYCOPACTEN PRECISSOR 13 CLYCOPACTEN PRECISSOR 14 CLYCOPACTEN PRECISSOR 15 CLYCOPACTEN PRECISSOR 15 CLYCOPACTEN PRECISSOR 15 CLYCOPACTEN PRECISSOR 15 CLYCOPACTEN PRECISSOR 16 CYCOPACTEN PRECISSOR 17 COPPORTEN PRECISSOR 18		5	8	-	1	1		$\frac{1}{1}$	
ELICATOMOTEN PRECUISOR		٦	1	7	-1	=======================================	1		+
ELGLYCOMOTERN PRECURSOR	DETTE)	٦	7	7	1055-1080		1		\dagger
ES GLYCOMOTEM PRECISSOR		٦	709-80	771-797 10	1036-1081	1	1	1	+
ES GLYCOMOTEM PRECUSOR ES GLYCOMOTEM PRECUSOR ES GLYCOMOTEM ES GLYCOMOTEM ES GLYCOMOTEM GLYCOMOTEM PRECUSOR		7	1	7	-	1	1		+
EL CLYCOPROTEM PRECUESOR. EL CLYCOPROTEM EL CLYCOPROTEM EL CLYCOPROTEM EL CLYCOPROTEM PRECUESOR CLYCOPROTEM P	AVIAN DOECTIOUS BRONCHUTIS VIRUS (STRAIN RB1523)	317-641	T	20, 20, 20,	÷	AAC DAM	\dagger		ł
EL GLYCOPROTEIN EL GLYCOPROTEIN EL GLYCOPROTEIN E PRÉCINSOR	1,000	T	Τ	T	1				+
EL CA COMPOSEDE EL CA COMPOSEDE CA COMPOSEDE DE DECISOR CA COMPOSEDE DE DECISOR CA COMPOSEDE DE DECISOR CA COMPOSED CA COMPOSED DE PRECISOR CA COMPOSED DE PR	Ī	174.701	T	l	T	T	T		L
GLYCOPROTEM PRECINSOR		178.201	T		\dagger				-
G.YCOMOTEM B PECURSON	EPSTEIN-BARR VIRUS (STRAIN 849-4)	Γ	П						Н
GLYCOPROTEIN B PLECIASON GLYCOPROTEIN B PLE		335-358		150-111	-				
GLYCOPROTERS PRECINSOR			107.133	151.378					+
GLYCOPROTENS PRECINSOR GLYCOPROTENS B PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPPORT PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPROTENS PRECINSOR GLYCOPPORT PRECINS		13:104						+	+
GLYCOPROTEN B PRECIRSOR		13-103						1	+
GLYCOPIOTEN B PRECINSOR GLYCOPROTEN B PRECINSOR GLYCOPROTEN B PRECINSOR GLYCOPROTEN B PRECINSOR GLYCOPROTEN B (PLACAGENT) GLYCOPROTEN B (PLACAGENT) GLYCOPROTEN B (PLACAGENT)		13-103							+
GLYCOMOTEN B PRECINSOR GLYCOMOTEN B PRECINSOR GLYCOMOTEN B (FRACAGNY) GLYCOMOTEN B (FRACAGNY) GLYCOMOTEN IN PRECINSOR	10%)	2			1				+
GLYCOMOTEN B PRECINSON GLYCOMOTEN B PRECINSON GLYCOMOTEN B (PRACMENT) GLYCOMOTEN I PRECINSON		8.6			1	1			+
GLYCOMOTEIN B PAECIASOR GLYCOMOTEIN B FALCIASOR GLYCOMOTEIN B FALCIASOR	3	2	1	+	+	1			+
GLYCOPROTEIN B (PLACARENT) GLYCOPROTEIN PRECURSOR			113 144	\dagger	1	1	1	+	+
CLYCOTROTEDY PRECURSOR	MARINES SOUTH A VINOS IT THE 67 STRAIN CLANDA 1103)		m (m)	\dagger	\dagger	Ţ			+
	STATE TO AND THE PARTY OF THE P	T	745.767	\dagger	\dagger	1	\dagger		+
SCHOOL STATE OF STATE	BOUTAS 16 BPE (VIEL 4 TYPE 1 STRAIN COOPER)	Τ		†	T	l	T		\mid

4	IPINCTIZIP	All Viruen (No Becterlophages)	T	Т	77.4	7	7 7 2 4	. 4284	AREA 6	AREA!
FILE MAKE		VIRIUS		1	700	Т	T	1	Т	
PVGE HSVE		EQUINE HERPES VIRUS TYPE I (ISOLATE HVS2SA) (EHV-I)		1		+		-		
PWELD HEWE!		EQUINE HERPES VIRUS TYPE I (STRAIN AB!)		1		-				
PVCL HOVEA		EQUINE HERPES VIRUS TYPE I (STRAIN ABI)	136.73			+				
PWC I HEVE		EQUINCE HEAPES VIRUS TYPE I (STRAIN AB4P)	130-131			1		-		
PACE HAVEL		EQUINE HEXPESVIRUS TYPE I (STRAIN KENTUCKY D)	736-753		1	+				
GWH LEWS		AAREKS DISEASE HERPESVIRUS (STRAIN RB-18)	7	Ť		+		1	ľ	
PVGL BUSVA		KERPESVIKUS SAIMIĮU (STRAIN II)	483.508	1	201-710	+				
WATER WA		DESCRIOUS LARYNGOTRACHEITIS VIRUS (STRAIN 432)	٦	1	201	1	+	+	Í	
PWR B B TW		INFECTIOUS LARYNCOTRACHEITIS VIRUS (STRAIN SA-2)	Т	7	2	1	<u> </u>			
PVG LTV		INVECTIOUS LAKYNCOTAACHEITIS VIRUS (STRAIN THORNE VBIZ)	٦	Т	20.00	-				Ī
WALL BOWN	CALVODARDITED B PRECURSOR	LAMBER CYTOMEGALOVIRUS (STRAIN SAIITII)	┪		736-765	1				Ī
1 1 1 m	CA VOCABOTERA ON PRECURSOR	PSEUDORADIES VIRUS (STRAIN INDIANA-FUNKLIAUSER / HECKER)	101-218		1				1	
		VALICELLA-ZOSTER VIRUS (STRAIN DURIAS)	=							Ī
TO TO TAKE	CLACOPOLITION OF PRECIDENCE	EXPES SUCHEX VIRUS (TYPE 1/STRAIN 17)	3.22	447-493		-				
	TO COMPANY OF THE COM	GRAPES SOURCEX VIRUS (TYPE I / STRAIN KOS)	1-22	467-403						
- CONT CONT.	SO COMPLETE DESCRIPTION	HEAPES SOUPLEX VIRUS (TYPE 2)	435-458	-	<u> </u>	-1	: :	;		1
1	CHANGE AND THE PARTY OF THE PAR	STRAIN 333	430-459					-	;	:::::::::::::::::::::::::::::::::::::::
1	ALTONO DE L'AMBRECO DE CONTROL DE	POVINE ISEBESVIETS TYPE I ISTANIN COOMIN	475.484							
PVOLC HSVBC	CLTCOTTO AND PROTO MEDICAL	FOLIDATION SOCIALIST TYPE 4 (STEATS 1942)	644.459	-		•				
PVGLC HSVEA	GLICUTACIEN CTRECONOM	COME LEGIS SVIRITS TYPE - (STRAIN ARV) AND ISTRAIN KENTICK	427.442			_				
PVGC HSVE	G TOTAL CHECORSON	ALABERT DAGE AND LIFE DECKNOTE (STRAIN BC.1)	399-421			-				
VGC RVG	SECRETURY CLYCOPROJEIA CP17-2 PRECURA	ALABORA DACE ACE DICEBER LICE ALL ROLLEY	199-421			_				
Vac My	SECRETORY CLYCOPROTEIN UP37-43 PILE CURX	MANCA 3 DASEASE HENCES WOODS TO THE TANK THE TAN	198-420			-				
PVOLC HSVND	SECRETORY OF TOOMSTEIN GP3743 MELURA	MANUEL DESCRIPTION OF THE OWNER AND	160.671				 -			
PVGLC HSWIDM	SECRETORY OF YCOMOTEIN GP5745 PRECURSOR	MAKEN S COSCASE RESPECTIVE CONTRACTOR STATES AND CONTRACTOR OF CONTRACTO	180.107	446.472		-		-		
PVGC MVB	CLYCOPROTEIN GILL PRECURSOR	CALCACTURE A SACRED WAS IN CASE AND PARTY OF	4717		-	-				
PVOLC VZVD	CLYCOPROTED GPV	VALUELLA-LUSIER VIRUSISIANIN UNRANS	27			 -				
PVOLC VZVS	OLYCOPROTEDIOPY	VARCELLA 2031EA VIIIOS (SIRAIM SCOTT)			1			-		
WOLD HEVIL	OLYCOPROTERY D PRECURSOR	PENDES SUPPLEA VIACO (1775 17 21 AND 1775 AND 17				-				
PYOLD HSV1	OL YOU'N OTED! D PIBCURSON	HEAVES SOUTHER VINCE (1978 AND 197	,	117117	Ī			-		
PVOLE HSVII	OLYCOPROTEIN E PRECURSOR	PERIORS SOUTHER VINOS (1175, 17.3) RAIN 17.)	Т			+				
PVOLI VEVO	OLYCOPROTED/ E PLECURSOR	VAULELLA-COSTER VIACO (STRAIN COMPANY)	304.331	241.389	482.504		-			
PVOLU BASVA	FUSION OF YCOPROTEDN PILECUISOR	AND THE PERSON OF THE PARTY OF THE PERSON CONTRACTOR	205-221	Т	484-306	l	-	-		
WOLL BASW		BOVING ACCOUNT OF THE PINCE OF COMMENT OF COMMENTS	204.23	T	464.506		-			
IVOL) BOSYL		POVING PASTONAL STATE THE TIME STATES OF PASTONS TO	136.361	Τ	\$42.589	-	-			
200	FUSION OL YCOMOTEDI MECURSON	AND DESIGNATION STANCTION VIRIAL STREET IS		Т	484.506					
	-	LE LANGE COMPATORY CYNEYTIAL VIRILE (STRAIN A2)	205-221	Г	24.506			_		
	-	HEMAN RESPONSTORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN LO	122-221	Т	484-506					
	REMARKS OF VANCOUS OF THE CAR COR	HIMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSS-3)	305-223	082-592	484-506					
	Т	MEASUES VIRUS (STRAIN EDMONSTON) and (STRAIN HALLE)	114-145		451-477					
1000	T	MEASLES VIRUS (STRAIN IP.)-CA)	227-248		454-480	4		-		
VALUE AND A	Т	MEASLES VIRUS (STRAIN YAMAGATA-1)	224-245	٦	451-477	1	+			
TARREST AND A	т	MONDES VIBLUS (STRAIN SBL-1)	5.20	٦	446-467	1		1	1	
Way Mason	_	MONGYS VOLUS (STRAIN MOYAHARA VACCINE)	276-292	646.467		+	+	1		
TYCH MACH	Т	HONO'S VIBLUS (STRAIN RW)	276-292	٦		+		+	1	
PVGU MODOS	1	MONGES VOICES (STRAIN SBL.)	270	110-101	100-001	+			1	
WOL NOVA	1	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/12)	273-269			+		+		
MON STONE	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	273-248		+	1		+	1	
WOL NOWE	FUSION OLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE YALUS (STRAIN HEAV))	273-209		1	+	1			
PVOI LOVI	1	NEWCASTLE DISEASE VIRUS (STRAIN BI-HITCHNEWAY)	273-209			1		+		
WOL LOW	т	NEWCASTLE DISEASE VIRUS (STRAIN LAS/46)	273-289			1				
TYOU YOU	FUSION OL VCOPIOTEIN PRECUISOR	NEWCASTLE DISEASE VIRUS (STRAIN MIYADERAS)	213-289		1	1		+		
PVOIL NOVO	FUSION OF YCOPROTEIN PRECUISOR	NEWCASTLE DISEASE VIRUS (STILAIN QUEENSLANDAM)	27.1.289			1		+	Ţ	T
PVCL YOY	_	NEWCASTLE DISCASE VINOS (STANDA TEANS)	371.780		+	$\frac{1}{1}$	1	-		
MON NOVICE	┑	NEW CALLE CALCAL TOOLS OF TEACH OF THE ATT	223-280		-		-			
300	╗	NEW CASE DISTRICTED AND CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR AND CONTRACTOR OF THE CONTRACTO	269-215	303.126	167.313 1331.558	<u></u>		-		
PVCL PHODY	FUSION GLYCOPHOTEIN PRECURSOR	FROLING DISTERS IN THESE		7	1					

WO 96/19495 PCT/US95/16733

					I			-		ł	
MI F WALL	PECTIZIT	All Virgo (ne Betterophegn)	Т	AREA 2	ARFA 3	ARCAS	ARLAS	AREAG	AREA 7	AREA	AREA 9
PVQL RIHC	FUSION CLYCOPROTEIN PRECURSOR	MAN PALAINFLUENZA 1 VIRUS (STRAIN C19)		; _	1		Г	Т	Ŧ-	Т	T
PVGU PUR	FUSION CLYCOPROTEIN PRECURSOR	HUMAN PARATIFICENZA 2 VIRUS (PIV.2)	450.471								
PVGLF MIMO	FUSION OLYCOPROTEIN PRECURSOR		450-471								
PVGLF PLINT	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA ? VIRUS (STRAIN TOSIUIA)									
PVGL PUB	FUSION GLYCOPROTEIN PRECURSOR	BOYINE PAKAINFLUENZA 3 VIRUS	2	٦						-	
70 E	FUSION CLYCOPROTEIN PRECURSOR	HIDAAN PARAINFLUENZA J VIRUS (STRAIN MII 47005)	T	╕	453-474					1	
No.	PUSION CLYCOPROTEIN PRECURSOR	RINDEAPEST VIRUS (STRAIN KABETE O)	770-74	283-298	447.473				+	+	T
Supply Supply	PUSION OF VOCABUTEIN PRECINGOS	SENDAL VIEUS (STRAIN 2 / 1905T MILTANTS)	Τ	Τ						\dagger	1
WCL UND	PUSION OF YOUR OTHER PRECINSOR	SENDAI VIRUS (STRAIN FUSITIALI)	10.41							<u>:</u> :	:
WOLD SENON	FUSION CLYCOPROTEIN PRECURSOR	SEMBAI MIRUS (STRAIN HARUS)	179							t	
Wat som	FUSION GLYCOPADTEIN PRECURSOR	SENDAL VIRUS (STRAIN HVJ)	460-431							\vdash	
Was serve	PUSION CLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN 2)	460-481								
PVQLF SV41	FUSION GLYCOPROTEIN PRECURSOR	SEGAN VIRUS 41	453.476			•				+	Γ
PVQLF SVS	FUSION GLYCOPROTEIN PRECUASOR	SDAIAN VIRUS 5 (STRAIN W1)	Ì	646.467							
INCL! TATV	FUSION CLYCOPROTEIN PRECURSOR	TÜRKEY KHIMOTRACHEITIS VIRUS	٥	482-474		-					
Vac 687	SPIKE GLYCOPROTEIN PRECURSOR	INFECTIOUS HEMATOPOIETIC NECROSIS VIRUS (STRAIN ROUND BUT	17.98								
VOLO INEVE	-	KABIES VIRUS (STRAIN E.K.)	1			1				1	Ī
MOLO PASY	-7	RABIES VIRUS (STRAIN HEP-FLURY)	Ī	24.474						+	
Ward Mary	SPIRE CLYCOPROTEIN PRECURSOR	RABLES VIRUS (STRAIN PV)							1	+	1
WOLD BADYS	┱	INDIES VIRUS (STIAIN SAD BI9)								+	
WELD IN	7	KABLES VIKUS (STRAIN STREET)	2/7/						1	+	T
WG.00	MANOR SURFACE CLYCOPROTEIN G	TURKEY INGRACHEITIS VIRUS	12.510		I	-				+	
MONO WOOM		VICAL REMOUSHAGIC SEPTICEMIA VIRUS (STRAIN 07.71)	7	Т						+	T
PVOLM HOVA	CALYCOPHOTEIN H PRECURSOR	HUMAN CYTOMEGALOVINUS (STRAIN ADIBS)	107-117	Т	374.398			1	\dagger	\dagger	
	┰	THE PARTY OF THE P	T						$\frac{1}{1}$		T
ACT IN TOTAL	CALTOURISM HIMELUNGON	MENTES SUMPLEX VIXUS (1778 17 STANIN 17) VEHICLE CHAIR BY URITE 77 VIX 17 CTS AND INTERN	Т		720-100	1		1		\dagger	Ī
200	_	DESIGN STATE OF USING CAME A ASSESSMENT OF THE COMM	T			ŀ		Ī		\dagger	Ī
AND HEAVE		FOUNDE HEAVENANCE TYPE 4 (STRAIN 1942)	Т	814.830						$\frac{1}{1}$	Ī
PVQLH HSVED	GLYCOMOTEIN W PRECURSOR	EQUINE HEAPESVIAUS TYPE I (STRAIN ABAP) and (ISOLATE HVS2SA)	Γ	201-100		-				\mid	Ī
PVOLH NSVSA	•	HEADESVILUS SAIMIRI (STRAIN 11)	Γ	658-670							
PYGLA MOAYS		MURINE CYTÓMEGALOVIRUS (STILAIN SMITH)	670-690								
PVGLI HOAVA		HEDGAN CYTOMEGALOVIRUS (STRAIN AD 169)	138-180								
PVOLI MSVII	GLYCOPROTEIN!	HERPES SOULEX VIXUS (TYPE I / STRAIN 17)	\$								
WOL BOYES	CLYCOPROTEIN I PRECURSOR	EQUIDE HELLTESVIRUS TYPE I	£5)	1				1		1	
DAGE VZAD	GLYCOPIOTED I	VAUCELLA-COSTER VIRUS (STRAIN DUMAS)	278-297					1	$\frac{1}{1}$	\dagger	1
17 17.0	-	BINAVA VIBILE LA CENCES CICCA ATE I 241	T		116,001	1134,1544	0171 1011			+	T
PVOLIA BURGH	-	BUNYAVIKUS SNOWSHOE HARE	T	Τ	Τ			\dagger		\dagger	I
PVCLM MANY		BUNYAWERA VIRUS	=	ş	Τ					+	
WOLK BUGBY	M POLYPROTEIN PRECURSOR	DUCINE VINUS								-	Ī
PVQLM KANTE	PVOLJA KANTB [JA POLYPROTEDN PRECLIRSOR	HANTAAN VIRUS (STRAIN B-1)	П	Г	600-915	999-1019				-	
PVCLM HUNTH	M POLYPROTEDY PRECURSOR		П		1000-1020					-	
MAKE HAME	_	HANTAAN VIXUS (STIVAIN LEE)			1001-1021				_		
TACK MOV	_	HANTAAN VIRUS (STRAIN 76-118)	2		=						
TYGEN DASA	M POLYTROTEEN PRECURSOR	DAPATIENS NECROTIC SPOT VIRUS (INSV)	7	74°.783	346-367	31:33	3			1	
VOL N	M POLYPROTEIN PRECURSOR	PROSPECT MILL VINUS	Т					1		1	
ALL POAL	M POLYTROTEIN PRECURSOR	PURITA LONG PRILEDUVIAUS	743-765	9101.04	1775-1702			1		+	T
	-	PUBLISH VIDIOS (STRAIN COTE ALIO)	T	Т				1	$\frac{1}{1}$	1	
	-		2/1-461	Т	22211	1111-7401		1		+	1
ZALAN MARKE	4=	(STRAIN 211-548 M12)	Τ	Т	2000	1154-1174		1	1	+	T
PYCEM REDU	1		155.371	Г	\$10.00 \$10.00	\$101 346		T		ł	Ī
PYCHA SECUR			П		Г	1000-1020		 		ŀ	
PYCELM SEOUS		AIN SR.11) (SAPPORO RAT VIRUS)	П	П	П	994-1019				H	П
PYGLM USE	M POLYPROTEIN PRECURSOR	UUKUMEMI VIAUS	261-565	655-674	126-842	150-576	684-996				Π
			:								ĺ

PCEVAL	THE TENT	All Vivers (Ne Betirringhages)	Т	ARTA!	AREAS	AREAS	AREAS	ANEAS	AHEA?	AREAS	ABEAS
FILE RAME	PROTEIN	WINUS	250.00	F	١.						
PVGLP BEV	PEPLONGA GLYCOPROTEIN PRECURSOR	BEANE VIACOS	Γ								
PVOLX HSVEB	GLYCOPROTED! X PRECURSOR	EQUIPE HEAVESTANCE ITTE (STRAIN ABOV)		T		-					
PVCLX HSVEK	GLYCOPROTED GX PRECURSOR	EQUING HEAVES VIALUE (STRAIN REPLICANT A)									
PVCLX HISVEL	GLYCOPROTEIN GX	EQUING HEAVES VINCE I (STANIN MENTOCK) OF	149.176								٠
PVGLX PRVIL	SECRETED OLYCOMOTEIN GX	PSEUDORABLES VIROS (STRAIN RILE)	15.7								
PVCLY RINGH	GLYCOPROTEIN POLYPROTEIN PRECURSOR	JUMIN AMERICA VINCO	17.71	37.336	426-448					٦	
PVCLY LASO	OLYCOPROTEIN FOLIPROTEIN PRIELUXSUR	LABOR VENEZA CETEATA INCIARIA	Γ	238-250	437-469						
PVCLY LASS	CLYCOPROTEIN FOLVPROTEIN PRECURSOR	LASSA VIANO (SINGE CONTROLLIS CITIES (STEAD) ARAISTRONG)	51:51								
PVOLY LYCVA	_	SCHOOL CLOSE CALCENDACITIS VIBILS (STRAIN WE)		19:10							
PVGLY LYCV		Library Marie	13:35	435447		1					
PVCLY MOPE	CLYCOPROTEIN FOLYPROTEIN PRECURSOR	MUTELA VIANOS	Γ	41.466	-						
PVOLY PIANY	GLYCOPROTEIN POLYPROTEIN PRECURSOR	PRODUCE ALENAVIRUS	Τ			ŀ					
PVCLY TACY	GLYCOPROTED FOLVPROTED PRECURSOR	TACALDE VIRUS				ŀ					
PVCLY TACVS	OLYCOPROTEDI POLYPROTEDI PRECURSOR	TACALIDE VIRUS (STRAIN VS)		Ī	1	ŀ					
PVCL V TACVI	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACABLEE VIRUS (STRAIN V?)			T	-					
PWELV TACVE	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACABLE VIRUS (STRAIN TRVL 11596)	T	101		1117.11	1160.1164				
AND BRIDA	т-	COWPEA MOSAIC VIRUS	T	Т	Ť					Ī	
AND WOME	т	COWPEA MOSAUC VIRUS	1	5	1	1					
WEST ENV	7	EPSTEIN-BARR VIRUS (STRAIN 895-8) (HURIAN HERPESVIRUS 4)	1		1	+					
Val fany	Т	EPSTEIN-BARR VIRUS (STRAIN BOS-8) (HUMAN HERPESVIRUS 4)	24.87								
VAN BOV	PROPARI FILITAMEANE ANTIGEN GPOS	EPSTEIN-BARK VIRUS (STRAIN B95-B) (PIURIAN HERPESVIRUS 4)	67.56	Т						Ī	
100 E	STRIPTIMAL TR. YCOPROTEIN PRECURSOR	EBOLA VIRUS	26.53	_[621-673	-					
200	CTRICTIBEAL OF VIOLENCED PRECURSOR	MARBURG VIRUS (STRAIN MUSOKE)	536-562	242							
	THE PARTY OF VANCE OF THE PARTY OF THE COR	MARBURG VIRUS (STRAIN POPP)		607-627		-				I	
	SECURITY TO DESCRIPTION OF THE PROPERTY OF THE	VACCINIA VIRUS (STRAIN COPENHAGEN)	76-92	103-121		ا					
A COL	TAUTED TOTAL TOTAL PROPERTY OF TAIL	VACCINIA VIRUS (STRAIN WR.)	76-93	105-121		1					
WHO! WACE	PROTEIN-1 TRUSING TOWNS TOWNS TO SEE	VARIAL VRUS	76-92	105-121		-					
PVHOI VAKV	TAULEUM I TRUSHED FROM THE	VACCINIA VIRUS (STRAIN WR)	10-97								
1 A C	CALCINETINE IN	VARIOLA VIRUS	70-97								
1	SECRETARIA CANTON	FOXTAL MOSALC VIRUS	182-205			1					
	PROPERTY OF THE PA	PAPAYA MOSALC POTEXYIRUS	153-168			*					
	1 POOT OF	VACCINIA VIRUS (STRAIN COPENHAGEN)	120-135								
7 1000	PROTEIN	VALIDLA VILUS	130-135								
	PROTECOLD	VACCINIA VILUS (STILADA COPENHAGEN)	194-220								
	PROTEINIS	VACCINIA VIRUS (STRAIN WR)	24-220								
VALUE OF A	PEDITEMIS	VANOLA VIRUS	194-220								
A TOTAL	PROTEIN 14	VACCINIA VIXUS (STRAIN WR)	104-128	3.63							
VANA VANA	PROTECNIA	VAUGLA VIRUS	108-121	20.00							
PVIO VACOC	PROTEDVIT	VACCINIA VIRUS (STRAIN COPENHAGEN)	13.34	344-767							
PVIOU VACCV	PROTEIN !?	VACCINIA VIRUS (STRAIN WR)									
PVIOT VARV	PROTEIN !?	VAUOLA VIRUS		200							
PYIOR VACOC	PUTATIVE BYA HELICASE IS	VACCINIA VICUS (STRAIN CUPENHAGEN)	104.313								
PVIOR VACCV	MINITIVE BUT HELICASE IS	VACCINIA VILLE (STRUIM WR)	196-212	117							
PVICE VARV	╗	INDIANA CYCLOSIA OVINCE (STRAIN AD169)	77.100	81.15							
PVE! HOWA	Т	MINISTER CONTROL CONTROL TOWNED	77.100	33.350							
WE HOW	SS KD BOGDIATE-BALLT PROJEIN	HERAN CYTOMOGGAI OVIRUS (STRAD) AD 169)	14.33	155.406							
MES HOW	Т	MEMANIC YTOMOGGAL OVIRUS (STRAIN TOWNE)	14.32	388-405							
ME3 HOW	┑	MIRINE CYTOMEGALOVINUS (STRAIN SMITH)	231-372								
L COL	Т	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	14.32								
TARES HAVE	Т	HEAPESVRUS SADADU (STRAIN II)	65-80								
V. CO (2)	Ť	AUTOCRAPHA CALIBORNICA MUCLEAR POLYHEDROSIS VIRUS	100-116	173.290							
A STATE OF THE PARTY OF THE PAR	7	EPSTEIN-BARR VIRUS (STRAIN B95-8)	73.100	281-521	207-102						
WOH OWN	_	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	68-89	28.2		İ					
PVDQ HSVII	_	HEAPES SO/O'LEX VIRUS (TYPE I / STRAIN 17)	03-120	20.270	,	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	161 191	91.60			
PYDAD HISVED	_	EQUING HELPES VIRUS TYPE I (STRAIN ABAP)	24-49	200	Т		76:100				
PVDA HSVSA		HERPESVINUS SAIMIN (STRAIN 11)	1/0-1/1		1						

									-		ſ
THE KAME	PROTEIN	YARUS	AREAL	AREAL	AREAZ	AREA	AREAS	ARIAA	AREA? A	AREAL	AREAS
PVD-0 VZVD	PROBABLE INTEGRAL MEMBRANE PROTEIN	VANCELLA-ZOSTER VIRUS (STRAIN DUMAS)	21-47	- X-18-	230-252						
PVIDI VACCE	PROTEIN II	VACCINIA VIRUS (STRAIN COPENHAGEN)	99-110			•					İ
PVJDI VACEV	PROTEIN 11	VACCINIA VIRUS (STRAIN WR)	89.110								
PVIDI VAKV	PROTEIN JI	VANOCA VIRUS	19.110							٤	İ
PVK64 VACCC	PROTEIN K4	VACCINIA VIRUS (STRAIN COPENHAGEN)	87.113	PEE-802	319.337						
PYKON VACEV	┪	VACCINIA VIRUS (STRAIN WR)	87-113	Ž	319-337					1	
VKO5 VACCE	7	VACCINIA VIRUS (STILAIN COPENHAGEN)	10-133						1	 	
PW. BY VACE	_	VACCINIA VIRUS (STRAIN COPENHAGEN)	Ţ					-		-	:
Wes VACE	7	VACCINIA VIRUS (STRAIN WR)	<u>ا</u>			-	İ		:	÷	
A NOTE A	- 1	VAUCA VILUS	39-61			-			-		
WAS VACOT	MOTERAL	VACCINIA VIRUS (STRAIN COPENHAGEN)	20.00	100.70	207.315	-				1	
WED WACEV	PROTEINLS	VACCIPIA VIRUS (STRAIN WR)	3	2	31.313					1	
WES VARY	PROTEIN L.	VAUGLA VIRUS	107-163	(A. 20)	291-314 201-314					1	
WAS VACC	PROTEIN L3	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENTAGEN)	16.38		-	-	:	:	-		
PVLOS VARV	PROTEIN LS	VARIOLA VIRUS		1	1	-					
W. COW	PROBABLE LI PROTEIN	COTTONTALL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	≃			-					
PVL. IOVIE	MOBALLE LI MOTEIN	HUMAN PAPILLOMAVIRUS TYPE IS	26-35			:				1	
74	PROBABLE LI PROTEIN	HUMAN PAMLLOMAVIRUS TYPE 4)	9			-			1	1	
PVL1 REOVO	MAJOR CORE PROTEIN LANGBDA I	REDVIRUS (TYPE 3 / STRAIN DEARING)	327.146	351.366	152.774					+	
PV1.2 10 V08	PROBABLE L2 PROTEIN	HEMAN PAPELOMANING TYPE 6	254-270			-				+	
	PROBABLE LA PROTEIN	HUMAN PAPILLUMAVIRUS LYPE II	32-38							1	
10A	PROBABLE LA PROTEIN	HUMAN PAPILLUMA VIRUS TYPE 13	35.58								Ì
200	PROBABLE LI PROTEIN	HUMAN PAPELCHANVIRUS TYPE 16	34-40							1	
10A	PROBABLE LI PROTEIN	HOMAN PAPEL CHANGING TYPE 18	33.59								
WIT HAVE	PROBABLE L2 PROTEIN	HUMANY PAPELICINA VIRUS TYPE IA	213.228							1	
Y	PROBABLE LI PROTEIN	HUNGAN PAMLLONIAVIRUS TYPE ZA	911-114			+				1	
TAN POAR	MOBABLE LI PROTEIN	HUMAN PAPELOMAVIRUS TYPE 11	9	443-462		^					
TAN TAN	PROBABLE LA PROTEIN	MUMAN PAPELONIAVISUS TYPE))	85.55	8-15						1	
201 2 100.03	PROBABLE LA PROTEIN	MUMAN PATILLIMA VIRUS 1 VTE 33	200	,,,,,,					1	1	
1000	PROBABILE 13 PROTEIN	MINISTER PAPELL ON A VIBILIS TYPE 42	11.10	144.130		Ī				1	Ī
PVL3 HPV47	PROBABILE L3 PROTEDA	HISTAN PAPIL CHANVILLS TYPE 47	250-265								Ī
PVL3 HPV55	PROBABLE L3 PROTEDY	HISALAN PAPILLICALAVIRUS TYPE ST	33-58							$\frac{1}{1}$	Ī
TVL3 HVS	PROBABLE LI PROTEDI	HUSAN PAPILLOMAVIRUS TYPE SI	13.59	98-114					l		Ī
PVL HVGB	PROBABLE L3 PROTEIN	HIBADA PAPELONA VIRUS TYPE 68	33-50							l	
MLS PAIVE	PROBABLE L3 PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS	30-54								
WY NOW	PROBABILE LA PROTEZIO	RUESUS PAPILLOMAVIRUS TYPE I	49-71							H	
	PROBABILE LY PROTEIN	HUMAN PAPELOMA VIRUS TYPE SB	6.28								
W IEGWO	MONOR CORE PROTEIN LANGUA	REOVENS (177E) / STRAIN DEALING	714-737						-	1	
	MUNCH COME PROTEIN LANGUA 3	ACOVICUS (1 TPE 2) STACIN DISJONES)	714-737	627-622						1	Ī
	I AL MANYEN	THE DATE OF THE TANK AND TANK THE PROPERTY OF THE TANK TH	11.00	30	116 707					+	T
MAN SAME	PROTEIN MI	VACCING VIBILATE AND CORNINGEN		119 106	100			1		1	Ī
VACV	-	VACCINIA VIRUS (STRAIN WE)	63-100	136.144	300-107			1	1	\dagger	T
PVADI VALV	-	VANOLA VIRUS	100	124-142	228.240					\dagger	Ī
PYMI LEOYD	MENOR VIDUON STRUCTURAL PROTEIN MU-2	REOVINUS (TYPE 1 / STRAIN DEAUNG)	141-166	227-245	280-304	324.347	414.436	456-477	ł	-	Ī
PVMI REOM.	•	REOVIRUS (TYPE I / STRAIN LANG)	141-164	227-245	180-304	Т	Т				
PYNO! REDVD	П	REDVIRUS (TYPE) / STRAIN DEARING)	164-192					T	l	t	Ī
Proces REOVO		AEOVIRUS (TYPE 3/STRAIN DEALING)	164-192							-	Γ
PVACE REDVI	MAJOR VIDION STRUC PROTEIN MU-INAU-IC	REOVENUS (TYPE 2 / STRAIN DISJONES)	164-192							İ	Γ
PVAL REOVL	MAJOR VIRION STRUC PROTEIN MU-IMU-IC	REDVIRUS (TYPE I / STRAIN LANG)								-	
PAG REOVO	7	REOVINUS (TYPE) / STRAIN DEARING)	2	521-540							
PYMAT BUSYA	7	BOVING RESMINATORY SYNCYTIAL VIRUS (STRAIN ASINGS)	Т								
WAT BY	MATRIX PROTEIN	CANDA BECOM ATORY CONCYTAL STREET AND AND	148-165	283-309							
200	MATRIX PROTEIN	LA PEDAD-MICHOACAN-MEXICO VIRUS	11:11	201-461				1	\dagger	\dagger	T
PYNAN NEASE	MATRUX PROTEIN	MEASLES VIRUS (STRAIN EDMONSTON)	283.309							\dagger	T
								1	1	1]

MATLIX PAOTEN MA		10. 10. 10. 10. 10. 10. 10. 10. 10. 10.	19-20 19-20 19-20 19-20 19-20 19-20 19-20 19-20	316-310 316-310 316-310 316-318 316-318 316-318						
MA TRUX PROTEIN MA TRUX PROTEIN MATRIX PROTEIN MA	AIN AUSTRALLA-VICTORIAVI31 AIN BELOETTE C41) AIN BELOETTE C41) 15 (STRAIN C3) 15 (STRAIN TOSIIBA) (PV-4B) 15 (STRAIN 64-313) (PV-4B) 17 (STRAIN 64-313) (PV-4B)			116-310 116-310 116-310 106-329 106-329 281-309						$\ \cdot\ _{\underline{\ }}$
WATELY HOOTEN WATELY WOOTEN WATELY HOOTE	AIN AUSTRALLA-VICTORIANI) AIN BEAUDE FITE CAS) (STAAIN CS) (STAAIN TOSIIBA) (PIV-A) (STAAIN TOSIIBA) (PIV-A) (STAAIN TOSIIBA) (PIV-A) (STAAIN TOSIIBA) (PIV-A) (STAAIN TOSIIBA) (PIV-A) (STAAIN TOSIIBA) (STAAIN STAAIN BIKIN) (STAAIN STAAIN STAAIN STAAIN STAAIN STAAIN STA			100-310 100-310 100-310 100-310 100-310 100-310 100-310 100-310 100-310						
MATELY PROTEIN PROTEIN MATERY PROTEIN MATE	MAIN AUSTRALIA-VICTORIA/33) MAIN BEAUDETTE CA/3) 18 (STRAIN C59) 18 (STRAIN TOSHIBA) (PV-3) 18 (STRAIN TOSHIBA) (PV-4) 19 (STRAIN TOSHIBA) (PV-4) 10 (STRAIN TOSHIBA) (PV-4) 10 (STRAIN TOSHIBA) (PV-4) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN) 10 (STRAIN BIKEN)			110-310 110-310 100-329 100-329 100-329 100-328 100-328						
MATTILE PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN	KAIN AUSTRALIA-VICTORIAJIS) AND BEACH COST S (STRAIN COSTIDEA) (PIV-2) US (STRAIN TOSHIBA) (PIV-4) US (STRAIN TOSHIBA) (PIV-4) ETE D) SETE D)			116-330 306-329 306-328 331-309 241-328						
MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN MATTALE PROTEIN EL GL. VCOPROTEIN MOVELMENT PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL PROTEIN MOTETAL P	AAIN AUSTRALIA-VICTORIAJI) RAIN BEAUDETTE CAS) SI (STRAIN TOSIIIDA) (PIV-A) SI (STRAIN TOSIIIDA) (PIV-A) US (STRAIN 40-333) (PIV-AB) RETE O) VETE O) CEPIALITIS VIRUS (STRAIN BIKIN) (RAIABDOVIRUS CANNA) US MED(S) ESTE) OG CS 1) TARN 859			305-329 306-328 311-369 311-369 311-369 311-369 311-369]
MATRIX PROTEIN	ALM BEAUDETTE CASI 15 (STAAIN COSHBA) (PIV-2) 15 (STAAIN TOSHBA) (PIV-4) 15 (STAAIN TOSHBA) (PIV-4) 10 (STAAIN TOSHBA) (PIV-4B) 10 (STAAIN BEA) 10 (STAAIN BEA) 10 (STAAIN BEA) 10 (RHABDOVIRUS CARMA) 10			261-328 361-328 381-309			-			١
MATRIX PROTEIN	18 (STALIN CA) 18 (STALIN CA) 18 (STALIN TOSHIBA) (PIV-A) 19 (STALIN TOSHIBA) (PIV-AB) 19 (STALIN TOSHIBA) (PIV-AB) 10 (STALIN STALIN STALIN BIKEN) 10 (BHABDOVIRUS CAPHA) 11 (BHABDOVIRUS CAPHA) 11 (BHABDOVIRUS CAPHA) 12 (BHABDOVIRUS CAPHA) 13 (BHABDOVIRUS CAPHA) 15 (BHABDOVIRUS CAPHA) 16 (BHABDOVIRUS CAPHA) 17 (BHABDOVIRUS CAPHA) 17 (BHABDOVIRUS CAPHA) 18 (BHABDOVI			383.308 383.309 383.328 383.338			T			
MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN MATTALK PROTEIN EL OL VOOPROTEIN MOVELMENT PROTEIN MOVELMENT PROTEIN MOVELMENT PROTEIN MOVELMENT PROTEIN MOVELMENT PROTEIN MOVELMENT PROTEIN MOVELMENT PROTEIN MOVELMENT PROTEIN	15 (STRAIN TOSIUBA) (PIV-1) 15 (STRAIN TOSIUBA) (PIV-4) 15 (STRAIN 46-333) (PIV-4B) 15 (STRAIN 64-333) (PIV-4B) 15 (STRAIN 64-333) (PIV-4B) 15 (EPIALITIS VIRUS (STRAIN BIKEN) 15 (RHABDOVIRUS CARPIA)			283.309 283.309 263.338						
MATTUR PROTEIN ROTEIN	US (STAIN TOSHIBA) (PIV-4A) US (STAIN 64-333) (PIV-4B) SETE D) SETE D) SETE D) CEPIALITIS VIRUS (STRAIN BIKEN) US WEBUS) ESFE OG CS 13 FRAIN ASP			311.309		İ				
MATRIX PROTEIN	US (STRAIN 64-333) (PIV 4B) VETE 0) CEPIALITIS VIRUS (STRAIN BIKEN) (RHABBOVIRUS CARNA) US MEB 05 TATAIN 439 TRAIN 189			181.309	-	-				
MATALE PROTEIN	SETE O) CEPHALITIS VIRUS (STRAIN BIKEN) (PARABDOVIRUS CADYA) MED STREE STREE CG C3 TARIN AS9 TRAIN AS9			388.309	F					
MATTUR PROTEIN	CEPIALITIS VIRUS (STRAIN BIKEN) CEPIALITIS VIRUS (STRAIN BIKEN) US MEBUS) STRE MEBUS TATRAIN ASP			306-338		 				İ
SENCE MATRIX PROTEIN SENCE	CEPIALITIS VIRUS (STRAIN BIKEN) CEPIALITIS VIRUS (STRAIN BIKEN) US MED(S) ESFE OG CS 1) TARN ASP			204.)28	-		F			
SEPTION AND THE PROTEIN SEVEN SI CA VOOP OT SIN CANAN SI CANAN SIN SIN SIN SIN SIN SIN SIN SIN SIN SI	CEPITALITIS VIRUS (STRAIN BIKEN) (PARABDOVIRUS CARMA) MEBUS) STREE STREE STREE STREE STREE STREE STREEN STREEN			36.33	ŀ					
MATRIX PROTEIN MATRIX PROTEIN MATRIX PROTEIN MATRIX PROTEIN MATRIX PROTEIN E GLYCOPROTEIN				100.32	-	:				
MATRIX PROTEIN MATRIX PROTEIN MATRIX PROTEIN MATRIX PROTEIN MATRIX PROTEIN EL CLAYCOPROTEIN	 			304-328	-					
MATRIX PROTEIN MATRIX PROTEIN EL GA VOOROTEIN EL GA VO	RUG (RIABDOVIRUS CARPIA) VIRUS AIN MEDUS) AIN 2586) AIN 2586) (STRAIN ASP) (STRAIN PRO)									
MATRIX PROTEIN MATRIX PROTEIN II GLYCOPROTEIN II GYOTE	RUS (RHADDOVIRUS CARYA) ANN US ANN MEDUS) ANN 1296) ANN 1296) ANN 1296) ANN 1296) (STRAIN AS) (STRAIN AS)	5 5			-,				- 1	_]
EL GLYCOMOTEIN EL GLYCOMOTEIN		55 55			-				1	
EI GAYCOMOTEIN		33			•		1	İ	1	
II GLYCOPROTEDM II GLYCOPROTEIN II GLYCOPROTEIN II GLYCOPROTEIN PRECINSOR II GLYCOPROTEIN PRECINSOR II GLYCOPROTEIN PRECINSOR II GLYCOPROTEIN II GLYCOPR		25	137.161	171-190			1	1		
II GLYCOMOTEIN EI GLYCOMOTEIN EI GLYCOMOTEIN PECUASOR EI GLYCOMOTEIN PECUASOR EI GLYCOMOTEIN PECUASOR EI GLYCOMOTEIN PECUASOR EI GLYCOMOTEIN					1	1		1	1	
EL GLYCOMOTEIN EL GLYCOMOTEIN EL GLYCOMOTEIN PRECINSOR EL GLYCOMOTEIN PRECINSOR EL GLYCOMOTEIN PRECINSOR EL GLYCOMOTEIN PRECINSOR EL GLYCOMOTEIN		1	Š	137.161	1	1	1	1		
EI GLYCOMOTEIN EI GLYCOMOTEIN MECHASON EI GLYCOMOTEIN MECHASON EI GLYCOMOTEIN MECHASON EI GLYCOMOTEIN		10.37					1	+		
EI GLYCOMOTEIN PRECINSOR EI GLYCOMOTEIN PRECINSOR EI GLYCOMOTEIN		10.37			-		1	1	T	
EI GLYCOMOTEIN PECINSOR EI GLYCOMOTEIN		Т			1	1		1		
I II CANCOMOTEIN MECINSOR II CANCOMOTEIN	PORCINE THANKAISSIBLE GASTROEVTERITIS CORONAVIRUS (STRAI	160-160	14-16)	1	1			1	T	
II I IL YCOMOTEN II GLYCOMOTEN II GLYCOMOTEN II GLYCOMOTEN II GLYCOMOTEN II GLYCOMOTEN II OLYCOMOTEN IIOVENT ROTEN IIOVENT ROTEN IIOVENENT ROTEN IIOVENENT PROTEN IIOVENENT PROTEN IIOVENENT PROTEN	JACO (STRUM MAY)	T	171.611	90,14	T		\dagger			
IS I CLYCOPATOREN EI	TURKET ENTEREC CURKEN VIAUS						T			
ET GLYCOPADTEIN ET GLYCOPADTEIN ET GLYCOPADTEIN FOGABLE EKSERANE PROTEIN FOGABLE FROTEIN FOGYELET	DETTE:	74-101			F		T	Ī		
ELOUVOMOTERN MOVEMENT MOTERN MOVEMENT MOTERN MOVEMENT MOTERN MOVEMENT MOTERN MOVEMENT MOTERN MOVEMENT PROTERN	1	74-101								
MONTALE MEMBLANE PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN	Ť	74-98						П		
MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN		Ħ	178-203							_]
AGVENENT PROTEIN AGVENENT PROTEIN AGVENENT PROTEIN AGVENENT PROTEIN	[41]	П	147.164	167-791			1			
HOVELENT PROTEIN HOVELENT PROTEIN HOVELENT PROTEIN		1	103.164	107-701			1	1		
MOVEMENT PROTEIN MOVEMENT PROTEIN MOVEMENT PROTEIN	CALLET OWER MOSAIC VIRUS (STRAIN BBC)	Ť	3	R			†	1	T	
MOVEMENT PROTEIN	100			200		1		T	Ī	
MOVEMENT PROJECT		Т	2	102.03						
		T								
MOVEMENT PROTEIN	1	1113:111	160-181 180-181							
			371-298						1	
MAJOR SURFACE ANTIGEN PRECURSOR	DUCK HEPATITIS & VIRUS (BROWN SHANGHAI DUCK ISOLATE \$1)	П	£				1	1	Ī	
MAJON SUNTACE ANTIGEN PRECURSOR	T	Т	268-794	1			1	†	T	
MAJOR SURFACE ANTIGEN PRECURSOR	DUCK HEPATITIS B VIXUS	20.15	231-237		T	1		\dagger	Ī	
MAJOR SURFACE ANTIGEN PRECURSOR	INCHAI COCK ISOLATE STIT	T.	231.765	180.105	T		1			
WHOSE INCHES SUIT ALE ANTIHORN THE UNSOR	MEDIN MEDINATION VIEW	Τ	201.130		Ī					
PARTY HERE MAKES SUBSICE ANTICENTAL CONSON		Г	200		Ī	T				
MANNE SIMPACE ANTICEN PRECURSOR	(SUBTYPE ADW2)	185.202	344.370							
LAND CIMPACE ANTICEN PRECURSOR		Г	344.270							
MAJOR STREACE ANTIGEN PRECUNSOR	STRAIN 991)									
MAJOR SURFACE ANTIGEN PRECURSOR	AI)	_	235-239				1	1		
MAJOR SURFACE AVITOEN	- 1	2	g		1		1	1		
PYNESA SPRYL MAJOR STREAMS ANTIGEN PRECURSOR	HEPATITIS BY VICTOR (SCHOOL AND A STRAIN INDURES INTO WASO)	ı	911.310	1			1			

INCERNE	Prochase	All Vivan (Ne Becierlesbases)				Ī			-	\mid	Γ
PILE NAME	PROTEIN	VARUS	ARCAI	AREAL	AREAJ	AREAD	AREAS	AREAS	AREA? AF	AREAT	AREA?
PYACSA HEBYL	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIRUS (STRAIN LSH / CHIMPANZEE ISOLATE	134-191	652-562		1				П	
PWKKA HPBVN		HEPATITIS B VIRUS (SUBTYPE ADR / STRAIN NC·1)	₽.:	8.2							
PYACKA MOBYO		HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN OKINAWARODW202)	174.191	233-259		-				-	
	MAJOR SURFACE ANTICEN PRECURSOR	HEPATTIS B VIRUS (SUBTYPE ADW / STRAIN PHILIPPINOTEDW294)	207.501	244-270		1				+	Ī
100 A		REPATTICE VIEW (CIRTINE AR)	2	200		ľ			+	+	
PVACA HOBVW	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIRUS (\$UBTYPE ADW)	134-191	233-259						†•	Ī
		HEPATITIS B VIRUS (SUBTYPE AYW)	134.191	233-239			İ	Ī		_	Ī
		HEPATITIS B VIRUS (SUBTYPE ADYW)	174-191	33)-159		·					
П	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS I	207.134	166-243	178-393	·					
PACK WINS	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS 59	212-239	274.200	393.398						
	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHACK MEPATITIS VIRUS 7	212-239	274-298	183-398						
PWCA WIN	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHLCK HEPATITIS VIRUS I	212-239	24.70	383-398	·	-	:	-		
		WOODCHLCK HEPATITIS VIAUS & (INFECTIOUS CI.ONI;)	212-239	274.298	383-398						
PWGA WHYWA		WOODCHUCK HEPATITIS VIRUS WER (ISOLATE PWS2)	125-149	234.249							
		DATUENZA A VIRUS (STRAIN AANN ARBORAGO)	25.46			-				1	
WITH THE	MATRUX (MA) PROTEIN	INGLUERZA A VIRUS (STRAIN ABANGROWITY)	25-46			•				1	
Т	MATRIX (MJ) PROTEIN	INCLUENCA A VINUS (STRAIN AFORT WARELATING)				7				1	
TAN TAN	MAINIX (NO) MOIEM	THE LUCK A VIKUS (STRAIN ATOML PLACUE VIKUSRUS TUCK)				1		1		+	
Т	MACINIA (MU) THUI BLA	INCLUDES A VINUS (STRAIN AND METANOS VINUS WETBADOS)	27.67			1	1	1	1	+	I
Т	MANUAL MA	INCLUSIVE A VINOS (STRAIN AN ENTRE AND AN ENTRE AND AND AND AND AND AND AND AND AND AND	1			Ī	1	1		\dagger	Ī
_	MATRIX CON PROTEIN	DELIENZA A VIRUS (STRAIN AAALI ARDAEW YGRKA79071)					Ì	Ì	+	\dagger	1
PWATZ IAPA	MATRIX OCH PROTEDI	INFILIFICA A VIRIUS (STRAIN APPERTO RICOVICA)	1			ŀ	1	Ī		\dagger	
PANTE LASON	MATRIX (MD) PROTEDA	INTLUDICA A VIRUS (STRAIN ASDIGAPORE/1/31)	***			Ŧ	T	1	+	\dagger	Ī
PWATE LAUDO	MATRIX OAT PROTEDI	DOTUBLIZA A VIRUS (STRAIN AUDORINIO7/12)	37.44			l				\mid	T
PWATE TAWAL	MATRIX (P.D.) PROTEIN	BUTLUENZA A VIRUS (STRAIN AWILSON-SMITHO))	25.46			-	T	Ī		+	
PVACTO MYXVL	INT-5 PROTEIN	MYXOMA VIRUS (STIAIN LAUSANNE)	226-241							-	
l	NONSTRUCTURAL PROTEIN NS34	BOVINE ROTAVÍRUS (GROUP C / STRAIN SHINTORU)	334.351			·				H	
PARTY PAST	16 7 KD PROTEIN	POTATO VIRUS & (STRAIN PERUVIAN)	25								
	NB CLYCOPIOTED	DOLLUZAZA B VIRUS (STRAIN DOELIING/IAT)	13.39			7					
PVNS DEDG	NB CLYCOPROTEIN	DOLLERZA 8 VIRUS (STRAIN BHONG KONGA71)	-			-					
TANG DIELE	NB CLYCOTIONER	INCLURACE B VIRUS (STRAIN MALE/40)								1	
PAN DES		DOT TOOLER WINDS (STRAIN BALENI MANUE)								+	T
WG PANO	NB CL YCOPROTEIN	INFLUENCA B VIAUS (STRAIN BAEMPHISTARS)	97.13			T	Ì	Ī		\dagger	
PVNB DOOR	NB GLYCOPROTEIN	DIFLUENZA B VIRUS (STRAIN BYOREGON'S/10)	97.78			T		T		+	T
PWCS ADVO	NONCAPSID PROTED/ NS.1	ALEUTIAN MINK DISEASE PARVOVIRUS (STRAIN G)		169-190						-	
PANCE AEDEV	NONCAPED PROTEIN NS. I	AEDIES DENSONICCI EOSIS VIRUS (STRAIN GKV 002 002) (AEDES DENS	635.690							H	
PANCE PANCE	NONCAPUL PROTEIN NC.	HAAKSTER PARVOVIRIS HI	100.16		+	1	1	1	1	1	
PYRS) ALSY4	NOWSTRUCTURAL PROTEIN NS!	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 47 STRAIN VACCINE)	275-272		\dagger	Ť	T	Ť		$\frac{1}{1}$	
PYRSI GALA	NOWSTRUCTURAL PROTEIN NS!	INFLIEDZA A VIRUS (STRAIN AALASKANIT)	3:5	114-117	167-192	Ī	T	T		\mid	T
Т	NONSTRUCTURAL PROTEIN NS	Delleca A Virus (Strain Alaba Arbotana)	31.30	114-137	167-197					$\ $	
WISH MCAG	MONSTRUCTURAL PROTEIN NS	INTELLERY A VIRUS (STRAIN ACAMELINGUECOLIANZ)	10.00					1			
L	NOWSTELL TIME A PROTECT AS	DEL GENZA A VIBIIS (STRAIN ACHICERMERIAN VALVO)	2 5		74.147	1	1	1		\dagger	Ī
Т	INONSTRUCTURAL PROTEIN NS!	DELLENZA A VIXUS (STRAIN ACHICKEN/JAPANZA)	28.43	1	1		1	1	+	+	
	NONSTRUCTURAL PROTEIN WSI	DIFLUENZA A VINUS (STRAIN ADUCKVALBERTAKO76)	31.50	167.192		T	1	1	$\frac{1}{1}$	\dagger	T
PVNSI LADEI	NONSTRUCTURAL PROTEIN YSI	INTLUENZA A VIRUS (STRAIN A/DUCK/ENGLAND/1/36)	28-47	3	T	T	<u> </u>	Ī	-	+	T
PYNSI MDUJ	NONSTRUCTURAL PROTEIN NSI	INFLUENZA A VIRUS (STRAIN A/DUCKAUKRAINE/1/6))	26-47	164-189			T	T		-	
PVNSI IAFOM	NONSTRUCTURAL PROTEIN NS!			114-137	167.192					-	
PVNSI IAFOW	NOWSTRUCTURAL PROTEIN NSI	INFLUENZA A VIRUS (STRAIN AFORT WARRENIYSO), ANDISTRAIN A		14-13	167-192					H	
PVISI IAPR	INCASSINCE UNIVERSITY OF THE PROTECT			167-192						\parallel	
PWRI MED	NONSTRUCTURAL PROTEIN NS	DOLUMA A VIRUS (STRAIN AA ENINGRADAM)	2 5	14.113	7 (a)	1	1	1	1	+	T
PWS1 LAMA6	NONSTRUCTURAL PROTEIN NS!	(TA/18/76)		167.197	7.1.70	Ť	†	†	1	+	1
		1	1		1	1	1	1	1	$\frac{1}{2}$	7

MCENE	Priceize	All Viruses (No Bacteriophoges)			П		П		П	л	
FILERAME	PROTEIN	VIRUS	ANTAL	785	ARTAL	AREA	2424	1	1	4	1
PVNSI IAMAN	MONSTRUCTURAL PROTEDNIS!	INFLUENZA A VIRUS (STRAIN AMALLANDMEW YORKA 15071)	21.50	167.192		4					1
PYNSI IAMAO	HONSTRUCTURAL PROTEIN NS!	DOLLIENZA A VIRUS (STRAIN AMALLARDMEW YORKWI7471)	<u>.</u>	167-192						1	
PVNS1 JALMYN	NONSTRUCTURAL PROTEDY YS!	DOT UENZA A VIRUS (STRAIN AMYNAWAANEDA-THAV76)	28-47	<u>5</u>		.				1	
PWSI MB	MONSTRUCTURAL PROTEDNINS!	DIFLUENZA A VIRUS (STRAIN APINTAIL/ALBERTA/11979)	167-192								
MASI JANII	HONSTRUCTURAL PROTEDY NS!	INTLUENZA A VIRUS (STRAIN APINTAIL/ALBERTA/131/79)	31.50	167-192		1					1
PWRI LAND	MONSTRUCTURAL PROTEIN NS!	DOLUMENZA A VORUS (STRAIN APINTAD/ALBERTA/261/78)	8 :	107.197	1					Ť	T
PVACSI LAPUS	NONSTRUCTURAL PROTEIN NSI	DIFLUENZA A VIRUS STRAIN APINTALIALBEATA/15079)	2.5	74-70						1	T
WASI LANUE	MONSTRUCTURAL PROTEIN NSI	INTLUENCA A VIRUS (STRAIN APUERTO INLUMBA)	2			-				Ī	T
PARSI LATES	MONSTRUCTURAL PROTEIN NSI	INTLUENZA A VIRUS (STRAIN ATURAR TARE INTERIOR - CLILI 1/1972-6	2 2		1	1				T	T
MAGI LATRC	MONSTRUCTURAL PROTEIN NSI	INPLUENCA A VIRUS (STRAIN AT UNKETA ANALARI)			1	-				T	T
WIGH WITH	NONSTRUCTURAL PROTED/ 1/51	DIFLUENCA A VIRUS (STRAIN ATURIXE YORECONTI)	S-1			-				1	
PVNGI LATAS	NONSTRUCTURAL PROTEIN NS!	INTELLEDIZA A VIRUS (STRAIN A/TERNISOUTH AFILICARI)	28.73							1	Ī
PWG! LATRY	MONSTRUCTURAL PROTEDY MS I	INSTLUENZA A VIRUS (STRAIN A/TENATURIX)	R:	167-192						Ì	
MASI IAUDO	HONSTRUCTURAL PROTEIN NS!	(DELLIEDZA A VIRUS (STRAIN ALDORWOOTT)	9	14.13	167.192	1				1	
SSTYT ISAM	NONSTRUCTURAL PROTEIN NS:	INTLUENZA A VIRUS (STRAIN AUSSAMOTT)	8	1	167:192	-				1	
PVICE LAZII	NONSTRUCTURAL PROTEIN NSI	DOLLIENCA A VIRUS (STRAIM ASWINGAOWA/1930)	35.50	167.192		-					
PYCH BICAA	NONSTRUCTURAL PROTEIN NS!	INGELUENCEA C VIRUS (STRAIN C'ANN ARBONVISO)	222.248			=					
PWSI NCCA	NOWSTRUCTURAL PROTEIN NSI	INFLUENCEA C VIRUS (STRAIN CYCALIFORMIA/18)	222-348		1	4				1	I
PVNS2 BTV10	NONSTRUCTURAL PROTEDNINGS	BELIETONGLE VIRUS (SEROTYPE 10/150LATE USA)	145-16		1	+				1	
PUNES BTV17	NOWSTRUCTURAL PROTEIN NS2	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	167161			•				1	Ī
PANES BYVIS	MONSTRINCTURAL PROTEIN MS2	BLUETONGUE VIXUS (SEKOTYPE I / ISOLATE SOUTH AFRICA)	103-101		1	-					
1	HOMSTRUCTURAL PROTEON NS2	BLUETONGUE VALUS (SEKOTYPE 10)	143-161		1	1			†	1	Ī
_	HONSTRUCTURAL PROTEDNINGS	EPIZOOTIC HEMORIAHAGAC DISEASE VIRUS (SEROTYPE 27 STRAIN AL.								1	Ī
	MONSTRUCTURAL PROTEIN NS2	DELUEZA A VEUS (STRADA APUERTO IUCONO4)	2		1					1	T
یاو	MONSTRUCTURAL PROTEIN NS2	DOLUEYCA A VIIIUS (STRAIN AT ELINSOUTH AFRICANT)			Ť	1				1	Ī
- 1	NOWSTRUCTURAL PROTEIN 1	PREUMONIA VIXUS UP HOUS			1	1				T	T
L	NOWSTRUCTURAL PROTEIN 1-1	PORCERS INANSMILLE DAS INDEMIES CONORA VIAUS (STRAI			Ī	1				Ť	
PWRS CVIEW	MONSTRUCTURAL PROTEIN 1-1	TURCATE INCOMESSION CONSTRUCTOR INCOMESSION CONTRACTOR (STRONG				-				T	
PUNE CARD	MONSTRUCTURAL PROTEST AND	Inches States value	9			-				İ	Ī
2	INCOMENCE IN THE ALL PROFITED A	HIBAAN CORONAVIRUS (STRAIN 229E)	814			F				Ī	Γ
.1	MONSTRUCTURAL PROTEIN 4	MURDING COROMAVIRUS AGIV (STRADAS)	17.30								
Ι.	HONSTRUCTURAL PROTEIN 4	PORCENS TRANSPOSSIBLE CASTROENTENTIS CORONAVIRUS (STRAL	16-31								
DE LO	HONSTRUCTURAL PROTEIN 4	PORCINE TRANSMUSSIBLE GASTROEVTEATES CORONAVIAUS (STRAI	1431								
PVNSA CVMUA	HONSTRUCTURAL PROTEIN 4	PORCEME RESPONDED CONONAVENUS (STRAIN EAR)	17		1			1		1	
WAST MELY	NONSTRUCTURAL PROTEIN PSA	MALLE STATE VIAUS		8 95	1					T	
700 Jan	MONSTRUCTURAL PROTEIN 554	FEI ING ENTERIC CORONAVIRUS (STRAIN 79-1681)	7 5	į						T	Ī
Valle Priva	NONSTRUCTURAL PROTEDY 7	FELLING INFECTIOUS PERITONITIS VIRUS (STRAIN 79-1146)	35								
PVICE MILE	NONSTRUCTURAL PROTEIN C	HIDAAN PARATHTUENZA I VIRUS (STRAIN C) S)	76-97								
PWSC PILIFIC	NONSTRUCTURAL PROTEIN C	HUBALM PARADALUENZA I VIRUS (STRAIN C19)	76-92								
PWSC MIND	NONSTRUCTURAL PROTEDIC	HEIGHAN PARAINGLUENZA I VIRUS (STRAIN CH.S/?))	76-92	179-197						1	
PVIC MIKE	NONSTRUCTURAL PROTEIN C	HUMAN FALAING LUENZA I VINUS (STRAIN CHIVES)	70-92		1					1	
TANKS CARE	LANGE THE ALL PROTEINS NOT NO.	INCLUDIZA C VILIS (STRAIN COREAT LAKES) 167/41	223.348							\dagger	T
1	MONSTRICT BAL PROTEDIS NSI-NS2	DITLEDIZA C VIDUS (STRAIN CYCHANGSBURG) MA	222.348	Ī	T					T	Ī
PVNST DICAG	NONSTRUCTURAL PROTEINS NSI-NS2	BOLUEKZA Č VIRUS (STRAIN CAUSSISSIPURO)	222-348								
PYNST_BICYA	NONSTRUCTURAL PROTEDMS NSI-NS1	DIFLUENZA C VIRUS (STRAIN CYAMAGATA/1001)	222-348								
PVNST PTPV	HONSTRUCTURAL PROTEDINS.S	PUNTA TORO PREBOVINIS	3								
PVNST STSV	NONSTRUCTURAL PROTEIN NS-S	SAMPLY PEVER MULIAN VIRUS			1					\dagger	T
rwst uuk	NONSTRUCTURAL PROTEIN NS-S	UNACUMENT VINCES	52.73	101	1					1	Ī
PANCA PRIVA	7	International Value (STRAIN MAILS)	137.176	1363-1363	1					\dagger	
PANIE FROM	NECTEOPROTEIN	EBOLA VINUS	139-176		T	T		Ī		T	Ī
PVNUC LANA	Т	DIFLUENZA A VIRUS (STRAIN AVANAS ACUTAPRIMORJEM99776)	173-197	266-287							
PVNUC LADYN	_	INTLUENZA A VIRUS (STILAIN AANN ARBOINGGO)	173-197								
PVNUC IMBIA	NUCLEOPROTEIN	INTLUENZA A VRUS (STRAIN ABRAZIL/11/18)	13-15]		1	7

		And Water State St		-					-	Γ
PA P MANT	PERMIT	VIRUS	AREA! AREA!	1 ABEA1	AREAI	AREAS	AREAS	AREA? AR	AREA & AB	AREA?
PWAC MAUD	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ABUDGERIGARMOKK AIDOVI 71)	133.187						-	Ī
PWINC LACAL	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ACALIFORMIA/10/18)	13.197	-					+	
PVAUC LACKO	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ACHICKENGERMIANYAVI9)	137-187	1	-				+	Ī
PWILL MOKE	MUCLEOPROTEIN	INTELENZA A VIRUS (STRAIN ACHICKEMPENNSYLVANIA/I/B))	13)-167		\downarrow				+	
PYRUC INDAU	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCK/AUSTRALIA/149/10	133-197	1				1	†	
PYNUC INDBE	HUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCKBELINGINE)	10.17	+	1				†	T
ZACC PECS	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADDUKACZECHOSLOVARIANO)	171.107	+	1			1		
PARC LADE	MUCLEOFICIENT	INTELLECTOR A VINUS (STRAIN AND CENTRAL AND HAS)	197-161	 -	-				l	Ī
THE PARTY	INCLEUMNO CLIN	INFI (FRIZA A VIRIS (STRAIN ADICKAIONG KONG773)	133.167			L			-	
N	TAIN PORTOTORY	INTELLEMENT A VIBER STRAIN ACTIONAL PROPERTY SANDER	13:167		-				-	
TANK TANK	MACCOMOTENA	DELIENZA A VIREN (STRADA ACHICICAANITOBALIS))	193.197	-						Γ
PVAIC LABAZ	MACH FORBOTTEIN	INPLUENZA A VIRUS (STRAIN ADUCKARW ZEALANDY) (76)	173-197		-					
PWAIC LADIN	MAICH EOPROTEDA	INFLUENZA A VIRUS (STRAIN ADUCKAIK RAINE 2560)	193-197		•					
PYNUC IAENS	MUCLEOPROTED	INFLUENCA A VILUS (STRAIN AENGLANDVIMS)	187-181		1					
PVAUC IN ON	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AFORT MONMOUTH/1/47)	193-197							
PWILC LABOW	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AFORT WALREWISO)	133-197		-				\dagger	1
PWACE LATE	NUCLEOPROTEIN	INFLUENCA A VIRUS (STRAIN AFOWL PLAGUE VIRUS/DODSON/DUTG 173-197	173-197						1	
PYNEUC LAFTE	NUCLEOMOTEIN	INSTLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIAUS/ROSTOCK))	137-197						1	
TYNUC MORE	NUCLEORGOTEIN	INTLUENZA A VIRUS (STRAIN AGREY TEAL/AUSTRALIA2/79)	17)-197		?				\dagger	T
PWRUC IAGUI	NUCLEOPROTEIN	INTLIENZA A VIRUS (STRAIN AGULLMARYLANDVS77)	173-197						+	Ī
	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AGULLMARYLAND/00/7)	175-197							T
PYNAUC LAGAIN	NUCLEOFROTEIN	DOPLUENZA A VIRUS (STRAIN AKKILLARARYLANDVISTATI)	173-197			-			1	I
PYNUC LACTA	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AGULLMARYLANDVIBIS/79)	17.197	1	1				1	Ī
PWADE INGUA	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AKKIL/ASTRAKIIAN227/84)	172-197						1	Ī
PVNUC MOUSE	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ACULLMASSACHUSETTS/2010)	111-111						\dagger	T
PYNUC JACUN	NUCLBORNOTEIN	DOTUTERZA A VINUS (STRAIN AKKILLAKINMESOTAMAKA)	172-197	+	7					T
WICE TARC	NUCLEOPROTEIN	DOLLDENZA A VIZUS (STRADA AMBCRUXAM)	137-137			1			1	I
PYNC MET	NUCLEOPROTEIN	DOLUCIAL A VIXOS (STRAIN ARCADINES/ILLINGTON)	147.103		-		I		l	T
WALCO LANGE	MULIEUTION	INTELLIGIAL A VIEW (STRAIN AFCRIME ACTION AND A CONTRACTOR AND A VIEW AND A STRAIN AND A STRAIN AND A STRAIN A	10.10	1	ľ					T
PVRICE INST	MULEURO EMPOREM	THE LESS A VIEW COME AND A MOND IN CONCURS.	172.107	-	†				t	
	MULEUROI EIN	INTELLEGISTA A CHELLE CENT A MANAGER CONTRACTOR	171.107	-	-	-			l	T
TANK MAG	NUCLEURING EIN	CARTIENT A VINITE RETEATE AND A PORT MARCH A COST CART	171.107	-	1				T	Ī
TYPEC MOR	NUCLEOTICS IEDA	THE TENNEY A VINING STRAIN AFORD STREET TOWNS (SEP) SAME	133.107	1	-	-			t	Ī
100 MAIL	WALCHEST TOWN	INGITIBILITY A VIRUS (STRAIN AIKIEVISOTO)	171.107			L			-	
PAGE LATES	NEICT POPEOTEIN	DOLLIERZA A VIRUS (STRAIN ALENINGRADISMI)	173-197		L				 	
PVAILE TALKAA	+	DELLENZA A VIRUS (STRAID AMALLARDASTRAKHAN24492)	141-671							
PARIC WAS	-	DIFLUENCA A VIRUS (STRADI AMALLARDINEW YORKA?SO79)	193-197							
PWALE LAND!	-	DOLLENZA A VIRUS (STRAIN AMINIK/SWEDENIW)	133-197	1					1	
PVNUC LUNTS	NUCLEOPROTEIN	DATILIENZA A VIRUS (STRAIN ANTRONS)	13:13	-					+	T
PVNUC LAONE	NUCL EOPROTEDI	INFLUENZA A VIXUS (STIZAIN ACHIONATI)	191.17						1	T
PWICE LAPAR	NUCLEOFICIEN	INCLUENZA A VINUS (SINAIN AFRANCI (ALI SINAI)	100.00						1	T
TANK MAN	NOCLEGIFICATION	CALLEY A VINIS (STRAIN ARITHMY TIRMSTONEMERS EVAN		1	ļ				1	Ī
PANAL PARE	March Edge Orten	DOTTENZA A VILUS (STRAIN ASEALAKASSACHUSETTS/1/10)			-				l	Ī
WATE LABO	MUCI EDMOTEIN	INFLUENZA A VIDUS (STRAIN ASHEARWATERVAUSTRALIA72)	133-193		L					
PVOUC LASIN	NUCLEOPROTEIN	INGLUENZA A YIRUS (STRAIN A/SINGAPORE/1/57)	181-181							
PVNUC LATE	MUCLEOPROTEIN	INFLUENCA A VIRUS (STRAIN ATEALACEL AND/2010)	173.197		Ц	Ц				
PVNUC LATICA	MUCL EOPROTEIN	INFLUENZA A VIRUS (STRAIN A/TURKEYAIINNESOTA/1661/81)	173.107						1	
PVAUC_LATKO	NUCLEOPROTEIN	INSTLUENZA A VIRUS (STRAIN ACTURICEY/ONTARIO/1) 2/66)	19.101							
PWILL LATES	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/TERN/SOUTH AFRICA®!)	173-107						1	1
PYNUC LATRY	NUCLEOPROTEIN	INTLUENZA A VIAUS (STRAIN ATERNATURKAIENIA/1972)	11:10					1	+	
PWOC LATX?	=	INTLUENZA A VIRUS (STRAIN A/TEXASIA)	137-187							
TYPE AUDO	-	INPLUENCA A VINUE SETA AND A CHECKEN MOUNTY	131-147		\downarrow				+	
PVAUC IAIRS	NUCLEOWOTEN	DOLUEZZA A VIRUS (STRAIN AUSSINGOV)	177-187	+	1	1		+	+	Ī
TYNC IN	- Control Con									1

		All Manager (No Decisionhoper)	П	П	П		Т	ABEA ABEA 9	A A B F A B	ABEA 9
PCCENE			I	25.2	o rose	4	2000	1	Т	Т
FILENAME	PROTEIN	ENZA Á VIRUS (STRAIN ÁMHALEAIAINEDIMA)	137-187	†	1	1	T			-
PWALE LAWOR	WOLLECT ROLL CAN	(NIPOS)		1	\dagger	1	T	-		
WALL LAWR	AND EXPERIENCE	1		\dagger		1	T			2
PVICE LAWIE	Wast Edwards th		A COL	1	t	T	Ī	-	_	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	INICIA POR OTREAT		W-17	1	Ì		İ			
TANK TANK	METEOROTEM		100	T	T	Ī				
VOLVE TANK	MIXTEONIOTEN .		131.103	T		Ī				
	NUCL ECHLOTEIN	DOLUENZA A VIRUS (STIAIN ASWINDOLINIAN 1720)								
1	MUCLEOPROTEIN	DELUCIZA A VIRUS (STRAIN ASWINERIONG RUNGS 16)	191	İ		-	<u> </u>			!
PVMIC LAZHS	NUCLEONACTED	DELLENZA A VIRUS (STRAIN ASWINIJIERINI, KIRMINIZIERE)	100	İ	†	I				
PVARIE IAZII	MICHEOPROTEIN	DELLEYZA A VIRUS (STRAIN ASWINEROWATS)		T						-
1167	NACH EGPEOTEDA	NOTUENZA A VIAUS (STRAIN ASWINEROWAII?)		T		ŀ	İ			
1107	Line of Forecomen	HELLENZA A VIRUS (STRAIN ASWINEMOW AND)		T		•		-		
TI VI NOTE OF THE PARTY OF THE	Mary Soveoften	INFLUENCA A VIRUS (STRAIN ASWINEATAL YAJWIV)	101			ŀ				
11611		RELUENZA A VIRUS (STRAIN ASWINE/)AMESRURGA?)				-				
VIVE VIEWS		INGLUENZA A VIRUS (STRAIN ANSWINGANAYON)		T		ŀ				H
TANK TO SERVICE		DOLUENZA A VIRUS (STRAIN A/SWINE/NETICEALANI) S/ 1,003)								
POPE LEDON	-	DELUENZA A VIRUS (STRAIN ASWING/UII)			İ	- 				
WAY TANK	-	DOLUCIAZA A VIRUS (STRAIN ASWINE/WISCOMSING)			T	ŀ				
PARK LATERS	•	DOLUDIZA A VIRUS (STIAIN ASMINE/WISCONSINGIA)	374.258							-
PANE BRAC	4=	DELIDIZA B VIIUS (STIAIN BANKA AMONINA INCOME INCOM	314.318			•				$\frac{1}{1}$
PVIRIT BALL	•	DELUENZA B VIRUS (STRAIN BARIN ALLICATION) (MILLO-1172)	314.318							
1	+-	DOLUENZA B VIRUS (STRADY BALEDAD)	374.34							4
WATER BORK	•	DOLLENZA B VIRUS (STRAIM BASIMOA POREZZZO 19)	Ţ	100		-				-
WATE WANT	_	NAMBURO VIRUS (STRADY MUSORE)	T	5						
SVERE LABOR	•	MANBURG VIRUS (STRAW POPT)	,	347.263	136-150	-				_
VACOR	•	VACCINIA VIRUS (STRAIN CUPEMIANEM)	Τ	Т	334-358					
VALUE VALVE	PLOTEDIOI	VALOCA VIRUS	Τ	Т						+
VOL 170V	133 KD PROTEIN	POXTAIL MOSAIC VIRUS		01010		-				+
PVOR! BOVY	IN KED PROPERIO	MARCHSONS MOSALC VIALUS	Ť	9001-986	1351.1270	1803-1980				-
PVOR! PVAGE	11) KD MOTEIN	POTATO VIRUS M (STIPATO ROBINIAM)								+
SWI MA	233 KB PROTEIN	FOTATO VIALUS SUSTEMINI PENDUNANI	1	374.256	201-301	1010-1030				+
PVOR! PVX	145 KD PROTECH	FUIATO VIRUS A	Γ	35.35		185.404	1010-1030			+
WON! MAD		POTATO VINUS A (STIMON CT)	Г	234-356	306-322	1010-1030			-	$\frac{1}{1}$
WOR! MOD	165 KD PROTED	POTATO VILLO A (STINAIN ACT)	L	135-175					1	+
PVORI BANEA	150 KD PKOTEIN	OS STANDELLE MAN TELLO TOTALO MAN AND AND AND AND AND AND AND AND AND A	131-146						1	+
PVORT WOW	FVORT WOWN 147 KD PROTEIN	WHILE CLOVER MOTOR CONTINUES (STRADE)	Г	606-430					1	+
PVOR! WOWD		LINE SECUMENT (A PARTE (STRADA II)	424-446	442-426	\$\$1.575	28-55	1031-1072			1
PVPO JEVSA	PROBABLE MENGRANE ANTIGEN 3	ATTITUTES A PALE IS DENICA NUCLEAR POLYHEDROSIS VIRUS	4-36	42.59					+	+
PVP10 NEVAC	PIO PROTEIN	CALONIA PSELIDIOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	4-31							ł
DAMIO MANO	PIO MOTOR	SPODOFTELA EXIGUA MUCLEAR FOLYNEDROSIS VIRUS (STRAIN US)			Т				+	╁
	FIG FIGURES	BLACK STREAKED DWARF VIRUS	31-49	£	103-126		1999	****		ł
	PROTECTION AT MACHEN PARTIO	WOUND TUNOR VIRUS (WTV)	٦	267-201					1	+
	POTENTIAL CONTRACTOR AND	5475	837-478	174-1165					1	
A PART	THOUSAND A SERVICE AND DAY MATUR PROTEI			34.364				+	-	+
	THOSE CLICATED ASSESSMENT A NATIONAL MATUR. P.		77-101	133-140	200-210					1
MAIS HOW	THOSE CANDINGS AND THE MATTER IN	HEMPESVOUS SADAGO (STRADA !!)	201.765						-	1
PVP 19 HSVSA	ALCO CAND ASSEMBLY AND THAT MATTER PROTEIN		Ī						-	1
DVZV SI AVA	CATSU ASSESSED AND CASS PERCITE SOR	SULFOLGEUS VIBUS-LIKE PARTICLE SSVI	53							-
W1 2W	Т	ARTICHOKE MOTTLED CHOKLE VIRUS	345						1	ł
	Т	CUCURAREA NECROSIS VIXUS	ş							ł
A	٦	CYNOBIDION RINGSPOT VIRUS	663					1		+
A STATE OF	COME PROTECTION P.3.	TOMATÓ BUSHY STUNT VIKUS (STRAIN CHERRY)	600						-	+
	7	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	141-165	187-201	707-107				-	ŀ
TIVE INVESTIGATION	Т	HEAVES SIMPLEX YOLUS (TYPE I / STRAIN 17)	197-220						-	H
TO STATE OF	PROBABLY CAPED PROTEIN VP33	HEAPES SDOPLEX VIRUS (TYPE 6/ STITATIN UGANDA-1102)	200							

N. C. C.	412 12-214	All Virges (No Beteriophages)		П	П	\Box	П	(-1	П	\mathbf{T}	
FILE HAME	PROTEIN	YIRUE	1434	4 10380	44.8	N	3000	1	7	Ť Į	1
OVZV LITAVI	PROBABLE CAPSID PROTEIN VP23	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	201	73.47		1	Ť				
PVP26 NEVAC	P26 PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYTEDROSIS VIRUS	1	Т		1			T	T	Ī
MAN ANSVA	OUTER CAPSID PROTEIN VP3	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4/STRAIN VALCINE)		767.90	1	97.00	T			ŀ	
PVP2 BTV10	OUTER CAPSID PROTEIN VP2.	BLUETONGUE VIRUS (SEROTYTE 107150RATE USA)		T	Т		Ī	Ī			
MP2 BTVII	OUTER CAPSID PROTEIN VP2	BLUETONGUE VIRUS (SEXOTYTE II / ISOLATE USA)		T	Т	167.734					
FVP3 BTV13	OUTER CAPSED PROTEIN VP2	BLUBTONGUE VIRUS (SEXOTYPE 17/150LATE USA)	161.161	T	Т					3	
PVF3 BTV19	OUTER CAPIED PROTEIN VP2	BLISTORGE VIKUSKSKOTYPE IV ISOLATE USA)	Ţ	19777	T						
ME BIVIA	OUTER CAPED PROTEIN VP2	BUBLICHOUS VIRUS (SERVITTE 1/190LATE AUSTRALIA)	Т	Т	420-438	189-159					
MAI BIVIS	OUTER CAPSID PROTEIN V72	SCURE CONCOLE VIANA (SEASO) THE THIRD AND THE SCOTT OF THE STATE OF THE SEASON OF THE	153,164	Т	Т						
742 EDV	OUTER CAPAD PROTEIN VP2	Extend a previous la cera en a se	101.117	Τ	\$32.563	677.63	764.789				
PVP2 ROTER	AMA-BOIDDING PROTEIN VP3	BOVDE KULAVILLS (STRAIN R.)	1110	Τ	T	763.790					
PV72 ROTEU	RNA-BINCOND PROTECN VP2	HOVING BUILD VIRUS (STRAIN OR)	301.001	Т	Т	Т	374.78				
PVP1 ROTHW	ANA-BRODEO PROTEIN VP2	MUMAN MUTATRUS (SERVITTE I / SIRAIM WA)		Т	Т	Т	107 37				
rvn kotrc	NA BROOKS PROTEDI VP2	PORCEDIG ROTAVIRUS (GROUP C / STRAIN COWDEN)		T	T	T	Τ	474.700	765.700		
PVP2 BOTS!	RNA-BINDONO PROTEIN VP2	SECAN II NOTAVILUS (STRAIN SAII)	10.00	T	Τ	-	T				
PVP IO MALEVP	INCHOR MUCLEOPROTEIN VP30	MAKBURO VIDUS (STRAIN MUSOKE)	20.00		1			-			ŀ
PAYS ASTE	PHOSPHOPROTEIN PT3	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	174-197		1						
PVP35 EBOV	POLYMERASE COMPLEX PROTEIN VP15	EBOX'V VILUX	233-534		1	1					
PVP35 LANVA	Т	MARBURG WINUS (STRADY MUSOKE)	\$.75	20-12		1					
PVPTS LLABVE	Т	MARBORIO VIRUS (STRAIN POPP)	\$-73	8		•					
AND STATE	INDAMBRICON MANY TOWN OPE PROTEIN P35	VACCINIA VILLIS (STRAIN COPENHAGEN)	278-304								
VALAN	BARCINEDONANAM DIVISIONE PROTEIN P35	VACCINIA VIRUS (STRAIN WR)	276-304								
VALVO STORY	BAAABADOAMIANT DAVELOPE PROTEIN P35	VALIDLA VIRUS	279-305								
TOTAL PROPERTY.	11 EN MANAGEMENTEDA	MALEKS DISEASE HEAPESVINUS (STRAIN GA)	255-270								
TO THE PERSON NAMED IN	+	MANEETS DISEASE NEW TRANSPORTED TO STRAIN NOT 1/75CA2)	255-270								
	Ť	ALTERCALANIA CALIFORNICA NUCLEAR POLYMEDROSIS VIRUS	296-311								
TAY IS AN AL	-	CARRYA PERINDINGLANA MAIL TICAPSID FOLVIEDROSIS VIRUS	107.134	214-240	91.3€ €	_					
DAVID STAN	MANUE CATABOLICAN	AFBICAN HORSE SICKNESS VIKUS (SEROTYPE ASTRAIN VACCINE)	1959	136-147	215-230	DAS-062					
	Las Pass Bacheru	RELIETOWCHE VIRIS (SEROTYPE 10/150LATE USA)	123-144	112-217							
	WAY COME THOUGHT	BLIGHOWGUE VIRUS (SEROTYPE 1771SOLATE USA)	133-144	112-224							
T I I	Ver coak recrition	BLUGIONCUE VIBUS (SEROTYPE 17 ISOLATE AUSTRALIA)	123-144	213-227		•					
Mary Park	VP) CORE PROTEIN	EPIZGOTIC HEMORRHAGIC DISEASE VIRUS (SCROTYPE I)	121-142	671-405							
AVOID PAVE	VP) COME PROTEIN	EPIZOOTIC HEMORUHAGIC DISEASE VIRUS (SEROTYPE 2/STRAIN AUS		7	╗						
V61 16V	MAJOR 114 KD STRUCTURAL PROTEIN	BUCE DWALL YIRUS (RDV)	100	340-340	167.393	2	742.76	24.70			
PVP) LOTIC	DONER CORE PROTEIN VP3	PORCING ROTAVIRUS (GROUP C / STRAIN COWDEN)	27.00	Т							
WY BOTS	DOUGH COME PROTEDN VP3	SOCIANTI ROTAVBUS (STRAIN SAII)	601-423		312-330						
Me EBV	CAPSID PROTEIN PAG	Epsted-bakk virus (strain 809-4)			T						
PVP60 HBVIII	CAPSED PROFESS PAG	HEADES SOCIETY VOLUS (TYPE 1 / STRADA 17)	101	Т	70,00						
PVP40 HSVED	CASE PROFESSION	EQUIDE MELPESVOLUS TYPE I (STEAM ABAP)	2		3						
PVP40 HSVSA	CAMB MOTEN No.	HEIGHTS VALUE AND (STIRAN II)	100								
7450 ETV		INTELLIGIS LAND MACHINES TANDS (SINGER TIMES CO.)	94.118								
PVP-0 MABYA	_	MACCONIC VENCO (3 I POLIT MICHORIA)	91130								
	-	EXCESSED TO THE PARTY CHARACTER CHAIR	323.242	34.37	Ī				L		
MAC DAVI	STRUCTURAL OLYCOPROTERS PRO	VANCETT A PORTER VIRINGISTRAIN DOMAS	4								
	1	ATTENDAMIA CALIFORNICA MICLEAR POLYMEDROSIS VIRUS	279-246	262.278							
	T	SDEAM II BOTAVBUS (STRAIM SAII)	483-506								
MAN POLICE	CONTRACTOR PROTEIN VA	SPEAN II ROTAVIRUS (STRAIN SAII)	395-411	483-508							
	7	AUTOGRAPHA CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	14.38								
SOME STAN	Т	ORGYNA PSEUDOTSUGATA MULTICAPSID FOLYHEDROSIS VIRUS	136-157								
WAY VARV	Ŧ	VALIDLA VIRUS	273-288								
WALE VACOR	7	VACCINIA VIRUS (STRAIN COPENHAGEN)	331-350								
CON DAK	Ť	VACCIMIA VIRUS (STILAIN WR)	X::X								
PVPG VARV	Т	VARUOLA VIRUS	2	7							
PVP BTV10	П	BLUETONGUE VITUS (SEROTYTE 10/1SOLATE USA)	134 161	237-76							
PVP4 BTV11	VP4 COME PROTEIN	BLUETOWOUE VIRUS (SEROTYPE 11 / ISOLATE USA)	1	T	- C						
PVP4 BTV13	VPA CORE PROTEIN	INCURTOMODE VIRUS (SEROITYE 117 ISOCATE USA)		407-767	2020						

THE MAKE WHY BITCH WHY BITCH WHY BOTH WHY	TEIN VIN	VIRUS		J									
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STEIN VP4		Γ	Г	Ī	-		Г	_	-			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	STEIN VP4	BLUETOWCKE VIRUS (SENOTYPE 2/ ISOLATE USA)	T	Т		+	 						
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		NEBIASKA CALF DIARAHEA VIRUS (STRAIN NCDV-LINCOLN)	I	7117	357.75	+	+	l	-	ľ			
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	PROTEDY PNS4	RICE DWARF VIRUS	Т	Ŧ		+	1	T					
	DTEN VP4	BOVING ROTAVIAUS (SEROTYPE & / STRAIN BALI)		1	1	-	\mid			Ī			
	OTEIN VP4	BOVINE ROTAVIAUS (STRAIN CASA)			-	+	-	T					
	OTEN VF4	BOVING ROTAVIRUS (STRAIN UK)	T	107.107		-				-			
	OTEIN VP	EQUINE ROTAVIRUS (STRAIN H-1)	Τ	7	105.507	-	T						
	O IEIN VIA	MUNICAN ROTAVIRUS (SEROTYPE I / STRAIN 1076)	Т	Т	107.69		-						
86 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	OTED VP4	HUNLAN KOTAVIRUS (SEROTYPE 2 / STRAIN RV-S)	2	Ī		+		T					
, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8, 8,	DIEDA VP4	HUMAN KOTAVIRUS (SEROTYPE I / STRAIN 6911)	Т		101 601	+	t	T		Ī			
	Office VPA	HUMAN MOTAVIRUS (SEROTYPE 2/STRAIN DS!)	٦	T	N. S	+	1	T	Ì	Ī			
		HADAGN ROTAVIRUS (STRAD) KI)	8	Т		.07	\dagger	T	İ				
	Action Co.	HELLAN ROTAVILUS (STRAID) KU)	76-91	╗	Т	Ř	†	1	1	T			
	A STATE OF S	HEIMAN ROTAVIRUS (STRAIN L26)	181-207	П	483:307	+	1	1	1				
	DIEL VI	INDICAMENTAVIBLE (SEKOTYPE I / STRADY MJ?)	161-207		482.507	-			1				
	CIETA VIA	IN BAAM BOTTAVIRUS (SEROTYPE 3 / STRAIN MCN13)	101-204	135-250	483.506	-	+			1			
	DIEM VIA	INDIAN BOTAVILLE (SEROTYPE) / STRAIN P)	161-207		483-507	<u> </u>							
	Olem viz.	SPINAN BRYANTIS (SEROTYPE 4/STRAIN ST THOMAS))	181-209	234-249	483.507	4		1		1			
	DIED VIA	MARAN BOTAVISIS (SEROTYPE 4/ STRAIN VATO)	181-207	483-507				1	1	1			
	DIEM VI	MATERIAL BOTAVEUS (SEROTYPE I / STRAIN WA)	181-307	463-507		-							
	OLENA VIV	PASSAGE BATAVINIS (SEROTVIE 5 / STRAIN OSU)	335-250	483-506		1	1	1	1				
	CORED VF	TANAMAN BOTANTHIS (CROUP C./ STRAIN COWDEN)	487-512			1	1						
	OTEN VF	PARAMER DOTA VIRILE (STRAIN COTTFALED)	234-249	483-507									
	OTEIN VIA	INCIDENCE BOTAVILIS (STRAIN YA)	235-250	183-508				1					
	OTEIN VZ	SKECK BOTAMBUS	443-506				1						
	DIEM VF	SECTION IN BOTAVILLE (STRAIN SAIL-PEA)	443-508			1	1						
	A PART OF THE PART	STATEMENT IN ROTAVIRUS (STRAD) SAIL-SEM)	395-411	45)-503		7	1						
	William VII	SOUTHERN BEAN MOSALC VIRUS	\$0-114	7	T	+		1		Ī	١		
	MOTEON PASA	WOUND TUNOR VIRUS	193-215	Т	Т		1						
	LOTELN VPS	BLUETOWOUE VIRUS (SENOTYPE 167 ISOLATE USA)	203-317	200	616.409	+	1						
	OTEDIVES	BLUETOWOUE VIRUS (SENOTYPE 11 / ISOLATE USA)	110	Т		+	T						
 	LOTEIN VPS	BLUETONOUE VINUS (SERUTYPE 11/15OLATE USA)	17.100	117.00		1							
	LOTEIN VPS	INCIDENCE VINCES (SCHOOL THE 17 ISOLATE AUSTRALIA)	200.300			-							
	ROTEIN VPS	BLUETONGUE VIRUS (SCHOLTTE 17 ISOLATE SOUTH A NOCA)	204.317			+							
	KOTEDA VPS	MULETOWOUR VICTOR SERVICE AND	STEEN PS	RUCE DWALL VIALOS	15.4	Т	361-376						
		A PROPERTY CALIFORNICA NICITERA POLYNEDROSIS VIRUS	321-537	438-462	-								
		INTERPORT IN VIRGING (SEROTYPE 10/15OLATE USA)	123	257.272									
	230044	MAINE BOURS DWARF VIRUS	130-146			H							
П.	TUINE SO INCIDENT	CHANTA PERIDOTSUCATA MULTICAPSID POLYPEDROSIS VIRUS	61.99	235-252	386-313				1				
Т	COROLLEIN PREC	ALTTOCHAPHA CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	84-103	338-355									
	A VIOLENTEIN	GALLERIA MELLONELLA MUCLEAR POLYMEDROSIS VIRUS	188-172			+	1						
Т		ALLIETONICIE VIRUS (SEROTYPE 11 / ISOLATE USA)	5.33	230.24	257-272	1	1						
VAC BTOTAL VAC PROTEIN		BLUETONGUE VIRUS (SEROTYPE, 13 / ISOLATE USA)	23	230.245	137.171	1	1	1	1				
١		ALUETONCIE VIRUS (SEROTYPE 11/1SOLATE USA)	23	228.245	131.171	1	1						
Ť.		BLUETONCIE VIRUS (SEROTYPE 1/ISOLATE SOUTH AFRICA)	2		201-270	†	1		T				
		BLUBTONGUE VIRUS (SEROTYPE 2/1SOLATE USA)	704-22			\dagger	1						
Ĩ	OTEIN M	WOUND TURKOR VIRUS	174 165			\dagger							
П	OTED! N	WOUND TUROR VIKUS (STRAIN PL)	344.334			T							
		AUTOCATA CALIFORNIA POLICA TOCTOCACOSIS VINOS	132.143										
П	PROBABLE NEWBRANE ANTIGEN 25	A INDICA A PARA CALIFORNICA MICHERAL POLYHEDROSIS VIRUS	274.301	605.420	678.704	T							
PVP P NEVAC PS ILD PROTEDI		INTERPORTER VIRUS (SEROTYPE 1) / ISOLATE USA)	197.111										
1	20	EPIZOOTIĆ HEMORUHAGIC DISEASE VIRUS (SEROTYPE I)	205-222	101.33									
Ţ	MANAGEMENT OF A PROTECT PASS	NCE DWARF VIRUS	400-416										
WALL THE PROTEIN PHS	I PROTEIN PAST	WOUND TUMOR VIRUS	262-285										

:

PCCENE	Practizit	[All Virgins (No Besterdoshares)	-	-	-			-	-	ſ
FILERAME	PROTEIN	Virius	AREA! AR	AREA! AREA?	J AREAN	ARCA 3	AREAS	AREA? AR	AREA! AREA!	
PVPED NOVAC	CAPSED PROTEIN P86	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDRÓSIS VIRUS		999					П	
AND MANO	CAPSID PROTEIN PR7	OROYTA PSEUDOTSUGATA MULTICAPSID POLYTIEDROSIS VIRUS	571-593							П
	MONSTRUCTURAL PROTEIN PR	BLUETOWGUE VIRUS (SEROTYPE 107 ISOLATE USA)	2							
	MONSTALCTURAL PROTEIN PA	SCULLIONCOLE VIXUS (SEROTYPE 11 / ISOLATE USA)	2	1						1
	MANUFACTURE AT BOOTEN BO	BUCKELOWAND VINOS (SCAO) TYC 13 TBUCK I E USA)	2 2	1	1			1		1
1/1/1	MANAGERICAL MAIL PROTEIN FO	BLUE LOWGUE VINUS (SCHOLLTE 177 ISOLATE USA)	2 2	1	+				1	-
PVP BTVIS	NONSTRUCTURAL PROTEDUPE	BLIRTONGIE VRUS/GEROTYPE I / ISOLATE SOUTH AFRICA)	104.130		+					T
PWR BTV2A	NONSTRUCTURAL PROTEIN PR	BLUETORGUE VIAUS (SEROTYPE 2 / ISOLATE USA)	104.120		 				1	T
PVP NDV	OUTER CAPSID PROTEIN PR (ALCE DWALF VIRUS	374-400		 -				<u> </u>	T
PVPE ROOV	OUTER CAPSID PROTEIN PS	RICE GALL DWAN' VIRUS	177.202 216	216-242 396-425	_					Ī
PVP VACOC	STRUCTURAL PROTEIN VP9 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	Г	Т						Ī
PVTN VACCV	STRUCTURAL PROTEIN VP9 PRECURSOR	VACCINIA VIRUS (STRAIM WR)	235.242	-	-				1	Ī
PVPS VARV	STRUCTURAL PROTEIN VPS PRECURSOR	VARIOLA VIRUS	225-242		·			1		T
PVP WTV	OUTER CAPSID PROTEIN PS	WOUND TUNOR VIRUS	L	214-241 251-271	379.405			-		Ī
VE EDV	MONSTRUCTURAL PROTEIN PASS	RICE DWALF VIRUS	Γ	Ι	Г					Ī
PVP RGDV	MONSTRUCTURAL PROTEIN S9	NUCE GALL DWARF VIRUS	151-175		-					T
PVPRE NOVAC	T	AUTOCHAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	Τ	225-245				+	1	Τ
PVPHE NOVOP		ORGYLA PSEUDOTSUGATA MOLTICAPSID POLYHEDROSIS VIRUS	Т		†			1		T
PVPRT_ADELL		HUNDAN ADENOVIRUS TYPE 12	191-191	-	<u> </u>					T
WART MARTY	PROTEASE	MOUSE MANDANT TURIOR VIRUS (STRAIN BRS)	979	-						T
PVPRT LONIV	PROTEASE	SINGAN MASON-PFIZER VIRUS	\$0.00	-				-		T
PVPRT SACKVH		SQUIRACE MONKEY RETROVIRUS	156-271						 	Ī
PVPRT SAVI	PROTEASE	SIMIAM RETROVIAUS SAV.1	8 8		ŀ			l		T
PVPU HIVIBI	VPU PROTEDI	HUBAAN BEACHODEFICIENCY VIRUS TYPE I (BIIIO ISOLATE HXRI)	12.5							T
PVPU HVIBS	VPU PROTEIN	HUDAAN INDAMPODEFICIENCY VIRUS TYPE I (BIIB ISOLATE)	133		_				-	Γ
PVPU HVIBN	VPU PROTEIN	HUMAN MOALPHODEFICIENCY VIRUS TYPE I (BRAIN ISO) ATE)	3.38		 					Ī
PVPU HVIBA	VPU PROTEIN	HEDRAM INDICIONCE VIRUS TYPE I (BRIJ ISOLATE)	1.17							Ī
PVPC HVIEL	VPU PROTEIN	HUMAN MANUNCOEFICIENCY VIRUS TYPE I (ELI ISOLATE)	1.26						<u> </u>	
	7	HUMAN INDADMODEFICIENCY VIRUS TYPE I (HXB2 ISOLATE)	4.27							
MAN HA	7	HUMAN DAMANDOE RETENCY VIRUS TYPE I (FICSF ISOLATE)	2.		-					
	7	HUMLAN DANGMODE/FCIENCY VIRUS TYPE I (AIAL ISOLATE)	3:31		•					
	VIOLEDING CONTRACTOR	HUMAN BONDHOOF KIENTY VIRUS TYPE I (AIN ISOLATE)	2.5		-					Ī
THE PART OF THE PA	VACINE THE CONTRACT	HUMAN MORUMORE FILENCY VIRUS TYPE I (NOK ISOLATE)	9.50		1					Ī
PVPU HVISI	VPU PROTEIN	HABAN BAA MADERICENCY VALLE 1776 1 (7421 300 ATE)	1.5	1						T
WINI WAY	VPO PROTEIN	MINAM DAM DAMBER FIFTH VINING TAPE 1 ACT ICAL A YES						+		Ī
WE WILL	VPU PROTEDN	HUMAN BOACHODERCIENCY VIRUS TYPE I (ZUCIDC. ZUA ISOLATE)	1.1							T
PWHU JSAV	VPU PROTEIN	SHEEP PULMONARY ADENOMATOSIS VIRUS (JAAGSIEKTE SHEEP RET	124-45		 -					Τ
PVPX HVIEL	VPX PLOTEDI	HUMAN BLOADMODEFICIENCY VIRUS TYPE 2 (ISOLATE BEN)		-						Τ
MYX HVXA	VPX PROTEIN	HRAKAN BOKUNDGFICIENCY VIRUS TYPE 2 (1501, ATE CAM2)	10-33		L			-	-	Τ
MAX HATD!	VPX PROTEIN	HIBACAN BEAUMODEFICIENCY VIRUS TYPE 2 (ISOLATE DIW)	16-33	_						T
NAX WARD	VPX PROTEDI	HIBAM BOANODE/ICIENCY VIRUS TYPE 2 (1501 ATE D205.7)	1531	I					-	
MAX MAXO	VAX PROTEIN	RUMAN BANDRODE FORMAY VIRUS TYPE 2 (ISOLATE GHANA.1)	10-13							П
COLON NAME	WAY PROJECT	THE STATE OF THE O	10.32	-						
THE PARTY OF THE P	The projection	INTERNATIONAL PROPERTY AND A THE ACT OF THE	10-31							7
AND AND	UNIVERSITY OF THE PROPERTY OF	INTERIOR DEGRACION PROPERTY (SOLATE SELESY)	10-13							
NA CANA	Ver se Avrent	HUMON DRINGLEFICIENCY VIRUS 177E 2 (ISOLATE ST)	10.32							
17017	VAN PROTEIN	INCLIAIS DEM TURCUEMASE ELEVATING VIKUS	145-165	1						
	THE POST OF THE PARTY OF THE PA	SHEAT MANAGERATERY VINOS (ISOLATE AGM / CLUME UN-1) (S			-					٦
SAN CIVAR	AND DECISION AND AND AND AND AND AND AND AND AND AN	SAMEAN DEMOCREPICENCY VISUS (NATIO 192-8) ISOLATE) (SIV-NAC)	10-33	1						
CANAL CANA	VPX PROTEIN	STATEM PARTICULAR PROPERTY VINCE (NOW INCH ATEXABLE)	200	1				1	1	7
NAX SIVE	VPX PROTEIN	SDOAN BOARNODEFICIENCY VIRUS (E) 16/34/01/4 ISO ATFLISHOTY M	-		-		\dagger	+	+	Ī
SANS XANA	VPX PLOTEDY	SDATAN BOADMODEFICTENCY VIRUS (PB/BCI) ISOLATE) (SOOTY MA					1	+	-	T
PYRINA BSAIV	ALPHA-A PROTEIN	BARLEY STRUPE MOSAIC VIRUS (BSMV)		939			1			Τ
PVSOS ROTTER	MONSTRUCTURAL PROTEIN MCVP2	BOVINE ROTAVRUS (S MAIN RF)	Τ	197	+	\downarrow	T	1	+	T
			1				1			7

TLE HAME	PROTECT	THE CONTRACTOR STREET,	Г	428.450 453.473		1	-	_	_	
VSOS ROTHE	MONSTRUCTURAL PROTEIN MCVP2		Ī	<u>i</u>	<u> </u>	<u>:</u> _		-	-	
PVS03 ROTPC	HONSTRUCTURAL PROTEIN WSSS	Par man and a series and a seri	198.414	:	<u>-</u>	:			-	
VSes ROTS!	NONSTRUCTURAL PROTEIN NCVP2	SIMIAN II ROTAVIRUS (STRAIM SALII)	202-225		-				اً	١
VSS ROTBR	VP4 PROTEIN	BOVING ROTAVISOS (STRAIN W)	5						1	
PVSOL ROTES	VP PROTEIN		201-125						 	-
VSOE BLOTTELU	VN PROTED		202-225					-	-	
VSOS ROTE	VP6 PROTEIN		201-125						1	
VSOS BOTEUL	VP6 PROTEIN	WYNARIN T BIARRIES ROTAVIRU	07-72					+	1	١
WEST ROTOR	VN MOTEDI								1	
WSM ROTO	We Profess	HULAVIAUS (CACUT OF STRAIN DES)	202-225							
WEST BOTH	VP PROTEIN	HOGAL TOTANTO (SERUIT TO 1 STANTA 1979)	58.43		-	-				
Wed tomic	-	HUMAN ROTAVIRUS (CRUOT C.) STANIT DIAGOCA	207.725	-		 -				
PVSod BOTHS	-	HEMAN ROTAVINUS (SERUITIFE 27 STRAIN 32)	302.235			_				
PVCS LOTINY	•	MUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	T	114.140	-					
PVSS BOTTE	-	PORCEME ROTAVIAUS (GROUP C/STRAIN COWDEIN)	١							
PVS06 ROTPG	VP6 PROTEIN	PORCINE BOTAVIRUS (STRAIN GOTTPRILED)	181							
PVSOT ROTEU	CL YCOPROTEDY VP?	BOVING ROTAVIRUS (STRAIR RM-4)	21.1							
PVSOE ROTHC	GLYCOPROTEIN VP? MECURSOR	PORCING ROTAVIRUS (GRUOT L'ASTANIA COMPEN)	100		-					
PVS08 ROTS!	MONSTRUCTURAL PROTEIN NCVP4	SECAN II ROTAVIRUS (STRAM SATI)			-					
WGO LOTTA	CL VCOPROTEDI VP1	BOVING ROTAVIRUS (SEROTVIE 6/ STRAIN 61A)			<u> </u>					
VSO LOTEA	*	BOVINE ROTAVIRUS (STRAIN Add)			+	-				
PVS# ROTES	ř	BOVINE ROTAVIROS (SEKOLTER 107 STRAIN BALLS)	187:101		-					1
PVSOP ROTEK	1	BOVINE ROTAVIRIO (STRAIN RAL)	1		-		-			
PVSOS EDTRE	•	BOVING ROTAVILLS (SELICITOR 1 / SILVAIN 1447)	17416		-	-				
PVSON ROTO	CLYCOPROTEIN VP7	CHICKEN HOTAVIAUS A (SEKUTYPE // STINKIN CHIS)	131-155							
PVSOP ROTEL	CLYCOPROTEIN V//	EQUING HOTAVILLO (STRAIN LOSS)	205-232		_	_				١
PV509 ROTGE	GLYCOPADTED VP7 PRECURSOR	ROTAVBUS (GROUP BY STIVAM LAW)	201-101	197-212	-		_			
PVSOB ROTH	г	MUMAN HOLD AT LAND (SENOT THE VIOLENT OF STRAIN MANY)	197.212			_				
PVSOF BOTHA		MUNICAL ROLL WINDS (RENOT VEST STRAIN DS)	197.212							١
PVSON ROTHE		THE TANK THE TANK OF THE TANK	197.212			4				1
HHUOTI GOSAG	CLYCOPROTEIN VP1	TANALAN BOTA WELL (STRAIN 1.26)	131-155	197.213		-				ļ
PVSOF BOTHE	П	LEPAZAN BOTAVIRIIS (SEROTYPE 1 / STRAIN M37)	131-155	167-313						
PVS09 NOTHER	П	INTERNATIONAL SERVICE (STRAIN NO AND STRAIN D)	131-155	107-212						1
PVSOF ROTHO	OLYCOPROTEIN VP1	MALAN BOTA VIRIS (SEROTYPE) / STRAIN ?)	131-155							1
PVSOF ROTIO		HITELAND BOTA VIRUS (SEROTYPE) / STRAIN RRV)	131.155							1
PVSOF ROTHER	7	HAMAN BOTAVILLS (SEROTYTE 1 / STRAIN 52)	197-313						1	
PASON ROTHS	CLYCOPROJECT VE	HUMAN ROTAVBUS (SEROTYPE 4/STRAIN VAYO)	197-213	-	1					
AND MOIN	Т	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN WA)	131-155	197.212	1					١
AND MOTHER	Т	PORCENE ROTAVENUS (SENOTYPE \$ / STRAIN OSU)	131-155	197-212	$\frac{1}{1}$					١
200	Т	PORCEME ROTAVIDUS (SEROTYPE 5 / STRAIN TFR-41)	131-155		1					
	CHACCOPROTEIN VP7	PORCINE KOTAVIRUS (SEROTYPE 4 / STRAIN BEN-144)	197-213		1	1	+			
	CL VCOPLOTED VP7	PORCING ROTAVIRUS (SEROTYPE 4/ STRAIN BAIL-1)	107-2112		1		+			
NOT OF THE	OLYCOPROTED VP1	NHESUS ROTAVIRUS			$\frac{1}{1}$	+				
PASSE ROTS!	OLYCOPROTEIN VP7	SDEAN 11 ROTAVILUS (STRAIDS SATT)	101-102		}		-			
VSII LOTON	Т	ROTAVILLE (GROUP B / STRAIN ADRY) (ADULT MARCHEA ROTAVIRUITATION	100		$\frac{1}{1}$		-			
AVSH IBSVA	T	MUMAN RESPIRATORY SYNCYTIAL VIRUS (3) INAIN AS			1					
WELLO!	Т	MANOS VIRUS (STRAIN SBL-I), AND MUNITY VIRUS (STRAIN SBL-)	3		-		-			
PVIH MAR	Г	MODES VILLS (STRAIN EDINGEURGH 2 = 9)			+	-	-			
WEH LEBER	Г	MUNUS VIXUS (STRAIN EDITING UNION 4)	20							
PVSH MINEA	Г	INCLUSION PRODUCTION PROCESSION AND CONTRACTOR AND	Z		L					
PVSH LAUROP	П	MONTS VINCE (STRAIN BELYAST)	3.39		-					
PVSH MUDGE	SMALL HYDROPHOBIC PROTEIN	MAINTE VALUE (STEADY EXALL YAN)	7.70							
PVSH MURO	T	MINDS VIRUS (STRAIN RICHAM)	1:39							
PVSH MONOX	Т	MUNDS (STRAIN BRISTOL I)	6.30		-					
						-	•			

	1914771919	All U (12, B		ŀ					Ì	
FILE NAME	PROTER	YRUS	AREAL	AREA ! AR	AREA? AREAS	ABLA S	AREA	AREA?	A NUMA	ARI'A 9
PVSH MURCPA	SMALL HYDROPHOBIC PROTEIN	MINGPS VIRUS (STRAIN RW)			_					
WSH MONT	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN TAKAJIASIII)	10-29							
75H M250	SHALL HYDROPHOBIC PROTEIN	ACOUPS VIRUS (STRAIN URABE VACCINE AMP)	10-39				٠			
PVSII REOV.	SIGNA I PROTEIN PRECURSOR	REOVIRUS (TYPE I / STRAIN LANG)	110-136							
PACH BEAU	SCHOOL STRUCKS	REDVIKUS (1 VPE 3 / STRAIN DEALUNG)	22:12						-	
PVS11 BEOVE	SUCALA SPONTEN	ACCURACY (TELL 27 STAKIN DOKANES)	2		1	+			1	
PVSLS REDVI.	SIGMA I.S PROTEIN	BEOVIEW CYPE 1 / (19 A IN CANC)	101.01	+	1				1	
PVST3 HEVBU	STRUCTURAL PROTEIN 2 PRECIMEOR	INDATTISE VIRES (STRAIN RIBLIA)	300-111	1	ľ		\downarrow		1	Ī
PVST1 HEWA	STRUCTURAL PROTED/ 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN MEXICO)		Ì			1			
PVSTI2 HEWAY	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN MYANAKAR)	111.00				1		1	
PYSTS HENPA	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN PAKISTAN)	111.00	-					1	1
PVSTT HEWELT	STRUCTURAL PROTEIN 2	PERATTIS B VIRUS (ISOLATE MIESUS)	2199			+			T	
PVT2 MYXW.	TURIOR MECROSIS PACTOR SOL RECEPTOR PREC	MYXONA VIRUS (STRAIN LAUSANNE)	261.283	-	1	+	-		İ	T
PVTS SPVICA	TUNOR NECKOSIS PACTOR SOL RECEPTOR PREC	SHOPE FLEKOWA VIRUS (STRAIN KASZA)	270-280				-		\dagger	Ī
PVTIA CUVI		CAPIDOXYING (STRAIN INS. 1)	114111					1	1	Ī
PVT4 SFVKA	TA PROTEIN	SHOPE FIREGLA VIRUS (STRAIN KASZA)	125-148	1	1			İ	1	
PYTER EBV	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-DARK YRUS (STRAIN 199-6)	ī	100	33.34		1 : :	Ī	!	1
PVTER HCMVA	PROBABLE DNA PACKAGING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	T	Т					\dagger	T
PYTER HSVII	PROBABLE DNA PACKAGING PROTEIN	HEAVES SPANLEX VIRUS (TYPE I / STRAIN II)	Τ	471-482			1		T	1
PYTER HSV6U	PROBABLE DNA PACKAGING PROTEIN	HEAPES SOUNEX VIRUS (TYPE 6/STRAIN UGANDA-1102)	Т	+						T
PYTER HSVEB	PROBABLE DNA PACKAGING PROTEIN	EQUINE HERDESVIRUS TYPE I (STRAIN ARAP)	Τ						T	Ī
PVTEA (ISVI)	PRODABLE DNA PACKAGING PROTEIN	CTALLIALD HEAVESVIRUS I	T		<u> </u>	:			-	:
PVTEA HBYSA	PROBABLE DNA PACKAGING PROTEIN	HEADESVIRUS SAIMIRU (STRAIN 11)	218-341			-			T	Ī
PVTER VZVD	PROBABLE DNA PACKAGNO PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	372.389							T
PX IPEOS	MOTERNX	CACADIO SQUIDEL HEPATITIS VIRUS	59-99						\dagger	Ī
PX WHY:	PROTEINX	#OODCHUCK HEPATITIS VIAUS I	58-83	_		-			İ	Ī
PX WHYS	PROTEINX	WOODCHLCK HEPATITIS VIRUS 59	SB-89						1	Ī
YX WHYY	PROTEIN X	WOODCHLICK HEPATITIS VIRUS 9	58-89			_				Γ
ZX WRY	PROTEIN X	WOODCALCK HEPATITIS VIRUS &	64-85							
A WANTER	TAULUM A	WOULD THE PATITIES WINDS I (INCECTIOUS CLONE)	20.00						1	
PY ION APPEN	WOLDER A	WOULD HEAD THE STATES WAS WERE (ISOLATE PWS23)	5							П
Viol Bavi	KYPOTHETHER TO BE BESTER!	NUMBER ANCHORUS I TITE /	1,7							
PY TOK MAY	HYPOTHETICAL 16 6 KD MOTERN	AAIZE STREAK VIRIN COUTTA ASSULATION AND	2:	+						
PY115 \$5VI	HYPOTHETICAL II I KD MOTEDA	SULFOLDBUS VINUS LIKE PARTICLE SSVI		1	+	1			†	
	HYPOTHETICAL 11 9 KD PROTEIN	PANICINI STREAK VIRUS	13-51	-					1	1
П	RAGAS KYPOTHETICAL IS 6 KD PROTEIN	REET NECKOTIC YELLOW VEIN MOSAIC VIRUS (ISOLATE GI)	1	-	-	-			\dagger	T
N CONTRACTOR	HYPOTHERICAL 12 4 KD PROTEIN	CYNGIDIUM MOSAIC VIRUS (STRAIN SINGAPORE)	0.30	-					t	T
	KITOTHETICAL MOTERN B-137	HUKAN ADENOVINUS TYPE 1	26.50							Γ
Ţ	WINDS HALL IN THE PROPERTY	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN BA)	34.55						l	
Τ,	MYPOTHETICAL 13 1 ED PROTEIN	CASAN VA LA IENI VIKUS (SITANIN NIGERIAN)	34-55							
PVISK TYLEV	HYPOTHETICAL 13 4 KD PROTEIN	TOWATO VELLOW LEAF CIRE VIRILE		1						
П	HYPOTHETICAL 14 SKD EARLY PROTEIN	HIDALAN ADENOVIRUS TYPE ?	104.113						1	
	HYPOTHETICAL 14 5 KD PROTEIN	CHEORIS STRUATE MOSANC VIRUS	92	+					1	T
٦	HYPOTHETICAL 180KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	_	141.162					T	Ţ
Т.	HYPOTHETICAL 20 6 KD EALLY PROTEIN	HUMAN ADENOVIAUS TYPE 1	50-73						\dagger	T
AVANT VALAR	MACO INTO THE ILAL AT THE PROJECT	REET NECKOTIC TELLOW VEIN MOSAIC VIRUS (ISOLATE F2)	163-188							Γ
THE REAL PROPERTY.	DANOTHE RALL POTENT	AUTOURANTA CALIFORNICA MUCLEAR POLYNEDROSIS VIRUS	90-106			L				Γ
Τ	OTEN	SOTBEAN CALLANDING MOI ILE VIAUS	65.80							
T		SOUTHWEST VIRISHING PARTICLE SSVI	122-143						_	
>		VACCIDIA VILIS (STRAIN WE)	4	1						
Т		MEASUES VIRUS (STRAIN HALLE)		+				1	1	
		SOVBEAN CHECKOTIC MOTTLE VIRUS	81.38	1	+			1	1	
PYDSK SSVI	OTER	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	I	144.131	Т	100 100		+		
			ı	1	7	100	1	1	1	7

POCENE	Pitchaip	All Virges (No Becterlephages)	П			1			
FILK HAMIK	PROTEIN			Т	_	T		Т	
TYL SOCIA	HYPOTHETICAL PROTEIN S	SOTREAM CHUMOIIL MINUS		+	1	-			
PY87 ADE01	HYPOTHETICAL 9 7 KD EALLY PROTEIN	HUNGAN ADEMOVIRUS 1 TPE 7			1				
PYMC3_SSVI	HYPOTHETICAL 9 2 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	1		†	+	1	1	
MALI EBV	HYPOTHETICAL BALF! PROTEDN	EPSTEIN-BARK VIRUS (STRAIN 899-1)	B17-502		1	-	-	Ī	
PYTHOI KOWPIN	HYPOTHETICAL BAIGG-ORF! PROTEIN	FOWLPOX VIRUS (ISOLATE HP-438(MUNICH))	¥7.				\downarrow		
PYBOT FOWPIA	HYPOTHETICAL BANGO-CAUT PROTEIN	FOWLPOX VIXUS (ISOLATE HP-438[MUNICH])	21-12		1			ľ	
PYTHOP FOUTM	HYPOTHETICAL BAAGG-ONFY PROTEIN	FOWLPOX VIXUS (ISQLATE HP-438[MUNICH])	49-47						
PYBIO FOWPM	HYPOTHETICAL BANDIL-ORF 10 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-404)MININCHI)	81-18		1				Ī
MANUA CURVE	HYPOTHERICAL BANGELORF 12 PROTEDY	FOWLPOX VIRUS (ISOLATE HP-434[AGNICH])	114-134	154-169		\downarrow			
PWELS STATE	NEL-2 PROTED	SOULAN FOALMY VIRUS (TYPE 3 / STRAIN LK3)	113-138		1				
AND LINE	MEL.S PROTEIN	HUBALN SPURARETROVIRUS	52-78		_	_			
AND INVEST	HAYS 24 9 KIN PROTEIN IN DAME TRECKON	HERPESVIKUS SAIMON (SUBGROUP C / STRAIN 488)	206-230						
SALE HEAVE	LIVE & CEN PROTEIN DUDIOR TESTION	HELPESVIKUS SADAIRI (SUBGROUP C / STRAIN 418)	69-90						
A TOTAL	LIVERAGE TATAL BY BECTFOR	EPSTEIN-BARK VIRUS (STRAIN 895-8)	200-223		_				
1000	INTERNATION OF THE BEATERN	MARRY INSPACE HERPSYRUS (STRAIN BC.)	175-190						
N N	7	MARKET PAGEAGE HERPES VIRUS (STRAIN MDS)	175-190		-	-	L		
	-4	SHIMAN CYTOMEGAL DVIEUS (STRAIN AD169)	161-191				L		
V. W.	-	VACCIMA VIBIR CITE ATUME)	16-102		_	_			
	STE FIGST BANKE ST AND THAT I SEE	LATERIA CONTRACTOR MANY	141-151						
3	HATE PROFIEM IN MOLECULARIO CON	ACTION CONCENTS NOT	×1:5:		[_		
ZYROK CVIII	INTERNATION IN PROCESSOR OUT ON	INCHEST CONCRACTOR LOCA	15.5						
ALC:	HIT PROJECT IN MALECOATED ON	PROCESSION AND AND AND BOLDS	67.60						
2	HYPOTHERICAL BLOCK PROTEIN	LABORAN AND AND AND AND AND	11.11			-			
PYLI3 ADEAI	HYPOTHERICAL BOLD PROTEIN	TOWERS BARBOTTE STORY AND BREET	26.100	172.151 215.261	110-350				
PYNOLD EBV	BLOUTS PROTEIN	ENSILEMENTAL VILUS (STANIN BY)	7	Т	Т		\downarrow		
PYLICE DAYS	HYPOTHERICAL 159 KD PROTEIN	SOULTIME DESCENT VIIUS (MSECT HUDESCENT VIKUS 1 YPE 22)	┰				+		
PYOR! ADEG!	-	AVIAN ADENOVIRUS GALI (STRAIN PIGLIS) (FOWL ADENOVIRUS I)	-		† 	+			
PYORI COYNY	_	COMPACIDIA YELLOW MOTTLE VIRUS	2						
PYOK! TTV!	_	THERMOPROTEUS TENAX VIRUS I (STRAIN KRAI)	9		 				
PYORE COYNY	HYPOTHETICAL 15 KD PROTEIN	COMPLETANA YELLOW MOTTLE VIBUS	27.62				\downarrow		
PYORE BAV	HYPOTHETICAL 15 CKD PROTEIN	EQUINE ARTENTIS VINUS	163-197						
PYON LELV	HYPOTHETICAL 24 4 KD PROTEIN	LELYSTAD VIDUS	136-213		7		-		
PYOU LVX	HYPOTHERICAL 11 BIED PROTEIN	LE Y VINS X	71-52						
PYON HAV	HYPOTHERICAL 14 KD PROTEDA	NAECHSSUS MOSANC VIRUS	7.30						
PYON PVX	HYPOTHETICAL 13 KD PROTEIN	POTATO VIDUS X	¥-			$\frac{1}{2}$			
THOSE WAY		POTATO VIELDS X (STRADA CP)	11:X			\downarrow			
TYDE WORM		WHETE CLOVER MOSALC VINUS (STRAIN M)	6.3		-				
PYON WOW		WHETE CLOVER MOSAIC VIRUS (STRAIN O)	_			-			
PYON ADEG!		AVIAN ADENOVIRUS GALI (STRAIM PRELIYS) (FOWL ADENOVIRUS 1)	-			-			
PYCH EAV	HYPOTHETICAL 28 7 KD PROTEIN	EQUING ANTEXITIS YINUS	139-158			-			
PYOR NOW	HYPOTHETICAL 10 KD PROTEDY	NATICESSUS MOSAIC VIRUS	10-26						
PYCH TTVI	HYPOTHESTICAL 16 6 KD PROTEIN	THERMOPROTEUS TENAX VIRUS I (STRAIN KRAI)	13-33			-			
PYORL TTVI	HYPOTHETICAL 16 5 KD PROTEIN	THERMOPROTEUS TENAX VIRUS I (STRAIN KRAI)	6.3			-			
PYONG TIVE	HYPOTHETICAL 31 6 KD PROTEDV	THERMOPHOTEUS TENAX VIRUS I (STRAIN KRAI)	12.102	233-236	1	-			
PYON TIVE	HYPOTHETHEAL 30 2 KD PROTEDM	THEIR MOPILITY TENAX VIXUS I (STITAIN KUA!)	91-13			$\frac{1}{1}$	1		
PYPM RTBV	HYPOTHETICAL PAPEOTEIN	INCE TUNCKO BACKLIFORM VIRUS	3.23	104-126		1			
PYPM KTBVP	HYPOTHETICAL PM PROTEIN	MCE TUNGRO BACELLEORIA VIRUS (ISOLATE PHILIPPINES)	52-23	97-126					
PYTHE NEVAC	HYPOTHETICAL 43 5 KD PROTEDM	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	-			$\frac{1}{1}$	+		
PYPEL NOVOP	HYPOTHETICAL 123 KD PROTEIN	ORGYIA PSEUDOTSUGATA MALTICAPSID POLYHEDAOSIS VIRUS (OP			-	$\frac{1}{1}$			
PYTHU NOVOP	HYPOTHETICAL 40 0 KD PROTEIN	ORIGINA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OP	-	215.230		$\frac{1}{4}$			
DANT BLATA	HYPOTHETICAL PTO PROTEDY	TOBACCO NECROSIS VIRUS (STRAIN D) (THV)			1	+			Ī
PYTON NOVLD	HAPOTHESTICAL 8 S KD PROTEDA	LYNANTRIA DISPAR MALTICAPSID NUCLEAR FOLYHEDROSIS VIRUS				1	4		
PYRU HEVED	HYPOTHETICAL PROTED/IU/1	HEAPES SDOPLEX VIRUS (TYPE 6 / STRAIN GS)	42.68						Ī
PYRUZ HEVRO	HYPOTHETICAL PROTEDM IST	MERPES SOURCEX VIRUS (TYPE 6 / STILAIN OS)	35.74						
PYRES HISVAG	HYPOTHETICAL PROTEDY IV!	HERPES SDIOLEX VIXUS (TYPE 6/STRAIN GS)					1		
PYRU IRVE	REPETITIVE PROTEIN ORF!	CHLO BURESCENT VICUS (CIV) (INSECT INDESCENT VICUS 177E 9)			$\frac{1}{1}$	1			
PYRY BY	REPETITIVE PROTEIN ORF4	CHELD BEDESCENT VIRUS (CIV) (INSECT INDESCENT VIRUS 1 TPE 9)		100 000		+			
PYNPS TAVE	REPETITIVE PROTEIN OUTS	CHLO IMDESCENT VIXUS (LIV) (INSECT IMDESCENT VIXUS 1 TTE V)	221-26	1		$\left \right $			

				Ì	l		İ	ł	-		
TURNE PARKE	PINCILLE	VIRIS	ARFAI	AREAZ	ABEAS	ARIA	ARFAS	ARFAG	ABEAT	ARFA B	ARFA
PYRA! EBV	HYPOTHETICAL BILL! PROTEIN	EPSTEIN-BADA VIRUS (STRAIN 095-0)	Г	Т		-	Т	1	Т		
PYRU EBY	HYPOTHETICAL BRUEZ PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 895-8)	164-182						<u> </u>	 	
PYSRI EBV	HYPOTHETICAL BSAFI PROTEIN	EPSTEIN-BARA VIRUŠ (STRAIN 895-8)	92-113								
PYTRI EDV	HYPOTHETICAL BIRF! PROTEIN	EPSTEIN-BARK VIRUS (STRAIN 895-0)	107-01								
ACES NAVO	HYPOTHETICAL 24 6 KD PROTEIN	ORGYTA PSEUDOTSUGATA MULTICAPSID POLYTIEDROSIS VIKUS (OP	133-152		1		1	1	$\frac{1}{1}$	1	
TANK WACCE	HYPOTHETICAL IS NO PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	2.9	200	1			+	1	+	I
PIVAL VACEV	HYPOTHETICAL SOLD PROTEIN	CINIA VIRUS (STRAIN COPE	1		T	Ī	1	\dagger	\dagger		T
PYVAT VACEV	HYPOTHETICAL 19 KD PROTEBY			İ	1	ŀ			+	\mid	
PYYBE VACCV	HYPOTHETICAL 10 5 KD PROTEIN	VACCINIA YIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE				·				l	Ī
PYVBG VACCC	INTOTHETICAL II 1 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	17.54	-		F		-	-		
PYYCA VACCE		VACCINIA VIRUS (STRAIN COPENHAGEN)									
PYVD2 VACCV	HYPOTHETICAL 8 6 KD PROTEIN	VACCINIA VIRUS (STIAIN WR), AND VACCINIA VIRUS (STIAIN COPE	\$7.5	36-52							
PYYDA VACCC	INTOTHETICAL 9 3 KD PROTEIN	VACCINGA VINUS (STILADA COPENDIAGEN)	12-38	П		•				-	
PYYDA VACCV		VACCINGA VIRIUS (STRAIN WR.)	3-18	22-38	44-64						
PYWA VACCE	HYPOTHETICAL 7 I KD PROTEIN	VACCINIA VINUS (STILAIN COPENHAGEM)	48-67			-					
PYYFF VACCC	HYPOTHETICAL & KID PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	13-42			:					
PYYOA VACCC	INTOTHETICAL 143 KD PROTEDM	VACCINIA VIRUS (STRAIN COPENHAGEN)	105-127							_	
PYYKA VACCC	INTIOTHETICAL 9 6 KD PROTEDI	VACCIPIA VIRUS (STIAIN COPENHAGEN)	54-70							Н.	
אמז נוצא	HYPOTHETICAL BZLF1 PROTEIN	EPSTEDUBARR VIRUS (STRAIN BPS-1)	130-166			•				_	
PY MK CSMV	HYPOTHETICAL 14 3 KD PROTEDV	CHELORUS STREATE MOSAIC VIRUS	54-80			·				Н	
PYISK SSVI	HYPOTHETICAL 18 9 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	100-125	141-163							
PYZOL ADEO?	INTROTHETICAL to 6 KD BARLY PROTEIN	KORAN ADENOVIAUS TYPE 1	50-73				1				
PY2SK BNYVF	KNA-3 HYPOTHETICAL 24 7 KD PROTEDA	REET NECKOTIC YELLOW VEIN MOSAIC VIRUS (ISOLATE F2)	193-188			-					
PY29K NEVAC	HYPOTHETICAL 39 9 KD PROTEIN	AUTOGRÁPHÁ CALIFORNICA MÚCLBAR POLYHEDROŠIS VIRUS	901-06			-					
772 SOCIA	HYPOTHETICAL PROTEIN 1	SOYBEAN CHLOROTIC MOTTLE VIDLIS	06-59			-					
PYTH SEVI	HYPOTHETICAL 31 7 KD PROTEIN	SULFOLDEUS VIRUS-LIKE PÄRTICI E SSVI	133-143			1					
PYGKO SSVI	HYPOTHETICAL 6 6 KD PROTEIN	SULFOLDBUS VIRUS-LIKE PARTICLE SSVI	776	+	1					1	1
A VACE	MYPOTHETICAL 74 KD PROTEIN	VACUALA VICUS (STRAIN WR.)	80.	1	1		1		+		1
27.43	WASHINGTON INCOME.	DELX	95	\dagger	1	ŀ	1		\dagger	1	T
PARCE SECO	INVOCATION OF SECTION	EVI	201.48	ונרואו	141.441	2 157 (1)7	744 744	$\frac{1}{1}$	1	1	I
V 602 IV	PAYOTHER AL PROTEBUL	SOVERAN CHARACTIC MOTTLE VIRUS	10.77	Т	Т	Т	5	1	\dagger	+	T
PWW ANGE	INVOCATIONAL OF PARTICULAR PROTEIN	HONZAN ADEMOVIREIS TYPE 7	11.77		1		Ì		+	1	T
PYWE2 ESVI	HYPOTHETICAL 93 KD PROTEIN	SULPOLOBUS VIXUS LINE PARTICLE SSV:	Τ	63.77	t	1	T	+	1	\dagger	T
PYALI EBV	HYPOTHETICAL BALF! PROTEIN	EPSTEEN-BARR VIXUS (STRAIN 1995-0)	2		T	Ī			t	\mid	T
PYBOI FOWEN	HYPOTHETICAL BANGE ON! PROTECN	FOWLLOX VIRUS (ISOLATE HP-A)EPATHICHI)	154-174			ĺ		-			
PYBO! FOWPA	HYPOTHETICAL BANGE-ONLY PROTEIN	FOWLPOX VIBUS (ISOLATE NP-434)AUMICH))	104-121						_		
PYBO FORM	HYPOTHETICAL BANGE-ORUS PROTEDI	FOWLPOX VEUS (ISOLATE IP 4) HADDINICH))	į.	1							
TARIO LORGA	WORDSTREET, BANKE CARTS BEDTEIN	FOR LOW VIEW COUNTY TO A 19th distriction	8	+	1	1	1		+	1	
PART DAVIE	NEL 2 PROTEIN	SDGAN FOAMY VIRUS (TYPE) / STRAIN LK))	Τ		\dagger	Ī		+	+	†	T
PYBLS FOAMV		HUMAN SPUNALETROVIRUS	27.72	T	T	T	Ī	+		+	
PYDHI HSVSC		HERPESVIRUS SAMARI (SUBGROUP C / STRAIN 488)	206-230		-			-	-		
PYDED HSVSC	HYPOTHETICAL 9 S KD PROTEIN IN DIGRESTREGION	HERPESYRUS SAMIRI (SUBGROUP C / STRAIN 488)	06-69					-	ŀ	-	Γ
YEC UNV	_	EPSTEIN-BARR VIRUS (STRAIN 895-8)	100-111								
MOA! HSWIG	_	MANEK'S DISEASE HERPESVIRUS (STRAIN BC-1)	23:180								
PYCA! HSVIDA	MITCHWEITCAL 21 6 KD PROTEIN	MALEA'S DISEASE HERPESVIRUS (STRAIN NDS)	2			1					
AND HONY	_	RUMAN CTTUNEGALOVIRUS (STRAIN AD169)	27:01:		+	1					
	INVESTIGATION TO SERVICE SERVICES AND SERVIC	LA BANE CAROLA MINISTER AND	201-00		1	1				+	
	INVESTMENTAL PROPERTY IN THE POCKASIO CAST	MACHINE CONCRAVING ANY	*	1	1	1		\dashv	+	1	
NAC SOUR	HYPOTHETICAL PROTEIN IN MICL EOCAPSID OFF	MAINE CORONAVILIS SOLV		1	\dagger	Ī		+	1	1	
PWC2 EBV	HYPOTHETICAL BKAP3 PROTEDY	N 895.83	90.0	\dagger	\dagger	T	\dagger	-	+	\dagger	Ī
PYLI3 ADEAI	HYPOTHETICAL 1 0 KD PROTEIN		53.73	\dagger		T	T		+	+	T
PYNEU EBV	BACK? PROTEIN	_		121.155 21	115.241	330.350	T	-	ig	ŀ	Ī
PYNEP IRVI	HYPOTHETICAL 15 9 KD PROTEIN	SIMULIUM INIDESCENT VIRUS (INSECT IRIDESCENT VIRUS TYPE 22)			П				-	+	
						İ					

97.7		All Virana (Ne Bacteriophages)		П	П	П	. 1		П	
THE WALE			ARKAL	AREA AR	ABEA AREA	I	ARKA JAHKAL	P P P P P P P P P P P P P P P P P P P	T T T	OBIA!
PYOR! ADED!		IELFS) (FOWL ADENOVIRUS I)	B .	1		$\frac{1}{4}$	-	+	1	
PYOR! COYNY			9		1	+		+		T
PYOK! TIV!		KAIN KRAI)	9		+	+				T
PYORE CONAV		TTLE VIRUS		1		+	-	+		T
PYORE EAV	INPOTICE TICAL 25 6 KD PROTEIN	EQUINE AKTERUTIS VIKUS			-	1			1	
PYOR2 LELV	INTOTNETICAL 28 4 KD PROTEIN	LELYSTAD VIKUS	31.63			+				
PYORU LYX	HYPOTHETICAL 118 to PROTEIN		9.4		-	+				
PYOR JORY	HYPOTHETICAL MK# PROTEIN	MALLISSUS MUSARL VINUS	7.	-		-	-	-		
705	HYPOTHETICAL IZED PROTEIN	CONTROL VIEW AND A PARTY OF THE	7	-		-	-	_		
7007 7007		S ISTRAIN AN	67.6		-	-				
PYON WOWN			2		-	-				
200		STROM ADEMONIBUS IN	40.84	-		-	-			
PYOR'S ADEQ!	MYOTHETICAL 31 S KD PROTEIN	_	136,158			•	-			Γ
MOS EAV	MYTOTHER TICAL 28 7 NO PRIOR EAR	STATES AND	10.76			+				
PYORE NAIV	HATTONE TICAL 10 KD PROTEIN	TABLESON HOSAN, VIACO	13.32		-	-		-		
PYON TIVE	HAYOTHETICAL 16 6 KD PROTEDY	INEXCENSION I ENAN VIANO I (STRAIN AND I				-	-	-		Ī
MOST IIAI	HYPOTHE TICAL 16 5 KD PROTEIN		19.103	211.246	+	+	-			Ī
PYORM TIVE	HYPOTHETICAL 18 & KD PROTEIN					+	-			
TOS T	HYPOTHETICAL 20 2 KD PROTEIN		١	104-126	-	+	-			
VEN LIEV	HYPOTHETICAL PROTEIN	CACE LONGED BACK FRANK VARIATION ATE PART INPRAFES	3.33	104-126	-	+	-			
PTP A RTBV	HYPOTICAL PICTURES	ALCE TORANG MAILTINGS AND FOR YOR YOR VIEDBOSIS VIEDS	200			+	-			<u> </u>
PYPAT NAVAC		AUTOMOTER CALIFORNIA PICAPAIN POLYHERANSIS VIRIS (OP	2.10			+	-			
	HTFOIRE ILA 12 2 ALD PROTEIN IN 19 3 PALSON	SACING SECTION SECTION AND THE APPLIES FOR YIELDS OF YIELDS OF	23.65	215.230	-	-				
		SAME APPLICATION OF THE PARTY AND THE PARTY	15.5			-				
TAY DAY	HYPOTRETECAL PIS PROTEIN	POLYHEDROSIS VIRUS				 				
	HTTO INC. 8 S BUT PROTEIN IN TAX.	HERPES STARTE WALLS CHYPE 6 / STRAIN GS)	\$ 2			-	_			
200	1	HEBPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	2.7		L	H				
	AND COUNTY OF ALL DESCRIPTION OF STREET	HERPES SIMPLEX VIRUS (TYPE 67 STRAIN GS)	32.56		-	H				
TO STATE OF THE PARTY OF THE PA	A CONTRACTOR OF THE CONTRACTOR	CHILD INDESCENT VIRUS (CIV) (INSECT INDESCENT VIRUS TYPE 4)	10-43			-				
	Speciment bankeli hera	CHILD INDESCENT VIRUS (CIV) (INSECT INDESCENT VIRUS TYPE 6)	474			į				
	ENDITOR PROTEIN ORF!	CHILD INDESCENT YIAUS (CIV) (INSECT INDESCENT YIAUS TYPE 6)	96-123	179-204 244	240-285	Н				
	WHOCH STICAL BASE PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 1995-0)	199-223							
AND STATE	HYPOTHETICAL BALLY PROTEIN	EPSTEIN-BALL VILUS (STRAIN BPS-1)	164-162			-				
WHITH	INTOTAL ISLUT PROTEDI	EPSTEED-BALIK VIRUS (STRAIN 1995-1)	73:113			1	-			
VIII IN	INTOTAL STATI PROTESM	EPSTEDLEAKK VIXUS (STRAIN 1995-1)	107-02			+		1		1
PYURI MYUD	Г	ORIGINA PSEUDOTSUGATA MULTICAPSID POLYNEDROSIS VIRUS (OP	22		1	\dagger				T
PWAL VACCE		VACCINIA VIRUS (STRAIN COPENHAGEN)	4.2	*1.0	+	+		+	1	
PYVA VACCE	Г	VACCINIA VINUS (STIAM CUPEMPACEM)		•	+	\dagger		+		
TYVAL VACCV		VACCIMIA VECUS (STEAMS WALLAND VACCIMIA VINUS (STEAMS COPE			+	+		 		
PYVAT VACEV	/ HYPOTHE FICAL 6 9 KD PROTEDI	VACUATA VINUS (STRAIN WAS AND VACUATA VINUS (STRAIN COPE			+	\dagger	+	-	-	
PWE VAC	7	VACTIMA VIETE (STEAD) COPEDALAGEN			-	\vdash	-			
WWO WACK	т	VACTORIA VIBILIA (STRAIN) COPEDALAGEON	18.35		-	-	-	-		
	—	VACCINIA VIRUS (STIJAIN WR), AMD VACCINIA VIRUS (STRAIN COPE	2.5	36.52	L	-	_	_		
	INVESTIGATION OF THE PROPERTY.	VACCINIA VIRUS (STRAIN COPENHAGEN)	100	1	-	-				
	U INVOCATION OF RESPECTED	VACCORIA VIRUS (STRAZIN WR)	1.5	22.38 44	19-17	H				
	WASTICAL FIED PLOTEDY	VACCINIA VIRUS (STILAIN COPENHAGEN)	49-67			Н				
PYYET VACCE	۳	VACCIDITA VIRUS (STRAIN COPEMIAGEN)	23-43			H		-		
PYYOR VACCE	┮	VACCINTA YIRUS (STRAIN COPENHAGEN)	<u>2</u>	_		+	+			
TYNG VACC	+-	VACCIDIA VIRUS (STRAIN COPENHAGEN)	2	1	1	+	1	1		T
WHILE EBV	F	(EPSTEIN-BALR VIRUS (STRAIN BOS-1)	150-166			-	-	-		

TABLE XIV

SEARCH RESULTS SUMMARY

FOR P23TLZIPC MOTIF

1991 1991				П	_		П	П	7 . 4	1
CHAPTER CHAP		liticxt4		T	\neg	ASSAL	1	2000	Т	7000
		CROILLE		٦				İ		
CHANGE BY THE CONTRICT CONTRICT BY A THE BY CON	~	NAMA POLYPROTEIN		1		İ		i		
CHANGE REVISION CHANGE REV	SAN TOP	RNA1 POLYPROTEIN		_	1001-100	_		-		
CHANGE BY THE PROPRETED CONTRACTOR CON	V SVS C	GENOME POLYPROTEIN		<u> </u>	650-1678	1110-1148		İ		
CHANGE OF TATION		ALTONA MANAGEMENT		Γ	560-1500	1110-1158				j
CHANGE OF THE CONTRICTORY CONTRICTORY		N. S. C. C. S. S. C. C. C. C. C. C. C. C. C. C. C. C. C.		T						
CHANGE FOR THE CONTINUENCE CONTINUENCE	Š	CEROME TO THE STATE OF THE STAT								
CHANGE FOR THE CONTACT CHAIN AND THE CONTA	YMY.			200						
CHAPTER CHAP	OXAZ			8						
CHAPTER TO THE CONTRICT OF T	17XC		CONSACRIC VIEW CONTRACTOR CONTRAC	601-161)			!			İ
CHANGE OF TYPESTER CONTRACTION CONTRAC			COXSACKIEVIRIS AN (STRAIN CARLILLOS)							
CONTROLLED CON	201									
CHECOL EL NY PROTEIN CONTRICTION FILE	FOLG COXB			101.						
CHOOLE BLY TROOLE 17.100 11.100	POI G COXB)			\$13.1615				Ì		Į
CREATE BY THE CONSTRUCTION CONST				99.	1313-1617					
				T,	404 4646	2401 3414				
CARDON FOR TWO IS NOT A COUNTY OF THE TOTAL MAN AND THE TOTAL MA			DELICITE CORTIC TYPE I (STRAIN SINGAPORE S275/90)	∹	117.6			Ì		
CHANGE REYATOR CHANGE READ			CINCAN PROPERTY CANADA	*:-=						
CETCORE FOR YEAR OF THE PARTY OF THE STREET HOUSE TO THE STREET				1	1113-1146					
CALCADE FOR TWO DIEST CALC					1					
	POLO DENZO									
	POLG DEN19									
	DEN ST. DE NO.			Γ	9117					
				Ì,						
	LA C DENZI									
CHANGE FOULTONING CHAN	CE DENIE	CENONE POLYPROTEIN	TVPE 21CHBAIN PRISOSI	.03	9					
	MAN CO DENS	CENOVIE POLYPROTEIN		200						İ
		NO FLORE OF VARIOUS IN	VINOS IVEL SICILIANIS IN THE SICILIANIS SICI		1100.1412					
			JE VIRUS 14PE 1							
CHANGE FOR THE PROPERTY 1995-1910 19	O DEN	CALMONIC TOTAL TOT						İ		1
The control of the	N I C I	GH MINGH FOR VERILLED	!	174.806						1
	2011	ALTONIA CON ALCONIA	I I I I I I I I I I I I I I I I I I I	64.1736	1463-1301					
Exception Fig. Fi		N. STORAGE STREET	ENCEPHALONYOCARDIES VIALIS		1010 000					
CEROLIE FOLVEROLIEN	THE PARTY		ENCEPHALOMYOCARDITIS VIRUS (SIRAIN FAIC-B NUMBIABE I UCITALL)							
CARDING FOUR FOUR FOUR FOUR FOUR FOUR FOUR FOUR	POI G ENICYB	CENUNIE FULL FROM	ENCEPTIAL ONLY OF ARDITIS VIRUS (STRAIN FAIC D DIAMETOGENIC)	17.04	130					
CENONE FOLYPOOLEN	POLG ENCYD	GENOVIE POLYPROTEIN	SOUT AND LIGHTING ACE VILLIS (STRAIN A10-61) (APITITIOVIRUS A)	_	1001					
CERONIE PRI VEROLEM COULYND MOUNTED STRAINS ON AND GRESS COURT COULYND MOUNTED STRAINS COURT	DIG INDVI	GENOMIE POLYPROTEIN	Γ	1036-1074	1041-1111	1167-1199	1465.1501			
CENDING POLYPROTEIN COLOUR VARIOUS FILES COLOUR VARIOUS COLOUR VAR	POLG FAIDVA	CENONE POLYPROTEIN		1001-1133		1465-1501				
CENTRE POLYPROTEN CONTROLLEY CONTROLLE	DAGMS STOR	GENOVIE POLYPROTEIN		1640.1670						
	1201	CENONIE POLYPROTEIN	HEPATITIS C VINUS (ISOCATE LITTING V)	1011 171	160.1511	211.11				
		2191042	HOG CHOLERA VIRUS (STRAIN ALFORT) (SWINE PEARS VIRUS)							
CENTRE FOR THE PARTY CONTRICT	۲. اعداد	GENORIE POLITICALE	HING CHILL FRA VIRUS (STRAIN BRESCIA) (SWING FEVER VIRUS)	19.13	260-13			::::	:	ı
	10 0 HCVB	CENTRE POR TITLE IN	The state of the s	16.4n.16.7u	1				1	;
CHAPTER CHAP	ME C. DE VIK	CI MINE TAX TELL IN		1640.1670					İ	
			III PATILIS C VIRUS (ISON ATE 11) (III. V)							
			HEPATITIS C VIRUS (150LATE HCV-476) ITIC V)	10.00						
	֓֞֞֜֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֓֡֓֡֓֡		HIFPATISTS CVINUS ITSOLATE IN 16) (IN. V)	711.741						
CERTITION CONTRICT	EV I		LINE AND LICE OF CHANGE AND CHECK	111.743	1003-1024					1
THE PROPERTY OF THE PROPERTY	PGI C IICVID	GENORI: FOLVITADITIN	THE PART OF THE PA	1640-1670			_			:
	ALC LICVIA	CENCORE POR YPROFFIN		11.50						
INTERPLIED INT			THE PAINTY CARTY SIZE AND THE TOTAL OF		-		!			i
	1 A HI 3 HA		III PAINIS C VIRUS (ISON ALL TAIWAN) (IR V	1040-1070						1
	MIN C: 18 4 18		INFPATITIS A VIRUS (STRAIN 24A)	1314-1550	106.20					1
	PPOLG HPAV		THE PARTY OF THE ACT OF THE PARTY OF THE PAR	1314-1350	1048.20m					1
CENOME POLYROLEN	PPOIG IPAVA			200	2064-2099	_				
CENTRALE FOLYPROTEIN	AVANT CITY		HEFAILIS A VIRUS (STINAIN 187)	1010	2015 SAN					
		NI STORAGE AND	HEPATITIS A VIRUS (STRAIN INF. 17.)							<u> </u>
INTERPRETATION INTE	IAVE OF L		TI FATILITY A VIBILITY OF IN A I							<u> </u>
CENDIG POLYPROTEIN CENDIN	LECH C. LIFAVI.	_	THE PAINT A VIETS (STEAT)	1313-1331	2009-2100					ļ
GENOME POLYPROTERN INTELNATIONALIST GENV-14 1094-1111 10	FINE GIFAVE	CHANGE FOR YERONI IN	STATE A VIDILE ACTION	191-161	1317-1333					1
GENOME POLYREOIEN INFANTA BINDOVINUS BIN	PPOLG 119 4VS	GENUNTE POL YPROTEIN	The state of the s	1094-1132	1005-3041					1
GENOME POLYPROTEIN ITAMAN MINNOVINIS 2 PLAN V. 191 100-1642	PPOLG 19 44	GENOME POLYPROTEIN	TICHAN WINOVINGS TATIONS	1453-1485	1816-1849	1983-2019				_
GENOME POLYPROTEIN HIGHAN BIRNOVRIS 2 (1917) 1405-1473 1405-1473 1511-1146 1905-1473 1511-1146 1905-1473 1511-1146 1905-1473 1511-1146 1905-1473 1511-1146 151	1 × 10 × 10 × 10 × 10 × 10 × 10 × 10 ×	GENOME POLYPROTEIN	III MAN WILL WIND TO (TAX TO)	1444.1494	1100.1542	1976-2012	L			
(2 NOME PIX PRACTEM CHINGALE PIX PRACTEM CHINGALE PIX PRACTEM STALK THE TRACTEM PARTIES STALK THE TRACTEM PARTIES CHINGALE POLYPROTEIN CHARACTER PIX PRACTEM CHOCKER POLYPROTEIN CHARACTER PIX		SENONE POL VPROIEIN	HILLIAN STINOVIRUS 2 (HRV-2)			9000				
100-115 100-	וב וב וב	-	INTERIOR PLINCOVINUS BY (PIRV-89)	3						
GENOME FILL TRAILER STRUCTURAL POLYMOTER TAPARESE ENCENIATION STATES AND STRUCTURES STRAIN SALIS GENOME POLYMOTER TAPARESE ENCENIATION VIRUS (STRAIN SALIS) GENOME POLYMOTER TAPARESE ENCENIATION VIRUS (STRAIN SALIS) GLOS (1833-1369 1516-1349	LLOI C INCAN		THE POSTATION TO START MANY	1100-1149						<u> </u>
STRUCTURAL POLYMOTEIN CAPAGE ENCEMALITIE VILLS (STRAIN SA 14) 61-95 133-1369 1316-1349 1516-1349	FFOR CHIPY	CHENOMIE FOIL VERGILLING	THE PARTY OF THE CAT INCRACE VIEWS (STRAIN CIT)	222-260						1
TARVI GENOME POLVPROTEIN INAMESE ENCEPHALISIS VINOS TERCINE POLVPROTEIN (61-9) 1331-1369 1316-1349	Protect Boyle		A CLASS CONTRACTOR AND CALLED AND CALLED	61.93	1233-1269		2775-2813	1114-1111		1
TAPARTY SALVENT ALL THE SALVENT SALVEN	IVAL C LOS	GENOMIE POLYPROTEIN	INTARESE ENGERITATION VINCE (STANIS OF THE	70.14	11211.1269			2779-2019 3274-3311		
Carconda Vola Carconda		CONTRACTOR VARIOTETIA	INPAMESE ENCEMIALITIS VIRUS (STRAIN SALVI)							

10000	910,711,912	All Vignace (na bacterlashanes)							
Į.	7.5.C.54	VIPUS	AREAI	AREAI	ABEA 2	AREA	ABEAS	AREAL	ABGA
Prot G JAEVI	GENOME POLYPROTEIN	IAPANESE ENCEPHALITIS VIRUS (STRAM IADARS902)		1233-1269	1316-1349	3779-2013	1110-0111		
PPOI G JAEVN	GENOME POLYPROJEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN NAKAYAMA)	1161-1197						
PROIS KUNIN	GENORIE POLYPROTEIN	K (MIIN VIRUS (STRAIN AIRAIGIC)	10.10	101.100	3275-3312				
PULC LANVI	GENOME POLYPROTEIN	LANGAT VIRUS (STRAIN IPSI)	1137-1166	1319-1331	2230-2264	1366-2398	1005-3133	İ	
PPOLG MCFA	GENOME POLYPROJEIN	ATOSOUTED CELL FUSING AGENT (CFA FLAVIVIRUS)	1174.1706	130.038				Ì	
1	GENOVIE POLVPROTEIN		2					Ì	Ī
PFOLG MVEV	CENONE POLYPROTEIN	MICHAEA VALLEY ENCLEPINALITIS VIRUS	146.174	7011107			Í		Ī
1000	CENORE FOR VEROITIN		936.000	4014.1134				Ť	
	CENCRIE POLYPROLLIN	FOLLOVIALISTYPE (STRAIN MAJONEY)	131.138						
	CENOME FOR YEAR IN	COLOCIALIS INTELISIBATIN SABIN	122.134					Ī	ĺ
1000	GENORIS POLYPROTEIN	POLICYIBUS TYPE 2 (STRAIN LANSING)	150 1137						
2010	CENONIE POLYPROTEIN	POLIOVIAUS TYPE 2 (STRAIN W.2)	130-1157						
100 0104	GENOLE POLYPROTEIN	POLIOVIRUS I VPE 1 (STRAIN 21127)	19:136						
Proi C Pol J.	CENONG POLYPROTEIN	POLITIVIALIS TYPE 1 (STRAINS PIALEONI) AND PIALEON (24) [II)	1119-1156						
	GENOME POLYPROTEIN	PLUNI POX POTYVIRUS (STRAIN D) (PPV)	1965-0965	1084-3113				Ī	
PPOLG PPVEA	GENOME POLYPROTEIN	FILMI POX POT YVIRUS (STRAIN EL ANIAR) (PPV)	1337-1364	1461-1490					
	GENOME POLYPROTEIN	PI (BI FOX POTYVIRUS (ISOLATE NAT) (PFV)	2044-2075	1066.3007					
	GENOME POLYPROTEIN	PLUM POX POTYVIRUS (STRAIN RANKOVIC) (FPV)	7930.3990	3013-3112					
PPOIG PSBMV	GENOME POLYPROTEIN	PEA SEED-DORNE MOSAIC VIRUS (STRAIN DPDI)	990-116	1411-1445	3149.3138				
PPOLG PVYIU	GENOME POLYPROTEIN	PUTATO VIRUS Y (STRAIN IITINGARIAN) (FVV)	1303-1336	1004-1011					
PROJECT PARTY	GENOME POLYPROTEIN	FOTATO VIRUS Y (STRAIN M) (PVY)	1302 (1316						
Proi G Pyrvi	GENOME FOL YPROTHIN	PARSMIP VILLOW FLECK VIRIS (ISOLATE F. 171) (PVI V)	210-262	1110.1139	1001-1031				
PLUIC SANIVA	CENCHE POLITICISM		245-274						
POLG STEVN	GENOME FOLVEROILIN		61.08	1301-1331					
Prolic SUMVS		SUGARCANE MISAIC VIRUS (STRAIM SC)	307.136						
PFOLG SYDYII	GENONIE POLYPROTITIN		1385-1617						
FFOLG SVDVI	GENONIE POLYPROTEIN	SWINE VESICITAR INSCASE VIRUS (STRAIN URG/21/7)	1818-1617						
PPOLG TBEVS	GENOVIE POLVENOTE IN			=	2164.2378	331:12	-	j	i
TO DEV	GENOVE POR VIRGILIA	:		-	304.11.2		-	-	:
PRIC IIV	NI I CAN PER C	1		-:					;
Proto Treve	CEMONE POLYPROCLES		1014	- 1	2				:
	THE PARTY OF THE P	1 ::			100			Ī	-
No.	CENCRES AX YESSES		_					İ	:
PPOI C TVAV	CLASSIC NE VPHILLIN	TOBLACT ON IN ABITTLE WINDER CLYNN	1498.3711	:	†			-	;
	CAMBRICAN TOWNS OF STREET	SAIC VIRIS II	198.189	:	 - -	!			1
	GENORIE POR VPROILIN		_	_					
PPR G YETVI	GENERAL FOR VERSIEN	VILLOW FEVE VIEWS (VIRALE VIEW)	20.1		=	306.3360	2	Ī	-
		10.100		32		7 1017	1000	Ì	!
	X 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	THE SICILITY AND A PRINCIPLE OF THE PRIN	-	1	:	•	:	•	
FFIRST WAY	GAMONI; POR YPROTEIN	-	34.33	-				İ	i
1	NONSTRUCTURAL FOLYFROTEIN	VENEZUELAM EQUINE FINCEPIALITIS VIRUS (STRAIM TRINIDAD INDIKEY)	3.5	14)6-1468					
) 1	NOW STRUCTURAL PUBLICATION	_	137.365						
.)	MON-STRUCTURAL POLYPROTEIN	_	2					j	
נכא	NOW YEAR THE ALL POR YEAR THE NEW YEAR		-	İ			i	j	-
	THE PERSON OF TH	THE FAILURE CONTRACTOR IN THE WINDS AND THE WASHINGTON	3	į			-	İ	1
AND IN CASE	MON-STRIKE HOME TO THE STRIKE	15						Ì	
100			13.16				-	İ	Ī
VOLUM NOTES	-	MIDDELAURG VIRUS	5					Ť	Ì
PPOIN ON VC	MONSTRIKETURAL POLYPROTEIN		144.1180	1404-1439				İ	
PPOLN RICOV	MON-STRUCTURAL POLYPROTEIN	DISEASE VIRUS (RIIDV	1	1981-1884					
> 25 X 7044	NONSTRUCTURAL POR YPROTEIN		1146-1175	1406-1441					
	MONSTRINCTURAL PUR YPROTITIN 1	SINONIS VIRUS (SULITYPE OCKELIDO / STRAIM EDSRYM 17:5)	1454-1424					1	
PPIN NAIN			144.1484			$\Big]$		1]

PCCONE	PIXTIZIE		ANCAL	AREAI	ABEAL	ABEAS	AKA1	ARGAE	ONTAL
TIT FASIE	CROCCIA	Γ	Г						
PPOLS CEEV	STRUCTURAL POLYPROTEIN	STRAIN VASSITEN PROFICES	133.50						
PPCILS FFEVS	STAILCTURAL POLYPROTEIN	INUS ISTRAIN TC-11)	101.101						
ALE S FLV	STRIK HIR AL POLYPROTEIN	THE PROPERTY OF THE VIEW OF THE WORLD OF THE	1203-1339						
Pron S. EE VVI	SIRUCTURAL POLYPROTEIN		150.1102	1201-1235	İ				
PHIN S ONNO	SIRIK HIMAL POLYPROTOTA		9			Ì			
NAME OF STREET	SIECK CHALL POLYPRITIN				Ì	-	Ï	i I	:
	SIRIN TURAL POLYPROTTIN			i		İ	1	Ī	!
	KINDS COME TO VENOTE NA		100		İ	Ì			
		F OCKELBO / SIRAIN EDSBYN BJ-SI	10.133						
			101:101						İ
PRIS SINDA			1111.1334						
					İ				
	William vot con		101.11					Ī	
		DOVINE INIMITINGIAL FICTENCY VIRUS ISOLATE 127) (BIV)	25.73						
PPO. BIV27	FOL FOR TPROJETY		10.00						
PPOL BLVAU	POL POL VPROTEIN		1	130 144		Ī			
17.17	PCE PCE VEDIEN	AIN CORK) (CAR'S)	3		÷			Ī	į
	ì		1234-1267	1484-1518	20		-		
A COLUMN	ı	CALIFORNIA TAREATA VIRIA VIRIA MILIONE 11401/EIAVI	26-193	206.539					
F0 54V	PUL POLYPROTEIN	COUNTY THE COUNTY AND THE COUNTY	164.198	\$06.519					
FP. ELAVC	POL POL YPROTEIN	PURINE IN CLINICAL AND ALCOHOLOGIC CONTINUES		110	Ī				
PPER TIAVY	POI YPROJEIN	FOURE PRECTIONS AMENIA VIRUS (ISOLATE WYCHING) ITTAN							
	POLY TON TON	IIIDNIAM SPUMARE TROVIRUS (FOAMY VIRUS)			j		i	Ì	-
,,,	1000		141.331						!
יייייייייייייייייייייייייייייייייייייי	TINE FULL FUNCTIONS	IN TYPE LISTRAIN A TRUTHILY II	657-688						
Prof. HTLIA	POL POLYPROTEIN	_	467 488				- 		
1111 IC	POL POLYPROTEIN	7			Ì	İ	Ì		i
	154 VEST 154		111.164	16.00		j			
			141 176	512.549					
	POR POLYTRUITE	:-	141.174	\$12.540					
PPOL HVIBS	POL POLYPROTEIN	Ī					l		İ
NO IN	POL YPROTEIN			316.384		1	İ		İ
131711	NI POLYPROTEIN	Ī	100	97. 77.					
			¥ :	<u>8</u> 5					Ì
NA PA	- 1	HINAM MARINDONE PETENCY VIRISTYPE LURCSF ISOLATE HINV-1)	135.361	304.541					
PPOL HVIR	- 1	THE PROPERTY OF STREET AND ROLL APER COLOR	110.141						
FROL HVINA		Ī	114 143	077 107					
POL HVIND	POL POLVPROTEIN					Ī			
PP INTE	FOL PULYPROTEIN					Ì	Ì		
CNIA	POLYPROTEIN	HINNAN INDICATE HERE YOU'S TYPE I (NOK ISOLATE) (IIIV-I)	10.00			Ì			
	1	HINIAM INDICIONOLITICIONEY VIRTIS TYPE I (OVI ISOLATI) (111V-1)]]	300.337					1
	:	HIGH AND INCHEST OF THE STATE OF VITA STATE OF VITAS AND A STATE OF VITA	10.13	\$12.540					
2	i	HALLE INGRESION VINENT VALUE OF THE ALENIATION ATENNIA VINE	310.363	499.516					
PRIN IN IEU		┰	170	100					
Prin EVIC	POL POLYFROITIN	THE PRINCIPLE OF A VICE OF THE PARTY OF THE PRINCIPLE OF							
Press 11V173		HINNIAN ININININININININININININININININI	101						
		HINNIAN INMINIMENDETICIENCY VIRUS TYPE 2 (ISOCATE CAND) (IIIV 2)	153 100				İ		1
	i	THE MAIN TAINETH WAS A VIRING TO IN STANK ATT MILLY THE TO	71.1B						
		TO A STANDARD OF THE REAL PRINCIPLE OF THE PRINCIPLE AND THE PRINCIPLE OF	154.117	!					
	Maria Maria	The state of the s	180.086						
FLCH IFIA	PUTATIVE PUL FOLVEROTTIN	HANDLE INTRACTORING A CANADA COLOR					ļ		
707	NE LUNCHEN			1	:	:	-		: !
ALTHUR THE	_		0.00		Ī		İ		
	Z 110000 200 200 200 200 200 200 200 200	OVINE I ENTIVIRUS (STRAIN SA.OMIVV)	¥.	07-130	-	746.37	-		
		THE STREET STATE STATE OF STAT	781.624	616-148	====				
FIR BIRV						:			:
FITH RIDY		ALL TONGETHER THE PRINCE OF TH							
12 × 12 × 12		SIMILAN FOAMY VIRUS (TYPE) STRAIM L'R JJ (SP V-J)							
1	POR POR VERDICIN	アリス・マン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン	111.75	2			-		:
		NITABEAN CHOUNCE AWITHE VINUS	17.55	33 64			•		
A WIN STATE	i	CINIAN BETROVIEUS SEV.	119-050						
POL SRVI	POL POLYFRUIEIM	10.41	10113	201.235	017.330				
POL VIL	POL POLYPROTEIN			970 610					
100 VII V	POL POL YPROTEIN	VISHA LEMITVINUS (STRAIN 1916/ CLUME LATERS)			***	Ī			
IN IN	POL POLYPROTEIN	VISNA LENTIVIRUS (STRAIN 1914 / CLONE LVI-1851)		201-202	200				
1	T	HERPES SUMPLEX VIRUS (TYPE 6 / STRAIN CS)	10.01				1		Ì
	1	(EDROSIS VIRUS	13.63						
PPIP NEVAL	٦								Y

FREE CSV	ויאר ועוד מוסטעניים								
11									
1	REPEAT ELEMENT PROTEIN	CAMPOLETIS SOMOREMSIS VIRUS (CSV)	Ī		Г	Т	Т	Т	
	MEV PROTEIN	NOVINE INDIGMENTIFICIENCY VIRUS (INDIANE 123) (NIV.)	26.198						
1	ELV PROTEIX	I CHINE IN CHINS AND MA VIRUS (CLOME 169) (FIAV.)	£.33						
		FOUNT IN LCTIOUS AND MIN VIRUS (CLONE CL22) (CAV)	2.2				_		
ı	AEV PROTEIN	EQUINE INFECTIOUS ANIMITA VIRUS (ISON ATE WYOMING) (ELAV)	74.100			-	-		
PREV SIVAR			29-62				-		
FRIRI ASFM2		-	630-666						
PRIRI LICHVA	RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE LARGE CH	HUNIAM CYTOMEGALOVIAUS (STRAIN AD169)	279-311	21710	440.473				
PRIRI HSVED	AIBONUCLEOSIDE DIPHOSPHATE REDUCTASE L'ARGE CH	EQUINE HERPESVIRUS TYPE I (STRAIN ADAP) (EHV-1)	\$.	501.531					
PRIRI VACCO	AIBONUCLEOSIDE DIPIOSPIIATE REDUCTASE LANGE CIT	VACCINIA VIRUS (STRAIN COPENIAGEN)	203.235					İ	
PRIR! VACCV	RIBONACLEOSIDE DIPLIOSPHATE REDUCTASE LANGE CH	VACCINIA VIRUS (STRAIN WR)	201-115				ŀ		
PRIR! VARV	INIBORUCL FOSIDE DIPLIOSPHATE REDUCTASE LANGE CH	VARIOLA VIRUS	201.213				İ	T	
PAIR! VZVD	RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE LARGE CH	VALICELLA-ZOSTER VIRUS (STRAIN DUNIAS) (VZV)	16.33	21.334	430.516			T	
STATE AVEVE	BALL CENTER HER OWING PROTEIN KINACE YEARS CONT	AVIAN BONG ACCOUNTS WHISE TWEET	140,117					t	
NA HAS	BAH CEBASTANE ONNE PROTEIN KINACE TRANCFORM					\dagger	T	T	
VACCO	BNA BOY WAREACT ACCOMINED THANCED TION COLUM	WEL AND VACCINIA VIBER 1878 AIN COPENIACE					ļ	T	
ANY PAR	BAA BO WASSACE ACCIONATED TRANSCRIPTION COECIS	VARIA VEIC				Ì	Ť	İ	
AUTO TOTAL			1101			Ì	†	Ì	
2797			_	707			+	ĺ	
A AND LONG			Т	143.438		+	1	Ť	
אליניי		AIN WELL AND VACCING VIRIS ACTEAN COPENSIAGE	72.00				l	t	
VALVA LOGICA	ONA DIRECTED BAY AND WASHACE IN TO BOX VPEPING		31.00	117		+	-	\dagger	
VACCV	INVA DISECTED BWA POR VACEDA CE 19 KD DOL VOED TINE	INTERNATION OF THE VISIT OF THE	ī			}	1	İ	Ī
100	PALA MARCHED BUY DON WAR HAVE TO THE WAR WESTING	-				\dagger		\dagger	Ī
1000	THAT DIRECTED AND BOX WATERAGE IN PARTICIPATION	11 02 707 0227				+	+	1	T
VIET ACT	BNA CIBELISO BNA POLYMERACE		35	1111.1111	1716 1463		\dagger	\dagger	T
		NOS (EAV)	1	1041.1077			$\frac{1}{1}$	T	
PREPI DAIVI	1	11/411/10/10)	T			ł		1	Ī
	ANA DIRECTED ANA POLYNGRASE SIRINGT PI	191	20.00	I				Ì	Ī
PRO INCO	BNA DIRECTED RNA POR YAGBASE STRIBBIT PI						1	\dagger	
FREE LAND	RNA DIRECTED ANA POLYMERASE SUBUMIT PT	ARBOR/4/60)	Τ	486.511			1	t	
	ANA DIRECTED ANA POLYMERASE SUBUNIT PI	VANBOI	Τ		Ì				Ì
PRIET LAFR		10\$10CKJ4)	915-900	Ī				\dagger	
PAREZ IAGUZ	RNA DIRECTED ANA POLYMERASE SUBUNIT PI		115.21	Ī			-	t	Ī
PRRF1 IAIRO	ANA DIRECTED RHA POLYNGRASE SUBUNIT PI			Ī		-	\dagger	Ť	Ī
PRRPJ JAHTE	RNA-DIRECTED RNA POLYNERASE SUBUNIT PI						├ 	1	
PRINT IAKOR	ANA-DIRECTED ANA POLYMERASE SUBUNIT PI		464.511					İ	
PRRFY IALE!	RNA-DIRECTED RNA POLYMERASE SUBONIT P?		100					t	
PRRF1 IALE2	RNA-DIRECTED RNA POLYNERASE SUBBNIT PI		484-518						
FRRP3 IAMAN	RNA-DIRECTED RNA POLYMERASE SUBUMT P2	LDAVE W YORKATSO/18)	404.510				-		
PRINTS IANTS	ANA-DIRECTED RNA POLYMERASE SUBUNIT PY		484-510				-		
PARP IAPRO	RNA-DIRECTED RNA POLYMERASE SUBUNIT P?	A11979)	414-5118						
FRKF2 IAPUE	RNA DIRECTED RNA POLYMERASE SUBURIT PZ	П	404-518						
PREZ IARUD	MAN-DIRECTED RIVA POLITICE AND SUBJECT FOR	MENEW JERSEY/47/85)	484.518						
PRACT IASIN	MAN-UNCCLED IN FOLIPERANE SUBORIL FA		484.518						
ı١	KAA-DIKELIED KAA PULI MEKASE SUUKII 17	VICES (STICKEN AT URKEYAMMESOTATION)	414-518						
PRESE IAVII	DAY DIRECTED BY TOUTHERASE SUBJECT BY		25.20						
	BAN DARCTED BAN DOLVING ACE CITITATE BY	INTEREST A VIOLE SERVING A MELLINGER PARTY OF THE	10-310		1			1	
1	PLA CHECKE SAN POR VARRACE CITEDATE DE			Ì		1			
	THE CHEST OF THE POST VICE AND THE PARTY OF	USE IS A TAKEN AND WINGING RUMON (2012)							Ī
17.00	PLA DISCUST BUY DO VIVEDARE CIMINITY DI	CIBILE (STRAIN ASWINGTOWN) VIOLENCE CONTROLLED	16-31				1	1	
200	THE CHECKED BLA POLYMERASE SUBJECT OF	A VIRUS (STRAIG AS WIND) ENABLS SELJION!)	1		1		1		
PART INCHES	BNA DIRECTED BNA POLYMERASE SUBORIT TO	MAN A VINES (STANIS ABOUGH BLANKER ABOUT)	1	25.41			 		
200	BEALTHOUSE THE CANADA C	A VIEW AS PARTY AND THACKE VIEW CONTROLLER	10.00				1		
PRRPS IAGUS	ANA DIRECTED ANA POLYMERASE SUBLIKET PE	A A VIBILIA COMAIN ACTUAL ANAMANANA		1			+	1	
PRRPJ IAGUA	RNA-DIRECTED RNA POLYMERASE SIRIPLIT PI	P. A. VIBLES OF PARTY AND PARTY AND PROPERTY OF THE PARTY AND PART		Ī		+	$\frac{1}{1}$	\dagger	
				1		1	1	1]

14 14 June	2.5		٦	1	T	T	I	Т		
,		YARUS	J	1000	4		T TOTAL			
L						T	+	T		
Т		INTUENZA A VIRUS (STRAIN AMALLANDMEN YORKA 1907)		T		Ī	\dagger	T	l	
		Т						T		
	RNA-DIRECTED RNA POLYNCRASE SUBUNIT PI		20.411					İ		
		T	365.613							
	RNA DIRECTED RNA POLYMERASE SUBURITY	INTERIOR A VIETE (CLEAN ASWINGTENESSEE)	305.611							
٦		INTERNAL WINEY STRAIN BANN ARBOWING ICOLD ADAPTEDIT	135.769							
٦			335.300							
_	POLYMERASE SUB		199.60							
w l			123.609							
٦	ANA DIRECTED HINA POLYMERASE SUBURITY		199.143	324.356			Ľ			
	212	THOUSE OF THE STREET STORY	410-443	113.745	1262-1295	1963-1999	2018-2112 24	2474.2508 3	3153-3191	
PRRPA_CVH23 RNA-DIR		TOWAR COROLL STATE AND STATE BANK	701.740	334.337	337.3785	1933.3961				
		MUMINE CORONAVIACIONALI (STRANIA PRIMA)	0.00 170	2117.2160	2173.2204	Ī				
Г		DERME VIRUS (BEV)	700	210.314	1419.1737	3646.2730				
Т		AN MINE CORONAVINUS MIN (SIRAIM AN)	200.000	711	7	316.3101	2006.2728	İ		
ī	ANA DIRECTED ANA POLYNGRASE		200		7			İ		
Г	RNA DIRECTED RNA POLYMERASE	MIIS COMUNAVIAUS					Ì			
PREPRICATE RNA DIR	RINA DIRECTED RINA POLYMERASE	T						Ť		
Т	RNA DIRECTED RNA POLYMERASE	CONCENTES VIRUS (STRAIN DEAUDELTE) (IBV)	010-010					T		
3	NA POLYMERASE	BUNYAMWERA VIRUS	100.00				+	t		
+	NA POLYMERASE	(GIC FEVER VINUS)					-	İ	I	
-	BWA BOI WATERASE BETA SUBUNIS	VIRUS (STRAIN A2)	226-201	(121:131)				Ì		
TO VINE TO STATE OF THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLU	PAN PASCIED BNA POLYMERASE	MARBURG VIRUS (STRAIN MUSOKE)	146-176	698-736	┪	1101:141	+	1		
_	ECTED BNA POLYMERASE	MANBURG VIRUS (STRAIN POPP)	_	2 . J.	=	2223-2253		1		
T	AND WHEN AND AND AND AND AND AND AND AND AND AN	MEASUES VIRUS (STRAIN EDMONSTON)		647-68)	718-025	1160-1192	1006-1914			
7	TAKEN ASE BETA CITATIONE		1807-1913					1		
PRINT MUNDAN	THE TOT THE MAKE BETTA CITICALLY	-	199-929	8		╗	-+			
T	SAME AND A CHARGE T		364-305				1621-1012	1023.201		
Т	VALEDACE IN TA SIBILINIT	HUMAN PARAINITIDINA J VIRUS (STRAIN NIII 47814)	91.10		_	1111.1139		1		
THE VIEW COMMENT	BILL PHY MITTAGE HETA SUBUNIT		60.90		⇁	1930-1962		1		
_	ENA POR YMERASE BETA SUBUMIT	AABIES VIRUS (STRAIN SAD DIP)	60.40	104-833	1365-1394	1910-1962		1		
THE VIEW THE	BAA DARECTED ANA POLYMERASE	AICE DWARF VIRUS (ADV)	1303-1323					1		
Т	LECTED RIVA FOL YMERASE	RIFT VALLEY FEVER VIRUS (STRAIN 214.548 MIT) (RVTV)	1016-105	1009-104				i		
ī	RNA POLYNETASE DE LA SEREINIT	SI MONI VIRUS (SIRAIN Z 1105T AUTANTS)	=:	23:24	3.					
7	VENEZA CONTROL	CIMEN VIRUS (SIMAIN PAIN RS)	ļ			1477: 1475	- A - C	İ		
	RMA PAKERASI: HETA SIRUMIT	SI MINI VIRUS (STRAIN Z)	25.2	337.760	735.764		2140-2177	Ì	Ī	
SEOUS	ANA DIRECTED RNA POLYNIERASE	SEOUL VIRUS (STRAIM 40.39)	100		1		1	1	Ī	
=	LYNGERASE RETA SUBUNIT	SIMIAN VIRUS 5 (STRAIN 21004-WR) (SVS)	22.28	171	<u>= </u>		1	1		
7	IFMA POLYMERASE BETA SUBUNIT		3	100		10.00	Ť	07 07 000	Ī	
م	RECTED RIMA POLYMERANE	IRIJS (BRAZILIAN ISCRAFII CTAMMININ DI) (15WV)	2	200		100	т			
	HVA INH YMPASI	(ICKUNI MI VIRUS (CUX)	200		Т	1443.1407	1054.1000	T		
	ANA POLYMERASE BETA SIBUNIT	CENTUCAR SIGNAL SITES VINOS	1011.1039	1976-1969	1					
-	FINA POLITACIONE DE LA SOBICIO	VEGICIE AB STORATITIS VIRUS (STRAIN SAN (UAN)	5	209.746	112.340	84 . FE	1011.101	1719.1772 2	1021.2017	
	Š	DEET WESTERN YELLOWS VIRUS (ISONATE FL. 1) (DWYV)	200							
	THE ALL AND AND CHAIN BUT AND		DARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDY)	23.53						
٦.	PHIATIVE RNA DIRECTED RNA POLYMERASE	HARLEY YELLOW DWARF VIRUS (150LATE P.PAV) (BYDV)	111.155				1	İ	İ	
_	PROBABLE RNA-DIRECTED RNA POLYNGIASE	CARNATION MOTTLE VIRUS (CARMY)	5		T		•	Ì		
-	PUTATIVE RIVA-DIRECTED RIVA POLYMERASE	CUCUMBER GREEN MOTTLE MOSAIC VIRUS (WATERAIELON STRAIN SM)	=	3.3	1005-1133	1865-1507		1		
PERIO CNV	PROBABLE RNA-DIRECTED RNA POLYMERASE	CUCUMBEA NECROSIS VIRIUS (CMV)	470-501							
-	PRODABLE RNA-DIRECTED RNA POLYMERASE	CYMDIDIUM RINGSPOT VIRUS	11-62	267.300	Š Š		1			
т	PUTATIVE RNA-DIRECTED RNA POLYMERASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 3270) (IBDV)	16-218	174-303						
Т	PUTATIVE RNA DIRECTED RNA POLYNGJASE	AVIAN INTECTIOUS BURSAL DISEASE VIRUS	2						Ī	
	PUTATIVE RNA-DIRECTED RNA POLYMENASE	INTECTIOUS PANCAEATIC MECROSIS VALUS (SEROTTYE JASPER)	RI S	149.318			1	\dagger		
П	PLITATIVE ANA DIRECTED ANA POR YMERANG	INI LUMBATAN KATATIL MA MAMA VINIMA MATATINA MATATINA								

PCGENE	PDC1121F	All Vicure (as batteringhages)	П	100	. 1	48644	9 7487	7 7 2 8 7	ABFA?
FILEPANE	LBOTELN	CONTRACTOR OF STREET STREET STREET AND ABLICUST.	3 2	2	2017	1	Т	Т	}
FRRPO LYCVA	NWA POLYMERASE	1	Т					Ī	
FRIEND I YOUW		I VARIETY VICCITION FOR MINING STATES WITH					Ì	Ī	
PRINCE STORY	PROBABLE RNA DIRECTED RNA POLYMERAST								
PRRPO PLRVI	PUTATIVE RMA DIRECTED RMA POLYMERASE		16-807						
PRETO PLEVE	PLITATIVE RNA DIRECTED BNA POLYAIERASE		276-603			7			
PRINT PPAVS	PHYTATIVE ANA DIRECTED ANA POLYAGRASE	PIPPLE MILED MOTTLE VIRUS (STRAIN SPAIN) (PPMV)	179.401	102-130	100.00	1004-1100	1311-1363		
PREPOR BONEV	PUTATIVE RNA DIRECTIONNA POLYANTASE	ALD CLOVI'R MICROTIC MITSAIC VIRIUS (ACMAIN)	278-314	320-353					
TAC SECOND	PART DIRECTED BAY FOR VALLEASE	RECVIRUS (14PE 27 STRAIN DY)ONES)	364-315						
	ANA MARCIED BNA POI VAISBAGE CIRITAIT VPI	DOVINE ROTAVIAUS (STRAIN RS)	13.60	165.005	347.376				
1000		POVING ROTAVIRIS (STRAIN (R.)	100.331	347.376					
201010101010101010101010101010101010101		PORTINE ROTAVIRUS (STRAIN GOTTFRIED)	100-111	147.276					
TREND ROING	MAN-DIRECTED ANA POLITICANSE SUBORITORIO	CALLAN TO COLA LYBRIC (CTB AIM CALL)	21.60	200.23	247.176				
PRAPO ROTS	RNA-DIRECTED RNA POLTMERASE SUBOMII VEI	STATE OF THE PROPERTY OF THE P	17.53	18	2070.2112				
PRRPO TACV									
PRRPO 185VC	PROBABLE RMA-DIRECTED RMA POLYMERASE	STRAIN CHERRY (THEY)							
PRING 1CV		ICANIP CRIMKLE VIRUS (TCV)	280-218			T	T		
PRRPO TMCAIV		TOBACCO MILD GREEN MOSAIC VIRUS (TMIV STRAIN UZ)	61.60	28.12	20.24	ī	430.483	20.45	
VALL OF STAN	MITATIVE BNA DIRECTED BNA POLYMERA	TOBACCO MUSAIC VIRUS (VURGARE) (TMV)	121-159	136-406	700.728	1513-1569			
	PARTY BANK CABECTED BANK DON WATERACE	TOBACCO MOSAIC VIRUS (STRAIN KOREAN) (TMIV)	128-139	176-406	700-728	1333-1565			
2	ALIAN MARKETER BAN POR VALERA	TOBACCO MOSAIC VIRUS (STRAIN TOMATOL) (TMV)	661-121	376-406	700.728	987-889	1333-1369		
	TO THE WAY OF THE PARTY OF THE	TOBACCO NECEDER VIRILS (STRAIN A) (TNV)	331-363						
ZAK C	MAN-DIREL IEU MAN TOL TRIEMASE	TOP ACTO ARCED CARLLE ACTORING TO TAKE	9	214.270					
	RNA-DIRECTED RVA POLYNITRASE	TOBACIO PECENSIS VIROS (SI PAIS DISTRIBUTION DE LA COMPANSION DE LA COMPAN							
	RNA POLYNERASE ALPIIA SUBUNIT	CANINE DISTERINGE VIADS (STRAIM ONIDERSTET CONTINUES)							
	ANA POLYMERASE ALPHA SUBUNIT	MEASURE VINUS (STRAIM EDMONSTOR)	366.6						
	RNA POLYNERASE AI PIIA SUBUNII		77.						
L	ANA FOLYNIERASE ALPIJA SLIBLINIT	IAGATA:1)							
PHREE MUNICIPAL	ANA POLYNERASE AI PIIA SUBINIT		211-240						
PRRPP MILLAPE	RNA POLYMERASE ALPIN SUBUNIT		212-249						
PRIED MINGH	INNA POLYNERASE ALPINA SUBUNIT		312.340						
PREP NOVA	-	(ACM) (E	230-355						
BYCH STATE	-	MEWCASTLE DISEASE VIRUS (STRAIN REAUDETTE CAS) (NUV)	330-077						
PREP PLIN	RNA POLYMERASE ALPHA SUBURIT		216-353						
PREP PIET	RNA POLYNERASE ALMIA SUBURIT	INTRIAN PARAING LIENZA 2 VIRUS (STRAIN TOSHBA) (PIV-2)	116-253						
PRILP PICHA	RNA POLYMERASE ALPHA SUBUNIT	HUNIAN PARAINE LUEMEA 4A VIRUS (STRAIM TOSHINA) (PIV-4A)	150-157	333.364					
PREST PARTIES	ANA POLYMERASE ALMIA SUBURIT	HUNIAN PARAINFL (FENZA 48 VIRUS (STRAFM 68-333) (PIV-4B)	120-157	133-364					
PARPO PIRYV	RINA POLYNGRASE AL MIA SUBUNIT	PIRY VIRUS	114.168						
PARPY BABVA	ANA POLYNERASE ALPHA SUBUMIT	AABIES VIRUS (STRAIN AVOI)	116-244						
PREP RABVC	ANA POLYMERASE ALPITA SUBURIT		116.244						
PRRP RABVE	IRNA POLYNERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN ERA), AND RADIES VIRUS (STRAIN THI	116-244						
PREP LABOR	ANA POLYMERASE ALPHA SIMURHIT I	RABIES VIRUS (STRAIN PV)	10-133	316-315					
PRILIT KABVS	RNA POLYMERASE ALPITA SUBUNIT	PABIES VIRUS (STRAIN SAD BIP)	116.244						
PARTY SENDS	TUNA FOLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN Z / 110ST NIUTANTS)	\$30.566						
PRAPP SENTS	RNA POLYMITANSE AI PIIA SIMIMIT	SI MINA VIRUS (STRAIN AND)	\$5. CE						
TREET CINE	BEA CH. YALL BASE AL PLIA SCRIPTION	A RIDAL VIRUS (STRACK) LINGING)	370.364						
PARP SENDA	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (SIRAIN HARRIS)	\$10.566						
PARPY SENDS	ANA POLYMERASE ALPHA SUBLINIT	SENDAI VIRUS (STRAIN 7)	\$96.068						
PRAPP SVS	ANA POLYMERASE ALPIIA SUBLIMIT	SIAHAH VIRUS S (STRAIN WS) (SVS)	199.136						
PARP VSVBJ	ANA POLYMERASE ALPITA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN MISSOUR	191.330						
PRRPP VSVIO	-	VESICH AR STONIATITIS VIRUS (SI ROLYTE NEW HERSEY / STRAIN OCHWIN)	143.310						
PKHK VACIO	_	VALCINIA VIRUS (NIRAIN CONTINUALAN)	19.43						
PSINC VALLY		VACCINIA VIRUS (STRAIN WR)	19.55						
PSODC VARV	•	VARIOLA VIRUS	3				-		
PSPIR AMEPV	SPHEROITIN	ANSACTA MOCRETENTOMOROXVIRUS (AND PV)	20.50	=======================================	627.459	100.100			
PSPII MYXVI	1	MYXONIA VIRUS (STRAIN LAUSAMME)	167.700						
PSPIJ VACEC	SERINE PROTEINASE INIIINITOR I	VACCINIA VIBUS (STRAIN COPT MIAGE'N)	2						!
PSFII VACCV				:				:	:
747 CAR				İ			İ		
F171.9 10WPV	TRAME, AC LIVATOR PROTICES IN		2]		

		S.		ľ			-	Г	
_	PIXCILZIP		415	ABEAL	AREAL	ARCAL	ABEA 2 AR	AREAL	ARIA!
AUG TO A	LARGE TANIKEN	PAIGAR FLEIDGING DISEAST VIRUS (HEDV)	Ī	٦	161.491	j	-		i
_	PACIFIE C. P. ANCICK N.		- -	Ì			_	j	j
-	MICHEL T ANICE N		8					j	İ
_	AUDOLE I ANTIGEN		اء			Ì		j	
PIAND POVIC	MINDLE TANTIGEN	V CRAWFORD SMALL PLAQUE	2			1		1	
FIASM POVBA	SMALL TANTIGEN	(KIRAIN AK)			Ì	1	1	\dagger	Ī
FIASAI POVIN	SAIALL TANTKITH	IN YOMAVIRUS IIK			Ì	İ	1	Ì	İ
PIASNI POVIIA	SAIALL I ANTIGEN				+		1	İ	ļ
PIASAI POVAIA	SAIALL TANTIGEN	S(STRAIN AZ)	2		†	Ť	1	İ	Ī
_	SMALL TANTIGEN					-	1	1	-
Γ	LARGE TEGUNENT PROTEIN	I IERFI SVIRTINA	Ì	sl	-	-	1	1	-
s	PRODABLE LARGE TECUNENT PROTEIN		1	٦	٦	÷	-	Ì	
7	LARCE TECHNENT PROTEIN		٦	٦	=		1037.7012		
т	LABOR TECHNISM PROTEON	I DUME HEAPESTRUS TYPI. I (STRAI). ARAPITEHV.I)			•	~	_		
7	TOTAL STATE OF THE PROPERTY OF		467.505	114.151	131.061	934.760	401-15 W 14	1431.3417	1
7			369.600						
	DAR LEANING THOUSEN		120.01				-		
1	BAANSI CANANG TROUGHT IN AN	ことがなっていても アーマニーン・コース・コース・コース・コース・コース・コース・コース・コース・コース・コース	1 1 1 1 1	105-1143					
Vans.	DAY IONGSAM KAST II			100.1101					
٦	DNA TOPOSONII LASI, II	A THE AND A STATE OF THE PARTY	×			İ			
٦	REL TRANSFORMING PROTEIN	1	2		İ	İ	<u> </u>		
	THY MIDYLATE SYMMAM.			Ī	İ	Ť	<u>!</u>	_	
			T			İ	ļ		-
	I CONSTEROID TOP GLUCOSYLIRANSI ERASE PRI CLIRGO	_		Ī	-	Ì			:
_	HYPOTHE TICAL PROTEIN UR.	1	3.50						,
	VIEW CROITIN BOR!	_	151.186		i				
7	THE PROPERTY OF THE PARTY OF TH		96+ +04						
	Z 11000 17 17 17 17 17 17 17 17 17 17 17 17 17	(CIV:1)	135.55	437.475					
200		11 B P C C 1 B C C C C C C C C C C C C C C C C	011 061					Ī	
	THE STATE OF THE S	C DESTRUCTIVE CONTRACTOR OF THE PROPERTY OF TH	Ĩ	\$02.510			-	-	
2,2,8	7. MCC C. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.		Ť		ļ			İ	i
DO MICHINA	INPOTITE TICAL PROTESS OF	COUNTY OF DESCRIPTION OF THE ACTUAL AND	1		Ì	<u>-</u>	<u> </u> 	Ì	-
_	GENE SEPONE			Ī		i 		<u> </u>	
OB LICKIVA	HYPOTHE TICAL PROTITIVES			Ť	Ì			†	i
	PROTEIN UL			1	\dagger	T	$\frac{1}{1}$	T	Ī
Г		(vzv)			t	Ì			İ
Pi.1.09 HSVII	ORIGIN OF REPLICATION BINDING PROTEIN		1		\dagger	Ì	+	İ	-
Г	DRIGIN OF REPLICATION BINDING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DISLAS) (VZV)	. J.		1	İ		-	::
1	CH. LE FROTLIN HENEN PK:		2			İ	1	ļ	-
	PROTEIN UL 16		25.21						Ī
Т	PROTEIN 10R	162)	103.176			1		1	Ī
PIR 31 CISVER	CENE 40 PROTEIN	r)(EIIV-t)	24. 32	1		1		1	
	PROTEIN ULTI HOMOLOG				1		1		Ì
_	CENE DE PROTEIN		-		•				
~	DAYONG UKAL PROJUMBA	THE PARTY OF THE PROPERTY OF THE PARTY OF TH		Ť	-		1		
٦	PROTEIN ULZ4 PONIULUG			Ī				l	Ī
Т	VINON PROTEIN ULZ		180			İ	l		
TO BYY	VICENCY OF THE PROPERTY.	N DUBIASI (VZV)	5 9	Ī			-		
20.00	VIDOR OCHE JOYNOLEM IN 10		917.68			İ		<u> </u>	
THE REMAND			- 101				<u>-</u>	<u> </u>	i
			161 191					İ	
200	BACKA AND E MAINE ENVELOPE CA YCOPROTEIN BELFI	- 6) (INDIAN HERPES VIRUS 4)	307-196				·		
M. 13 E.			Т	564-592					
P. 11.5V	PROBABLE MADOR ENVELORE OF LOCALISM CO.		Т						ĺ
100	ALCOR ENVELORE CULTURE CONTROLLE CON	Z	38.301			Ī			
	PROBABLE MAKINE ENVELOPE CLYCOPROTEIN 36	N DUNIAS) (VZV)	251-381		-				
PIN IN CIRCLE	. 1		96.130						
NI ILLIANA	INVESTIGATION ULUS	NH ADIG9	138.160						

PUGEN	IPDC1L21P	AB Vive o (no baterioghages)							
FILENAME	PROJUIN		4364	45.54	AREA	ARGAL	SELA L	AREAL	APIAL
MAN MENA	HTTOTHETICAL PROTEIN ULIA	FIGURE CATOMEGALOVINOS (STRAIN ADIEN)	2						
11.11	CELE 11 BOOKEN								İ
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CERE JUTICIES	LOUINE HEALT SAIMIN 1772 L'STANIN ANTIFETT : 1	107-701				Ì		-
H137 V2VB	CENE 21 PROPER	VARICELLA-ZOSTER VIRUS (STRAIN DUBIAS) (VZV)	548.679	704.734	174.106		1		
PIT JI HCAIVA	INTOTHETICAL PROTEIN UL 18	HUNIAM CYTONIEGAL OVINITS (STRATIN AD164)	23.18						
PIA.41 V2VD	HOST SHUTOIF VILLON PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DURIAS) (VZV)	174.307						
FI 49 HSVII	MENINAME PROTEIN (R.4)	HERPES SIMPLEX VIRIIS (TYPE I / STRAIN 17)	2.30			İ	Ī		
114.45 11SV11	GEM: 15 MEMBRANE MOTFIN	VARICELLA ZOSTER VIRUS (STRAIN PIJAIAS) (VZV)	\$	117.300					
FIR OF HICKINA	PROTEIN ULAT	(STRAIN ADIGO)	436.471	741.777					
PIR 47 HSVE4	97 KD ALPHA TRAMS IMDUCING PROTEIN		\$19.05						
TA 47 HSVED	97 KD ALPHA TRANS-IMIXICING PROTEIN	j (Eliv.1)	587-632						
M. 48 115VII	TECUMENT PROTEIN UL 49		226-259						
Mil 49 HSVIII	TECUNIENT PROTEIN ULA HOMOLOG		135.168						
F1.53 f.BV	PROMABLE DNA REPLICATION PROTEIN BSI F1	FPSTEIN-BARB VIRUS (STRAIN RMS D) (HUNIAN HERFT, SVIRUS 4)	182.617						
PIE 22 115V11	DNA REMICATION PROTEIN U.S.		90 620	20.00					
Full 52 HSVEn			٦	9.00	912-947				
FILL 11 INSVSA	PROBABLE DNA REPLICATION GENE SO PROTEIN]	2					
LIE II IICAIVA	FROTEIN U.S.	THINIAN CYTOMEGALOVIRUS (STRAIN ADJOS)	2						
TO SECOND	ULSS FROIL IN HILDARIS (K)		03:136			-			
LILES INCHIVA	GOVERNMENT AL PROTEIN ULBO					1	Ì	Ì	
THE HEAVY		IN MAKE CATOMICALOVINOS (STRAIN ADIOV)	Ī	20.02					
THE STATE OF THE S	VICON PROJECT CONTRACTOR VI	***************************************	ī			1	Ì	j	Ī
Z	TITOTHE IL AL FROITIN OLD	ALIA ALIABA)	T	2			j	Ì	
Y 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	STATES OF THE ST	THE REPORT OF STRAIN THE STRAIN THE STREET STREET		1		1	İ	j	
	THE PARTY OF THE P							1	
PIE INTOVA	MANAGEMENT OF PROPERTY IS OF					1	1	Ì	
	HV90116 11CAT PROTEIN AB	STATE OF THE PARTY OF THE PARTY AND A STATE OF THE PARTY	T						
FIRST HISVSA	HYPOTHETH'AL CENT TO PROTEIN		Τ			\dagger	\dagger	1	
MIN STATE	IIVPOTHE HE AL PROFITE BUNEA	DARCHINA IN RPLSVINIS 41	100		Ì			İ	Ī
PIR 92 HSVSA	HYPOTHETICAL GENE 31 PROTEIN :		31:10				Ì	T	
FIR 91 INTAINA	PROTICIN US.93		107.470			+		\dagger	Ī
rin. 51 Linv	HYPOHIE IKAL PROHINGELL)	PERPESVINUS 4)	=				İ		
LIA BE INCMYA	HYPOTHETHEAL PROTEIN IN THE		81.50	133.181					
VAM MI LINE			¥ .	:	- 	 	<u>-</u>		
VALUE OF THE PARTY	THE PROPERTY OF THE PROPERTY O	A THURST CALL DVINGS (STRAIN ADICA)	2		j				
TANKS IN									
PURC USV		I PSILIN TARE VIEWS (STEAMED) TO LEAST AND APPROVISION AND APP				1	†	İ	
HING VACCC	-		1117		İ		1	İ	
_		:		i	!	<u> </u>	:	İ	
	URACII. IMA GI. YCUS YLASE		1111						
7	HYPOTHETICAL PROTEIN HOLF?		43.13			-			
7	HYPOHETICAL FROTEIN HALFS	(STRAIN ADIES)	13)-190	П					
LOSON INCHAR	HYPOTHETICAL PROTEIN HALF	INDIAN (TICKIEGALOVIRUS (STRAIN AD169)	3			Н			
			2					i	
YAN		THE PART OF THE PARTY STRAIN ALTHUR	Ī	27.61					
TO INCHANGE	HITCHIE IR AL FROILIN HALFS		₹						
Van Heavy	HYDERIKAL TRUEIN HYLT		┪			•			
LOSIO MONA	MINISTRAL PROTEIN HYLLS	TILIMAN C TICKECALUVINUS (SIRAIN ADIES)	٦	Š			•		
HIS I WAY	MEMBRANG PROPERTY IN THE PARTY		2						
TANK BE WAY	CARL THE LEASE SECTION OF THE PROPERTY OF THE	TATION CALINATION (SINASMANICA)	76.73	j					
VAN SEL	TATOLIS IN ALL TAUST IN THE CO.	CALLMI CALICALES (STRAIN ADICA	3						
7		AN CATACATORINA ATTACATA ADIAN				1			
Т	TOTAL PROPERTY OF THE PROPERTY		21.00	1				1	
٦.			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1		1	1	

Process	PERCTURIT	sere (no hatteriophogre)	П	П	1 1 1 1 1 1 1 1 1	****		17.197
Т	PROTEIN		1	1	Т	Т	Т	
VIS ANY	13 KD PROTEIN	/ISTLATE LEIDER				+		-
Т	16 KD PROTEIN	FOBACCO NATILE VIRUS (STRAIN PLI)	70-7					1
ī	POLICASE	AUTOGRAPHA CALIFORNICA NUCLEMA POL VICOROSIS VIRUS	2		1	1	 	
PULL MENIV	17 KD FROIEIN	DARLEY STRIFE MOSAIC VIRUS (PSNV)	66.73		1		1	
L	IA PROTEIN	CLICITATION MOSAIC VIAUS (STRAIN LAV) (CNV)	1	1				1
Ī	Lan Proteix	AFRICAN SWINE FEVER VIRUS (STRAIN BASTV) (ASFV)			1	<u> </u>		 -
Γ	24 PROTETS	NACAD REAMAIOTILE VIRUS	ī	410 411	141 100	<u> </u>	 	<u> </u> -
ı	NI LUCAL VI	LOWPEA CHI OROTH MIDITLE VIRING CAIV)	T	Ī			<u> </u>	
z	Z-101-14	CONTINUE PRINCIPLE VIREIS (STRAIN INV)	ì				1	
÷	Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z	CUCININI & MUSAIC VIRIS (STRAIN Q) (CNV)					<u> </u>	
20.00	2A PROTEIN	TONIATO ASPERBIY VIRUS (TAV)						1
Ì.	NE KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN TCNI)	10.50			1		
Т	7.940	AROAD BEAN AND TILE VIRUS	133-117					
١	The state of the s	REDAKE MOSAIC VIRIS (BASV)	139.189					
1	DA PROTEIN	CHAPT A CHAPTER PRINTER CIBINS ACCURATION	98			L		_
,	1A PROTEIN	CHARLES AND						
PVIA GEVE	1A PROTEIN	AVIAN INTELLIGIS BROWLINGS VIROS IS I RAIN BEAUTION OF THE PROPERTY OF THE PRO					I	-
ł	JA PROTEIN	AVIAN INTECTIONS PROMOTHERS VIRUS (VIRALIN MAIL)				1		ļ
ı	Z-C-Z-V	AVIAN IN LCHOUS BROW HITTS VIRIES					I	 -
PVIA INVIS	TA PROTEIN	A CIAM INFECTIOUS BRONCINTIS VIRIS (STRAIN UK/183/64) (IIIV.)	~					+
L	SO E KD PROTETY	AFPLE CHLOROTIC LEAF SPOT VIRUS IACLSV)	8					
	NI TOTAL CHARGE	INI ET WESTEAN YELLOWS VIAUS (150) ATE PL. 1) (BWY'')	3					
	7.50	THE F WESTERN YELLOWS VIRUS (150) ATE GOL) (DWYV)	B: 35					
TANK BALAN		POTATOL EAFTER L VIRUS (STRAIN LIFT, RV)	26. 592					
	STATE OF THE STATE	POTATOL EAFROLL VIRUS (STRAIN WACIEMINGEN) (PL RV)	160.000					
	A LO PROTEIN	BABLEY CIBINE MORAL VIBING CRAIN	130.53					
ī	SAKD PROJEIN	CONTRACTOR OF CONTRACTOR OF THE PARTY OF THE	130.333			_		
PV 70K PLRVI	66 J KD PROTEIN	TO COLOR TO THE PROPERTY OF TH	130.301	Ī				<u> </u>
_	69 7 KO PROTEIN	FOIRIO LEARGEL VINOS (STRAIN WAGE PRINCIPLES)	101	Ī				
PV90K ANIVLE	90 KD PROTEIN	ALFALPA MOSAFL VIRUS (STRAIM 4227 1904.ATE LEUTEN)		Ī		<u> </u>	<u> </u>	
PVAD VACCC	PROTEIN A4	VACCINIA VIRUS (STRAIN COPEMIAGEN)		1	-	1	-	
PVADA VACCV	PROTEINA	VACCINIA VIRUS (STRAIN WR.)						
PVAO VARV	PROTEIN A4		107			1		
l٥	FROIEN ALL		2				<u> </u>	
	PROTEIN ALI	VARIOLA VIRUS						-
	34 KD ABORTIVE LATE PROTEIN	VACCINIA VIRUS ISTRAIN COPENIIAGENI	8		1			1
PVAIS VACCV	SO KO ABORTIVE LATE PROTEIN	S (STRAIN WR)	8					1
	36 KD ABORTIVE LATE PROTEIN		Ī					1
	PROTEIN A21	VALCTINIA VIRITS (STRAIN COPTINIAGEN)		10.00 10.00		_		
PVAN CANV	PROJECT AND	VARIOLA VIRUS		170.703				4
	PROJEKI A 11	VACCINIA VIAUS (STRAIN COPENIAGEN)	12.36					
1	FROITINAIL	VACCINIA VIRIS (STRAIN WA)	41.16					
PVA II VARV	PROJETE A31	VARIOLA VIRUS	13.76					-
	FROIT IN A 12	VALITIMIA VIRUS (STRAIN WR) AND VALITIMA VIRUS (STRAIN CHEINHAG)	5.3			_		:
	THEFT IN ALL	VARITH A VIKILS	2.5					
PVA46 VACCC	PROJEIN A40	VACCINIA VIRUS (STRAIN COPENHAGEN)	5					-
PVAGI VACCC	PROTEIN ACT	VACCINIA VIRUS (STRAIN COPERBIAGEN)	21.2			1		
PVA41 VACCV	PROJECT A41	VACCINIA VIRUS (STRAIN WR)	2.12					_
VAA I VAN	PROTEIN A4)	VARIOLA VIRUS	95.130				 - 	
אַנונע אַנונע	PECEL IN A C.	VAC INIA VIRIS (STRAIN CIPTINIACII NI	3.2	į		-	_	į
V. FIAN UANT		VALCINIA VIRING (STRAIN WIN)	107.143			1		4
Post i Brita	ALIPROTEIN	BEET CURLY TOP VIRUS (BCTV)	19:113					4
VALUE OF THE PARTY	ALI PROTEIN	REAN COLDEN MOSAIC VIRUS	19.410					
	A1 - PEO150N	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844	411.98					
	ALL PROTEIN	CASSAVA LATENT VIRUS (STRAIN MICHAIAN)	1113					
>	NI CITAL TOT	FOTATO VILLOW MOSAR VIRUS (1908 ATL VENEZIIT A)	10.11					i
A	2 10 10 10 10 10 10 10 10 10 10 10 10 10	TOWARD CONTRINSION VINES (1CANV)	9		4			1
7	ALL PROTEIN	TIMIN III VI I I I IV I I AI CIRI. VIRIN STRAIN MARKIANIN 1,1 VI VI						-
1 YI.C.V	ALI PROTEIN	TOWARD VILLOW IT AS CORT, VIRUS (TVICV)	2					-

	100000	Value of the Parish and Parish an			Г			П	Π
1	PROTEIN		TVIIV	AREAI	77717	ত চত্ত্ৰত	AREA! AREA!	र्वेष	4
P	AL) PROTEIN	BEET CLIALY TOP VIRUS (SCTV)	82-115						Ī
	AL SPROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 144)	77.113						Ī
	AL DESCRIP	CASSAVA LATENT VIRUS (STRAIN MICERIAN)	17:11)					1	Ī
PVAL TYTCH	AL PROJETY	IONIATO YELLOW LEAF CURL VIRUS (STRAIN MATAIANDE) (TYLCV)	71.116					1	Ī
	ALS PROTEIN	TONIATO YELLOW LEAF CURL VIRUS (TYLCV	77.13					+	1
PVAT CAMVC	APHID TRANSMISSION PROTEIN	CALIL IF LOWER AIOSAIC VIRUS (STRAIN CM-1841) (CANIV)	ŝ	=				$\frac{1}{1}$	Ī
PVAT CAMPO	APIED TRANSMISSION PROTEIN	CAIL IFLOWER MOSAIC VIRUS (STRAIN DAI) (CAMV	ŝ	103-130				+	1
1	APIRD TRANSMISSION PROTEIN		ŝ	===				1	1
Т	APIND TRANSMISSION PROTEIN		2	=				+	Ī
Т	APIED TRANSMISSION PROTEIN		2	=				1	Ī
Т	APHID TRANSMISSION PROTEIN	5	3.5	110					Ī
Т	PROJENOA	VACCINIA VIRIIS (STRAIN COPENIIAGEN)	174-156	409-525					Ī
PVBO4 VACCV	PROTEINS	VACCINIA VIRUS (STRAIN WR)	124-156	489.525					Ī
PVBO4 VARV			120-925						Ī
MANUE COWPX	INTERLEUKIN-I BINDING PROTEIN PRECURSOR		*					.	1
VACCV	INTERLEUKIN-I BINDING PROTEIN PRECURSOR		19.126					+	1
DOWN SIEVA	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN COPENTIAGEN)	213-244						1
9777	STREAM ANTICEN SPRECIRSOR		311-343						-
2000	SIREACE ANTIGEN SPECIFISOR		111.343						-
7877 01070	CIREATE ANTIGEN SPRECUTSOR		111.242						
07124	201 DEC 100 CO.	BEAN GOLDEN MOSAIC VIRUS	166-198						
A COLOR	C BECIEVA COURT ED BETER TOR MOMON OG CI		98.130						
TALES OF THE		VACCINIA VIRUS (STRAIN COPENIACI M)	109.130	113.2116					
		AN TIME AND THE PROPERTY OF TH	6116	103-215					
		VIEW A VIEW	100.00						<u> </u>
	THOUSE IN CASE	VALCINIA VIRUS ISTRAIN COPLINIAGO NI	19.91			İ			1
ארם אינור	TRUIS CONTRACTOR CONTR	CACTOS CREATERS	19.61						i
אַרני אַרני אַ		VARIOUS VIRIS	19.01						i
TANK STATE	TACING OF THE PROPERTY OF THE	CIBIOS STRAIN RASZALICA VI	10.03						<u> </u>
PYCO' STVKA	POTENTIAL PROPERTY		333.610			İ		L I	<u> </u>
TO ALCO	PODUCION		33.410					<u> </u> 	
A COUNTY	HVPO1071CAL PROTEIN CIO		12.131						
PVC 10 VACCC	PROTECTO	VACCINIA VIRUS (STRAIN COPENHACH M)	21.130						il
1	PEDITING	(タン) アンドラン (アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・ア	-						i
Ī	PROTEIN CIO	VARIUR A VIRUS	21:12E						
L	PROTEIN C11/817	VACCINIA VIRIIS (STRAIN COPENHAGIM)	1.)1						j
PVCAP FBV	MAJOR CAPSID PROTEIN	FPSTEIN DARR VIRUS (STRAIN DRS D) (HUNIAN HERPESVIRUS 4)	148-183	300-310					!
PICAP IKNIVA	MAJOR CAPSID PROTEIN	HINGIAN CYTCAL CALOVINIS (STRAIN ADICA)	=	2	240.746			1	_
FICAP IISVII	MAJOR CAPSID PROJETS	III BPLS SIAPLEN VIRUS (TVPE 1/STBAIN (7)						1	ī
PICAP HSV6U	NAJOR CAPSID PROTEIN	THE RESSERIE LA VINUS (1978 B.) SHALIN UCANDA-1102)	19:10	989 989	A91-191			+	Ī
PACAP HAVER	MAJOR CAPSID PROBLIN	THE PERSON OF TH		10.174	316.346	104.) IPPR		<u>j</u> T	İ
FVI AF JIVVA	MANUAL AND THE STATE OF THE STA	FSEUDORANIES VIRIS (STRAIN INDIANA SILPRVI	160.121	260.269					Ī
200	MAKON CAPCID PROFILE	VARICITA POSTI & VIRTIN STRAIN INIMIANI (V.V.)	3						
TO ALL PARTY	X = C = X = C		1 2 3					L	
PVCON! ADEB!	KENOR CORF. PROTEIN		11:11						
PVIDI VACCO	PROJETH DI	VACCINIA VIRLIS (SIRAIN COPTINIACII NI	2	104-107				-	-
Frimi VACE V		VALCENIA VIREIS (VERAIN VER	ا ! ج	~				<u> </u>	į
PVIDI VARV	PEC11:(N1)1		9	2				1	
PVINO FOURT	93 6 KD PROTEIN							1	1
PVD05 VACCC	PROTEIN DS	VALUNIA VIAUS (SI ILAIM LUPERIIAUEN)						<u> </u>	1
PVD05 VACCV			10.14					+	Ī
LADOS VALV	PROTEIN DA		1717				-	-	Ī
200		VACCIMIA VIRUS (SIRAIN DAIREN I)	99-1						
PVI B VACC	: : : : : : : : : : : : : : : : : : : :	VACCINIA VINCIS (SINAIN (TATEMIACION)	278-260	430-450	\$11.540				 !
PVI IS VACCV		VACCINIA VIRUS (STRAIN WR)	236-260	430-454	\$11.540			-	
									İ

		VARIAL VARIAS V	20 1 1 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	316-347	<u>- </u>			
		IN POL VIIEDROSIS VIRUS (ACAINPY) IN POL VIIEDROSIS VIRUS (ACAINPY) AN POL VIIEDROSIS VIRUS (ACAINPY) AN POL VIIEDROSIS VIRUS (ACAINPY)	10	187(16)				
		A POLYHEDROSIS VIRUS (ACAINPY) A POLYHEDROSIS VIRUS (ACAINPY) AN POLYHEDROSIS VIRUS (ACAINPY)	1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	9) 3)11				
		A POLYHEDROSIS VIRUS (ACAINITY) US TYPE I A POLYHEDROSIS VIRUS (ACAINITY) AA POLYHEDROSIS VIRUS (ACAINITY)		187.0				
		US TYPE I IR POLYHEDROSIS VIRUS (ACKINPY) AR POLYHEDROSIS VIRUS (ACKINPY) AR POLYHEDROSIS VIRUS (ACKINPY)		10.51				
		LA POL YHEDAOSIS VIRUS (ACAINIY) LUS TYPE I TR POL YHEDAOSIS VIRUS (ACAINIPY) AA POL YHEDAOSIS VIRUS (ACAINIPY)		117:00				
		A POL VHEDROSIS VIRUS (ACAINPY) A POL VHEDROSIS VIRUS (ACAINPY) AR POL VHEDROSIS VIRUS (ACAINPY)		111111111111111111111111111111111111111				
		US TYPE I REPOLYIEGROSIS VIRUS (ACKINPY) AR POLYIEGROSIS VIRUS (ACKINPY)		117:40				
.		US TYPE I R POLYHEDROSIS VIRUS (ACAIMPLY) AN POLYHEDROSIS VIRUS (ACAIMPLY)		115.6				
		US TYPE I R POLYIEDROSIS VIRUS (ACAINPY) AR POLYIEDROSIS VIRUS (ACAINPY)		111111111111111111111111111111111111111				
		US TYPE I IR POLYIEGROSIS VIRUS (ACKINPY) AR POLYIEGROSIS VIRUS (ACKINPY)		155.0				
i : :		US TYPE I R POLYHEDROSIS VIRUS (ACAINPLY) INV 1) AR POLYHEDROSIS VIRUS (ACAINPLY)						
: :		US TYPE I LA POLYIEDROSIS VIRUS (ACKINPY) LIPY I) AA POLYIEDROSIS VIRUS (ACKINPY)		117:10				
: [US TVPE I N. POLYJIEDROSIS VIRUS (ACAINPY) HIPV I) AR POLYJIEDROSIS VIRUS (ACAINPY)		115.0				
		US TYPE I R POLYIEDROSIS VIRUS (ACAINPY) IPV 1) AR POLYIEDROSIS VIRUS (ACAINPY)		1100				
		US TYPE I IR POLYHEDROSIS VIRUS (ACAINPY) AR POLYHEDROSIS VIRUS (ACAINPY)						
l I I I I I I I I I I I I I I I I I I I	KOPROTEIN NO PROTEIN EA PROTEIN EA PROTEIN EA PROTEIN ET PROTEIN ET PROTEIN ET PROTEIN ET PROTEIN		1.10 1.10 1.10 1.10 1.10 1.10 1.10 1.10					
I I I I I I I I I I I I I I I I I I I	KO PROTEIN KO PROTEIN ESA		25. 25. 25. 25. 25. 25. 25. 25. 25. 25.					
I I I I I I I I I I I I I I I I I I I	KOPROTEIN KOPROTEIN EA PROTEIN EA PROTEIN EA PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN		5.761 17.790 17.790 16.190 17.107 17.					
the last to be be the first to the	KOPROTEIN KOPROTEIN KOPROTEIN ESA RAGIEIN ESA RAGIEIN ESA RAGIEIN ESTRUITEIN ESTRUITEIN ESTRUITEIN		1.201 17.200 17.200 17.101 17.102 17.103 17.					
l led balakkut : i l	KOPROICIN KOPROICIN EA PROICIN EA PROICIN EA PROICIN EA PROICIN E PROICIN E PROICIN	1 1 1 1 1 1 1 1 1 1	7.790 1.190 1.101					
l lul lul-lelul : i l	KO PROTEIN KO PROTEIN KO PROTEIN EN AROTEIN ET AROTEIN ET AROTEIN ET PRO	1 1 1 1-1 1 1 1	20 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2					
late la	KD PROIEIN KD PROIEIN ESA PROIEIN ESA PROIEIN ESA PROIEIN ESA PROIEIN ESA PROIEIN ESA PROIEIN ESTRUILIN	1 1 1 1 1 1 1 1	8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					
let balalelet : i	KO PROTEIN KO PROTEIN KO PROTEIN EA PROTEIN ET AROTEIN ET PROTEIN ET PROTEIN ET PROTEIN ET PROTEIN ET PROTEIN	1 1 1 - 1 1 1 1	17:107 13:107 1:53 1:54 5:56 5:56					
and the last of the	KO PROTEIN ELA RACIEIN ELA PROTEIN ELA PROTEIN ELA PROTEIN ELA PROTEIN ELA PROTEIN ELA PROTEIN	1-1-1-1	5.56 5.56 5.56 5.56 5.56 5.56					
1 ()	NO PROTEIN ELA FROTEIN	1-1 1 1	2 2 2 2 2					
1 1.1 1	KO PROTEIN ELA PROTEIN ELA PROTEIN ELA PROTEIN EL PROTEIN EL PROTEIN EL PROTEIN	LVIEDROSIS VIRUS (ACRINPV)	3 3 3 3 3					
tal lata in the	KO PROTEIN EST PROTEIN EST PROTEIN EST PROTEIN EST PROTEIN EST PROTEIN EST PROTEIN		3 3 3 3					
	EA PROTEIN EA PROTEIN EA PROTEIN ET PROTEIN ET PROTEIN ET PROTEIN ET PROTEIN		3.56 3.56 3.56					
1-1.1	EA MOLEN EA PROTEIN E PROTEIN ET PROTEIN		2.5					
_1.1 • • • • • •	EA PROTEIN E PROTEIN E STRUCTION							
	ES PROTEIN				_			
	ES PROPEIN				1			
	ES PROJEIN				1		1	Щ
: [ESPROIEIN	INUS TYPE I	11.50	1	1		_	L
1			99.140	-		1	<u> </u>	
	N. J. C. Z.		91.128	_	-		 	
Ī			×.30	<u>_</u>				
		LICHTAN FAFIL CALAVIRIES FOR S	8.50					
١			47.01				_	_
PUET HEVOR ET PROTEIN				_	<u>:</u>	_	_	_
	· · · · · · · · · · · · · · · ·			_	_			_
TVI TOPICIO								ļ
MILITARY OF THE PROPERTY.	7		41.13					
	7		47.61				1	1
1			68-64					
TILL IN THE PROPERTY OF THE PR			41.64					
1			8		-			اِ
- 1	2		2		-			
PVET 10PV47 ET PROTEIN	Z	THEN PAPEL LINIA VIRIES LYPE A	7				_	
ļ		:		-			<u> </u> 	ļ
ryly lirva 1.3 cmoil IN	Z		55.90		+	1		ļ
_			47.83		1			1
NIBLORG ES PROSEIN			41.00					ļ
l.	2		19-03					1
T	-	SI VIETE DESK VIRUS (ACAINPVI	5	650-678				4
T.	NIJIO44 CA VA	ī	14.10					
Ţ		KANULOSIS VIRUS (1993)				-		
٠,	N. M. Cont.					-	-	
TALINA III.A	INVELORE TO STORE OF THE PRECISE OF	-					-	H
7	CAVELORE OF TOOLSON		21.10	1	+			
	A CELOTE PROPERTY	TYPE 3 (MCVII)						
ENV MC1.1 MAJOREN	MAJOR ENVELOPE PROTEIN		2		+			L
PVENV VACCC NAJOREN	MAJOR ENVELOPE PROTEIN		2		+			-
TENY VAFCE MAJOREN	NVELOPE PROTEIN		2					-
PVENV VACCP MAJOR EN	NVELOPI: PROTEIN		Ž					-
VINC VACCO MANDE IN			133-187	106-241				l

PCT/US95/16733

						-	_	L	
PCGENE		All Victors (no December 1)	ARCAL	Γ	ABEAL	AREA! AREA!	A3 AREAS	AREA 1	H
IL CRANK	IROTE	VALCINIA VIBIIS ISTRAIN COPENDIAGENI	Γ	61.93					7
PVF03 VACCC		VACCINIA VIRGS (STRAIN CO CONTOCO)		(6:19					
PVF03 VACCV	-	VACCINIA VIKUS (SIRAIN WA)	9				 -		
PVIPI FOWPY	_	POWLFOL VIAUS	217.267		<u> </u>	-			1
PUTPE FOWPY	-	TO SELVE A VIRGO	1						<u> </u>
TYPY CAPAK	PROTEIN F7	VACCINIA UBLICACIONIN CONTRACTOR	3						
LANCE:	I A KD F USION PARTIESIN	VACCINA VIETO CITA WELL	19-07			_			
ארני	-	VARIOLA VIRUS	19-12						ı
AVACA STATES		ICTALUND HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	317.146						-
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MITOTICAL CENE 1 PROTEIN	EQUINE HERPESYTAUS TYPE I (STRAIN ABUP) (EHV-1)	81:0						٦
2000	NE DEP	VACCINIA VIRUS (STRAIN WR) AND VACCINIA VIRUS (STRAIN CUFI:NITAGE	91.19						٦
	ISATIN BETA THINGENICABRAZONE DEPENDENT PROTEI	VARIOLA VIRUS	92.120						١
PVCO1 UPVI	INVESTIGATION OF THE PROPERTY	ICTALUND HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	9(1-801						Ī
TACE CON	CHANGE COME A LANGE AND DECTOR	INTALITATION HERPERVIALIS I (CHANNEL CATRISH VIRUS) (CCV)	24-83						
INCH SOL		VACCINIA VIRUS (STRAIN COPENHAGEN)	961.66						
374	TAULEN CO	VARIOLA VIRUS	96.136						ī
SALES VALUE	TO MISSION	VACCINIA VIRUS (STRAIN COPENIAGEN)	113-145						
77.00	23104	VARIOLA VIRUS	113-145						
		VACCINIA VIBIIS ISTRAIN COPENIIAGEN	103.33						
2000		VACCINIA VIRUS (STRAIN WR)	106-301						
200	THE PROPERTY OF THE PROPERTY O		101-118						
1000	DEPOSITION OF ALCENDARY PROTEIN	PESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	150-183						Ī
PVG13 HKVII		ICTALUND INDESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	106-243					_	Ī
A SAC STATE OF THE PARK A	HVPOTIGETICAL CENE 12 PROTEIN		901-17					_	Ī
STATE OF THE PARTY	CANCID BEOTEN		Γ	Г	414.452				
	INVESTIGATION CENE 22 PROTEIN		Г	647-678					
	LIYPOING TICAL GENE 23 PROTEIN	ICTALURID HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	30-108					4	ī
1	INPOTITETICAL GENE 26 PROTEIN	ICTALUNID HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	94-125					4	1
PVG23 HSVSA	HYPOTHETICAL GENE 17 PROTEIN		36.74					-	Ī
PVG28 HSVII	HYPOTHETICAL GENE 28 PROTEIN	VIRUS) (CCV)	101-331					1	ī
PVG2R AMEPV	IIYPOTIETICAL GIR PROTEIN	AMSACTA MOOREI ENTONIOPOXVIRUS (AMEPV)	2		1			+	ī
PVG2 SPV4	GENE 2 PROTEIN	SPIROPLASMA VIRUS 4 (SPV4)	10.74	1	†			+	1
rvc35 115VII	HYPOHIERCAL CEME 35 PROTEIN	TELECOTOR CALLES VINCE I (CITANNEL CALTESTI VINCE)].	2	1			ļ	ī
PVG16 HSVSA	POSSIBLE TYROSINE-FROIEIN RIPASE	CTALLIBID AS RESERVICING LICHARMS CATERON VIRIANICON	T	717.177	-			ļ	Ī
PVC NOVE	HISPOTIETICAL GENE 40 PROTEIN	III. LESVIRUS SAIMIRI (STRAIN II)	Ī					L	Π
INCEL TEXT	LIYPOTITETICAL GENE 41 PROTEIN .	ICTALITATIO FIGRITIS SYRUS I (CHANNEL CATFISH VIRUS) (CCV)	1	32:33					
PVG42 185VII	HYPOTHETICAL GENE 42 PROTEIN		\$21-16						1
PVG43 115VII	HYPOTHETICAL GENE 4) PROTEIN F		100-140	3.63	1			4	Ī
rvc46 HSVII	PROBABLE MAJOR GLYCOPROTEIN	HANNEL CATFISH VIRUS) (CCV)			1	1		1	١
PVG48 IISVSA	HYPOTHETICAL GENE 4 PROTEIN	INEACES VINOS DAIMIN (STRAIN 11)	25.137		1	1		\downarrow	T
PVG50 HSVSA	PROBABLE TRANSCRIPTION ACTIVATOR ELACT	ICTAL DRIVING STRUCK I ICTAL CATERIA VIRISMICA	3	67.73	T		<u> </u> -	-	ī
MAN CENT	٠.	ICTALURID HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	¥					L	Ī
PVGSS 115VII	HYPOTHETICAL GENE SS PROTEIN	ICTALUMD HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)						Ц	
PVGS6 115VII	HYPOTHETICAL GENE M.PROTEIN	ICTALUND HERFESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)		631-663	1091-1126				
PVGSE IISVII	HYPOTHEFICAL GENE SE PROTEIN	ICTALUND HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	25.33	200	1	1	1	4	1
PVGSB HSVSA	GENE SE PROTEIN	HEADESVIAUS SAIMIRI (STRAIN II)	9	3	1				1
PVC:S9 115V)1	_	ICTALLINIO BERFESVINOS I (CHARMEL CATEISTI VIRUS) (CCV)	=			+		+	Ī
TVG1 115 Y	SIYPOTILETICAL CENE 61 PROTEIN	ICTALUMID IERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	5.18	T	1,7	+		+	Ī
PVC64 HSVII	IIVPOTIETICAL GENE 64 PROTEIN	IL I ALUMD REALESVIRUS I (CHARMEL CATHISM VINUS) (CCV)	2		700		-	\downarrow	Ī
PVG65 IISVI	HYPOTHETICAL GENE 65 PROTEIN	ICTALIBED MENTES VINUS I (CHANNEL CATEISM VINUS) (CLV)						+	Ī
PVG67 HSWI	INTOTIBLICAL GENE OF PROFEIN	KINCHAN ACAM VIBIR COVIDERS II			Ť	+		\downarrow	Ī
ANCE SPVIA	CENE O TRUITING	HERICANIS CALLET STRAIN III	36.10		1			ļ	Ī
PVC) ISVA	MINESTER CONTRACTOR OF THE PROPERTY OF THE PRO		Т	128-751	115-116	1252-1265		\downarrow	T
PVOVE HOVE	INVESTMENT OF THE STREET OF THE STREET	ICTALUND HERPESVIRUS I (CHANGEL CATFISH VIRUS) (CCV)	<u> </u>	117.01			 -	ļ	T
::.20			1						1

PUGLNE	PERCEUSIF		Т	18643	ABEAS	ABEA	AREA S	AREAG	ARIA
II.E.NANE	PROTEIN	LIPEUS CATRICA VIRGINISTERY		Т	T	Г	Т		
ry Gre IISVII	HYPOTHETICAL GENE 16 PROTEIN		3						
PVGJ SPVIA	GENE 7 PROTEIN	STROPLASKIA VIKUS STV. REAL BEAUDETTE) (IIIV.)	1319.1347	1036-1301	3109-2146	160[-100[
F C 18/1	-7	HIGHAN CYTONICAL OVIRUS (STRAIN AD169)	51.0	135.185					
S	GLYCOPROTEIN HIGH PACTURED	DOCINE CORONAVIRUS (STRAIN F15)	1350.1304						
	ELOUTO TO THE PROPERTY OF THE	DOVINE COROMAVIAUS (STRAIN L®)	18.18						
•	STOCKED FINANCIAL SOCIETY OF THE SOC	BOVINE CORCHAVIRUS (STRAIN LY-138)	28.28						
	CONTRACTOR SOFT	DOVINE COROMAVIRUS (STRAIN MEBUS)	28-124						
1	STOREGIST SECTION AND AND AND AND AND AND AND AND AND AN	INDIVINE CORONAVIAUS (STRAIN QUEBEC)	2						
	CONTRACTOR OF THE PRINCIPLE SOR	DOWNE CORONAVIRUS (STRAIN VACCINE)	1239-1246		Ī				
		HIUNIAN CORD'A VIRUS (STRAIN 229E)	105						
	C. C. VOORDIEN PRECIESOR	AIURINE CORONAVIRUS MINV (STRAIN WILD TYPE 4) (ANIV-4)	267.1304	Ī					
	ES CI VEOSEOTERN PRECUESOR	ARLIAINE CORONA VIRUS BOIV (STRAIN ASP	212 122						
2000	FIGURE OF PRECUESOR	ATURINE CORONAVIRUS ABIV (STRAIN MINIV / VARIANT CL-3)							
	ET CLI VOGEOTEIN PRECURSOR		=						
PVG 2 CVPS	ET CL YCOPROTEIN PRECURSOR								
PUGES CVPAII	EJ GL YCOPROTEIN PRECURSOR		177.00	17, 11,	171				
PUGLE CVPR	EJ GLYCOPROTEIN PRECURSOR		Т		71.				
PYCE STATE	EJ GLYCOPROTEIN PRECURSOR	FORCINE TRANSMISSIBLE GASTROENTERITIS CORCHAVIRUS		104.1110					
PVGL2 CVFR3	ET GLYCOPADIEIN PRECURSOR	PORCINE RESPIRATORY CORONAVIRUS	Т	97.51	1104-1110				
CVPRNI	ET GI. YCOPROTEIN PRECURSOR	ACT BAIN MED	ī	714.742	1326-1361				
VGL) CVPRI	ES GLYCOPROTEIN PRECURSOR		ī	136.767	1331-1366				
	EJ CLYCOPROTEIN PRECURSOR	THE INTELLIBOR TENTONING VIOLE AND REALIBERTED VIOLE	181.181						
PVCL1 IBVB	ET CLYCOPROTEIN PRECURSOR	AVIAN INSECTIONS UNCACHING VINOS (STRAIN ADIAN)	T	151.70					
PVGLD INCAVA	GLYCOPROTEIN B PRECLIRSOR	THOUSE OF THE SECOND STATES OF	T	701.144					
PVGLD HCRIVT		TICHTAR CALLONIC STATES AND ALCOUNTY INCANDALLION	2						
PVCLB HSV6U	GLYCOPROTEIN R	DOWNE JERRECKIETS TYPE I	334-388						
בינוף מצים	GLYCOPROJEIN THE CHASON	HOVING HERPESYTHUS TYPE 3 (STRAIN HAIV) (HOVING ALANIMILLI IIIS VIRUS	145.324						
	CALVOURD TO THE PRESENCE OF TH	BOVINE HERFESVINUS TYPE I (STRAIN COOPER	111.181						
100 E	CHACOPROTEIN PRICEINSON	INFECTIONS LARYNCOTRACTIONS VIRUS (STRAIN 612) (B.IV.)	443.472						
rvean navs	C. V. OFBOILIN II FRI CHRSON		3						
PUCLO ILTUT	CL VCOPROTEIN IN PRICONSOR	MAIN THORNE VARD III.TV)	Ī						
	S GLYCOPROTEIN D PRI CURSOR	NICEIN CYTONICAL DIVIEUS (STEATH SMITH)	19:101	2					
PVGLC 115V11	GLYCOPACIEIY CPECUESOR		18						
1	GLYCOPROTEIN C PRECURSON		415.465						
PVG.C IISVI	STATE OF STA		416-466						
			475.507						
SALVE STATE	_	VARICITALA. ZUSTIR VIRUS (STRAIN DUMAS) (VZV)	Π	\$13.548					
PVGLC VZVS	-	VARICELLA ZOSTER VIRUS (STRAIN SCOTT) (VZV)	ī	\$13.548					
PVGLD IBVEA		(STRAIN ARI) (TINV-1)	2	į	-		. ! ! !		; 1
PVCH IS HISVER		CARNER AND SAME AND S	Ī	2 2 2					
PVCLD HSVEK	CLYCOPROTEIN DIRECURSOR		\$ 13						L
PVCLE HSVE	GLYCUROLEIM E		Ī	27967					
	STATE OF THE PROPERTY OF THE P		61-100	111-111					
	$\overline{}$	PULLINGALIST VIRIS (STRAIN RICT) (FRV)						 -	1
LVILL STAY		HUVING BESTERATORY SYNCYTIAL VIRUS (STRAIN ANTHU) (ITES)	ī	# SII			1		
PVCLF BR VC		DOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COFENIAGE!) (DRE)							
PVGLF BRSVR	1	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRADA ROY4) (DRS)							
ייכון נפוס	FUSION G. YCOPAO EIN PRECURSOR	CARINE DISTERIFER VIAUS (STRAIN OPOBRASIE/POURI) (CUV)	(1.5) N						
PVGLE HRSVI	7	Т	(15:51)						
PVCH FUMSVI.		A / STRAIN LUNG)	€ F 313						
PVGLF HASVA	Т	.US (STRAIM RSS-1)	3						
10.00	FLISION CLYCOPROTEIN PRECURSOR	ALEASLES VIRUS (STRAIN EDMONSTON)							

HILL BANE N'CLF HEAST N'CLF HE	PASIEIN	NEASLES VIRUS (STRAIN IP-)-CA	117-359	134.487					
		.A1A.11	Ι				_		
	FUSION GLYCOPRUIETS PRECURSOR			181-484					
MICAPE MICAPE MICAPE MOVI. MOVI. MICAPE	FUSION CLYCOPROTEIN PRECURSOR	ALIVIPE VIEW COMMANDED		446-474				1	
MUMPS MUMPS MUMPS MOVI MOVI MINC	FUSION CLYCOPIOTEIN PARLUANON	AND IPS VIRUS ISTRAIN MITTALIARA VACCINE)	2					1	
MUMPS MOOVE MINC	SOSION CALVE CONTRACTOR SOR	AIUAIPS VIAUS (STRAIN AW)	2	,,,,			\dagger	1	
7 20 V	POSICIA CLA COTACO PARTICIONALE PROPERTINA CONTRA C	AIUAIPS VIRUS (STRAIN SOL)					+	T	
MON.	FINANCIA VOORBOIEN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN ITALIEN4S) (NDV)	132-163				1	T	
	FIRITION CLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN LAS/46) (NOV)						T	
11	FINION GLYCOPROTEIN PRECURSOR	PHOCINE DISTEMPER VIRUS	211-20						
T	CIRCON CI VCOPROTEIN PRECUASOR	HUMAN PARAINFLUENZA I VIRUS (STRAIN C.19)	,						
	STRING CT VEOPROTEIN PRECURSOR	BOVINE PARAINFLUENZA J VIRUS						T	
T	FIRE CLYCOPROTEIN PRECURSOR	(4788)		444 446				T	
NU.	STRING CLYCOPROTEIN PRECURSOR (767-07	8			İ	T	
7	SI KIND CI VCOPROTEIN PRECUTSOR		767-07					Ī	
	CINCOL VOCEDIFIN PRECIDEOR	SENDAL VIAUS (SIRAIN Z / HOST ARUTANTS)	100						
T	GIRMON CH VOOPEDTEIN PRECUTSOR	SENDAI VIRUS (STRAIN FUSHINI)							
L	FIRION GLYCOPROTEIN PRECUASOR	SENDAI VIRUS (STRAIN STARUS)						T	
т	FINSTON GLYCOPROTEIN PRECURSOR	SEMDAI VIRUS (STRAIN HVJ)					+		
CUNE CENTRAL	FIRSTON CLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN 2)						T	
_	FUSION GLYCOPROTEIN PRECURSOR	SINITAN VIRUS 3 (STRAIN W1) (SV3)							
2	FLISTON GLYCOPROTEIN PRECURSOR	TURKEY RHINDTRACHEITIS VIRUS (TRIV)							Ì
-	GLYCOPIOIEIN G PRECURSOR	EQUINE HEADESVIAUS TYPE I (STRAIN ABOP) (EIIV-I)	107.76						
т	CPIKE GLYCOPROTEIN PRECURSOR	SONCINUS YELLOW NET VIRUS (SYNV)							
١	CHIKE CLYCOPROJEIN PRECURSOR	VESICULAR STORIATITIS VIRUS (SEROTYPE INDIANA / STRAIN CLASCOW)							
_	CPIKE CL YCOPROTEIN PRECURSOR	VESICULAR STONIATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN CODEN)	740-160					Ī	١
_	COLUMN CI VIOLETIN PRECUASOR D	VESICIA AR STOMATITIS VIRUS (STRAIN ORSAY)	930.00					Ì	
1000	CHEKE CH YCOPROTEIN PRECURSOR	VESICULAR STORIATITIS VIRUS (STRAIN SAN IUAN)	430.48						
_	CI VONTOTEIN II PRECURSOR	HUMIAN CYTOMEGALOVIRUS (STRAIN AD169)	417.144					Ī	١
_	CL YCOPROTEIN II PRECURSOR	HUMIAN CYTOMEGALOVIAUS (STRAIN TOWNE)	917-044					T	١
NO. II INVAC	CI VCOPEDITION IF PRINCIPASOR	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN GS)	22.50	200					
PACE IN MENEA	GLYCOPROJEIN II PRECURSOR	EQUINE HERPESVIRUS TYPE 4							
NOT IT SEVER	CI VCOPROTEIN II PAECURSOR	EQUINE HEAPESVIRUS TYPE 1	100./00						l
VALUE OF STREET	INTERNATION PARTY CONTROLLEN PRIX URSOR	HUNDAN CY IOMICALOVIRUS (STRAIN ADIEV)			9.00	1001		Ī	l
	L POS VERDITAR PRECINSOR	ININYAVIRUS GERAIISTON		3	0.01.2	100			
TVG.N.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HINNYAVIRIS I A CRINSI- USB A IT 1.74)	0.7			•	•	:	:
		THINA VIRIS SMIWKIRE HARL	2	=				Ī	ŀ
	200 Z 200 Z	HUNYARWERA VIRIIS	2	2	20.00				
-	LINE YEST THE CHANGE	BIGHT VIRIN							
TVC2 & LIANIB	ALPHA VIEDIUM TRICURANTE	HANDAAN VIRUS (STRAIN IS-1) (KURI)AN IRIANDRRIDARU - EVI, II VIRUS)			500				
TVCL M HANTE	M POL YPROTEIN PRECURSOR	SIANTAAR VIRUS (STRAIN HOIO)							
_	NI PON YPHOTEIN PRECIDENT					+			!
PVER MI HANIV	N. PAN. VPRODEIN PROCURNIN	LIAMIAAN VIRUS (SIRAIN 18-118)	196.363	1036.106.					
	NI POLYPROTEIN PRECURSOR	INITALIENS NILL MULIE STOL VINUS (INS.)	616.649	100	ļ				
FVGLM MIV	ALPOLYPRINE IN PRICURSOR	MINITA TOPO MILEDOVINIA	349.102	1375-1309					
PVGLM PTPV	M FOR YPROTEIN PRECURSOR	PHILIPAL A CORP. CORP. IN STATE MAKENIN	630-653	1093-1125					
PVGLIM PUURIII	M POL YPROTEIN PRECURSOR	TOWNS A VINITE ISSUED TO THE PARTY OF THE PA	\$3.65	200					
PVG IN PUINIS	MICHELYPROPERTY PRICESSOR	TOURIST VALUE OF THE PARTY.	420.450	130.00					
PVGLN RVIV	_	RIP I VALLET TEVER VIRGO, RIP 10 CONT. CON	99.46	199	1156-1185		-		
PVGLM RVIVZ	-	THE CALLEY PEYER CIRCUITS AND CHARLES AND	300	18					
PVCLNI SEBUB		STORY CHANGE OF A STORY CONTRACTOR OF THE STORY CHANGES OF THE STORY CHA	- - - - - - - - - - - - - - - - - - -	1083:1170			F		
PVCLAS SEOUR		SCOOL VIBILS IS IN ABOUT AND AND VIBILS	410-641	1081.11					
PVCIN SEPIIS	_	I DECEMBER AND	401	100					
PVG.F.	ACASTO CASTO	PERNE VIRUS (BEV)	1401-1320						
PAGE BEY	_	RICHIN AREMAVIRUS	\$7						
A PART	CL VOOPEOTE IN POL VPROTEIN PRECURSOR	LASSA VIRUS (STRAIN GAIN)	3. 3. 3.		4				
NCLY LASS	SCHOOL STATE OF STATE	I ACCA VIRIIS (STRAIN MISTAIL)	218.34						

20.0.0	1010CT1 21P	ster (no bacteriophager)	AREAL	ARCAL	ARTAZ	7	ANIAZ	1	
ILC HAME		SICHINDS ARENAVIRUS	2			1		T	
VGLY PIARV	GLYCOPROTEIN POLYPROTEIN PRECURSOR		Ī		1	1			
PVGLY TACV	GLYCOPROTEIN FOLYPROTEIN PRECURSOR	ICTEAIN VS	١	2		1			
VGLY TACVS	τ				1				
PVG.Y TACVI	CL VCOPROJEIN MR. VPROJEIN FRECURSOR	(1841)	2						
FVCLY TACVE	CLYCAMOLEIN TALVINOLEIM I NELONION		_	161.191					
VCNB CPAIV	GENOME POLYPRUIEM B		1	1100					
PVGNA! CPMV		(STRAIN DG)	,						
VCINE CPSM	GENUALE FOLITIONES PE								
PVCNA! RCNV	_	I IERPESVIAUS 4)							
VGP2 EBV	_	MAN REALESVINOS 4)							
PVCP3 EBV	_	ENHAGEN							
PVI02 VACCC	-1								
VIID) VACEV	_	VARIOLA VIRUS							
PVIIDS VARV	LATE PROTEIN HI	S (STRAIN COPENHAGEN)							
PV1105 VACCC	PROTEINIS								
PLYING VACCV	PROTEINIS	VARIOLA VIRUS	2						
PUTIOS VARV	PROTEINUS		107.143						
Prinet LSV	PROBABLE HELICASE	「アンニアものファマー」	34-82						
PLIBITY ACCC	110111711		2.5						
PUDI VARV	PROTEIN	STATE WE	55-68						
PURE VACEV	:-		55-68						
VIOL VARV	PROTEIN 16		391-624						
VIGE VACCC	PUTATIVE BYA HILICASE IS		361.674						
100Y) BE	PUTATIVE RYA IN LICASE IS		501-624						
P. 100 VARV	PUTATIVE RNA III LICASI: IA		141.231						
VIET SICKLY	SI KO MINEDIATE CARLY PROTEIN !		263-271						
TANK THE SECOND	SEED INDICATE EARLY PROTEIN !	HUNIAN CYTONI GALOVINOS (STRAIR 10% ALT 10% ALT	43.78						
	CHEST COLONIA POR SECURIOR		43.30						
•	CARIOS INFECTIVITY PACTOR		46.78						1
	VIETON INTERIOR INTERIOR	1	13.111	İ	ļ	Ī i			
			135.150						
781 417		THE RATE SAIROS A	100						
1000	PROPAGILE INTECENT. MINISTERANE PROP			120-121	250.282				
	PECKLANI IN INC. ALL ANNA AND PROPERTY				145.180	132-361			
1		COUNT MEMPISSIAUS TYPE I (STRAIN ARATICENT I							
TO THE PERSON	_	LIEBFESCIRUS SAINING (STRAIN II)	141.391	İ					
Veneral Print	-	Citi ton thans vinus like Partical Savi							
	52 77 77 78	VACCINIA VIRUS (STRAIN COPTINIAGIN)							
	SI NI SI NI	VACCINIA VIRUS (STRAIN WR)							
2017	- NOTE OF	VARIALA VIRUS	5						L
DIAN MACC	PROJETYKA	VACCINIA VIRUS (STRAIN COPENITAGEN)	9						
PLKON VACCV	-T	CACCINIA VIRUS (STRAIN WR)	14:103						
PVK03 VACCC	7	VACCIMIA VIRUS (STRAIN COTTO)	87-116						
PVK03 VACCI		CACCIONA VIRGIO GUARIN COPONIACIENA	39.36						
PVT.02 VACCC	PROTEINLE	CATCHER VIEWS CHAIN WELL	19.76						
PVT 63 VACCV	_	CARRIED A CITIC	39.36						
FVI 02 VARV	PROJEIN L3	CACCINIA COLIS CAPAIN COSENIACENI	292.323						
PULOJ VACCO	_	CANALA CIRCA CARANA	201-322				1		
PILOJ VACC	MOTERAL	VARIATION A VIBILA	181-181						
PVIOS VAR	_	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPEMIAGE							1
PILLOS VACC	=		Ŷ						
PVI.05 VARV	-	CALL DAIN THE CALL TAPE CA	113.404						
PATI HPV		LINE AND THE BARRIE TO SEE PAPEL CONTAVIRUS (STRAIN KANSAS) (CRPV)	15.2						1
FILT CRPVK		IN CASH DEPT COMANIBUS INTES							\downarrow
PVL2 IUVOS	PROBABLE L2 PROTEIN	A CALM COMA VIRUA TYPE 0						1	1
PLL3 HOVOS	PROBABLE LI PROTEIN	- In seem but a had when I TYPE IA	36-54						
PVL2 HOVIA	PROBABLE LI PROTEIN								

PCT/US95/16733

			Г	П	П	П		
T	121		IJ		PATAS LAZAS	14 48541	48546	141
THE SAME PARTY	DECEMBER 1 DECISION	VPE 39	╗	<u>=</u>				
T	PACKAGE TO PROTECT		74.13					
1	TOTAL TOTAL		24.57					
100 M	PECEL NI PEC		2					
Ī	PECINANI E L'3 PROTEIN		10.00	1		+		
T	PROBABLE LY PROTEIN		2	1				
Ī	ROBABLE L2 PROTEIN		Т	***		<u> </u>	-	
Ť	LOG PROTEIN	CT INDESCENT VIRUS TYPE I)	Т		1			
Įş	MINOR VIRION STRUCTURAL PROTEIN MU.2	2	1					
Ť	ALINOR VIRION STRUCTURAL PROTEIN MU-1			1	1			
900	NAME OF VIRION STRUCTURAL PROTEIN AND TAILUIC		64 - W	1			1	
Т	NIANOR VIRION STRUCTURAL PROTERNIU-IAIU-IC		641-89			 		
Т	VIRION STRUCTURAL PROTEIN MU-14/U-1C	REOVINUS (TYPE 2/STRAIN DS/JONES)	108-109			1		
	NAMES OF THE PROPER MULTANIC		10.19				1	
Τ.	MAINS NOWSTRIKTION PROTEIN MU-NS	NG)	31.16					
T	NIVERIA DESCRIPTION		20.00					
Ī,	A POSTER	(TRIV)	S :≅					
1	MAINA FROIEIN		103					
T.	El GLICORDIEIN		101.49					
	COMMONERA	459)	69-103					
CVNIAS	El GLICOPROTEIN		101-19					
THE STATE OF	COTACIENT		101-103					
TARE CVINE	EI OCICOMOLEIM	(STRAIN BEAUDETTE) (INV.)	13.101			_		
	COTACIENT	(AQ)	101-[1					
_	EI GLYCOPKUI EIN	Г	111:11					
┱	PROBABLE MENIBILANE PROJECT		91-136					
PWIP CERV MOVE	MOVEMENT PROTEIN		Γ	133.303	-			
٦.	MOVEMBER TROUBLY	ANGITAL DUCK ISOLATE STILLINGY)	201-338	169-307				
Т	PINCH SOFT AND	_		164-301				
Т	CONTRACTOR SECTIONS	1	157.190	131-264				
PANSA ILTERON MANAGEMENT	MANOR SOMETHE ANTIGEN PRECUESOR	SHANGHAI BUCK ISOLATE SHEEHBY)		164.302				
Ŧ	NAME STORAGE ANTIGEN PRECURSOR.		П	111.101				
7	MAIOR SURFACE ANTIGEN PRECUASOR:	П	2	136-269		1		
т	MANDE CITES ACT ANTICEN		10.08					
т	MANOR SURFACE ANTIGEN PRECURSOR.		344-372					
Т	MAJOR SURFACE ANTIGEN PRECURSOR		244-372					
т	MAJOR SURFACE ANTIGEN PRECURSOR.	STRAIN 991)	244-273					
Τ.	MAJOR SURFACE ANTIGEN PRECURSOR!	AI)	333.261				1	
1	MAJOR SURFACE ANTIGEN		20.02		-			
_	MAJOR SURFACE ANTIGEN PRECURSOR	/420)	13:361	1	+		+	
┍	MAJOR SURFACE ANTIGEN PRECURSOR	(10)						
٠-	MAJOR SURFACE ANTIGEN PRECURSOR.	(OLATE)			1			
_	MAJOR SURFACE ANTIGEN	T	17.11	Ī			+	
	MAJOR SURFACE ANTIGEN PRECURSOR	THE ATTERS BY VINOS (2001) 175 ADM 1 STRANG WAITER AND STRAIN OF THE STR	1	Ī			-	
	MAJOR SURFACE ANTIGEN PRECURSOR				+		-	
┪	MAJOR SURFACE ANTIGEN PRECURSOR		8 02				-	L
PULISA HOBUS MAJO	MAJOR SURFACE ANTIGEN						-	
_	MANOR SURFACE ANTIGEN PRECURSOR				1			
7	MAJOR SURFACE ANTIGEN PRECURSOR		107-117			+	-	
	R SURFACE ANTIGEN PRECURSOR	DAM)	Т		1		+	
PUNISA WILVI MAJO	SIAJOR SURFACE ANTIGEN PRECURSOR		ī		1		-	
_	A SUMFACE ANTIGEN PRECURSOR	•	Т	274.310			1	1
•	MAJOR SURFACE ANTIGEN PRECURSOR		П	274.310	1		+	
ř							+	
_	PROBABLE MAJOR SURFACE ANTIGEN PRECURSOR		Т				-	L
	MAJOR SURFACE ANTIGEN PRECUESOR I	WOUNTILLE HELD WINDS WENT IN THE PUBLIC		ĺ		<u> </u> -	1	
	MAIRIX (M)) PRO11-1N	INTELLINAL A VIRIO DI RASTA ACAMITETATA ACIA WAS		1	1			

	12101101	All Viruses (na bacteriafhages)	ABEA1 6		7717	2850	7		
100			Γ	141-130					
TAKE.	LYZOTT	USAME	136.46						
PVAILE MYXVL	ALTO PROTEIN								
PUBLIS ALYXVL	AIT-PROTEIN		•	T					
CONTRACTOR	PROJECT NO		7						
VACO.	PROTEINNY		7						
7	PECTEN NY		116-166						
	12 X X X 2 X 2 X 2 X 2 X 2 X 2 X 2 X 2 X	AIN COMPANY	Ĺ	103-691					
VN) ROIN	MONSING TO SECURE THE	\$ 2 (AAV?)	ī	16.31	439.471				
FVMCA AAVI	DNA REPUCATION TROPIES		T						
PVNCS PAVISO	PROBABLE MONCAPSED FREEDILIN POL	VIRUS (SEROTVIE 4/ STRAIN VACCINI.)	21.180			Ī			
4SI AIISV4	KONSTRUCTURAL PROTEIN NSI		16-146						
A TAKE	NOWSTRUCTURAL PROTEIN MS!	107/	110-100						
700	PROME THE TENTON PROTEIN MS!		19:10						
1000	LUCASE DE LITTE AL PROTEIN MSI		10.00						
WASI IACHI	MUNSI RUC LORDE LE DESTE DE LA COMPANSION DE LA COMPANSIO	(Asyal)							_
PVNS1 IACKG	MONSTRUCTURAL PROFILE PA		8						L
PVMS1 IACKU	MONSTRUCTURAL PROTEIN MSI	(9)	107.144						
PVNSI IADA?	MONSTRUCTURAL PROTEIN NS!	- THE LOCKEY AND AND INCHARACTE AND 1/56)	104-141						
14061	MONSTRUCTURAL PROTEIN MS!	INCLUENZA A VIRUS ISTRAIN AUGUSTICA INCLINATI	20.14						
	AND THE ALL PROJECT NSI		114.140						
MASI IADU	TACAS INC. CONT. C	1,1							
PVNSI IAFON	NONSTRUCTIONAL TRUITMENT								
	NOWSTRUCTURAL PROTEIN NO.	INTERNAL A VIRUS IS IN AND AFONT PLAGUE VIRUS/ROSTOCK/14)	07-164						ļ
PVNSI IAFPIR	NONSTRUCTURAL PROTEIN NSI	THE STATE OF THE PAIN AN ENINGRADULES!	14-144						
ı	NONSTRUCTURAL PROTEIN NSI	IN THE REAL PROPERTY AND	14.144						1
١.	NONSTRUCTURAL PROTEIN NSI	TAPLIENCE A VINCE COLORNIA POR A PORTA PER TARRIES	07-144						
1	CONTRACTOR AT PROJECT NS	INFLUENZA A VIRUS (STRAIM APIALLANDALBERT STATES	97.10						
	NAME OF TAXABLE PARTY O	INFLUENZA A VIRIJS (STRAIN AMIALLARISMEW TORUS SET							
WASI TANIAN	-	IN LUI: NZA A VIRUS (STRAIN ARIALLARIVNE W YORKABTUTI)							L
WSI INMINO	_		2						L
PVNS: JALIYN	_		107-144						1
PVNSI TAPIO	NONSTRUCTURAL PROTEIN NS!	THE COURT A VIBIR (CTRAIN APPINTALIJALDERTA/121/79)	107.144						\downarrow
MAKE TAPES	NONSTRUCTURAL PROTEIN MS!	TATLOCKY A VINCE AND A MINTAR ALL MENTAR AND	103.144						
PVNS: IAPE	NONSTRUCTURAL PROTEIN MS!	TATLETT STATE OF THE ABOUT AND A SECTION OF THE PROPERTY OF TH	107-144		į				
NSI IAPIJ	MONSTRUCTURAL PROTEIN MS!	INCLUSIVE A CHARLES AND A PARTY OF BIOCACA A	114-144						4
PVNSI IAPUE	HONSTRUCTURAL PROTEIN MS!	COUNTY A COMPLETE AND AMIDICEVARINI BARMICLE 17/1693-8-42)	107-144						1
VNSI IATKB	NOMSTRUCTURAL PROTEIN NSI	TAPLUENCA A VINCE (CTS AIM ANTIBLE VINCENDAM)	03-144						1
PVNS1 IAIKC	MONSTRUCTURAL PROTEIN MSI	INCLUENCE A CHAOL CONTRACTOR OF THE ACTION A	10.00						
WALL LATES	NONSTRUCTURAL PROTEIN MSI	INT. UENZA A VINCE CONTACTO CO	107.144						
WEI IATRI	NONSTRUCTURAL PROFEIN NS	INT. ULVE A VIRUS (STRAIN ALTERNATIONS)	114.644						
		INTUCAZA A VIAUS (STRAIN ACICAGO DO 1/2)	114.144					_	
SUPPLIED TO		INITUENZA A VIRUS (STRAIN AUSSRAGOT)							L
MSF IAUSS	CONSTRUCTION AT PROTEIN NSI	INTLUENZA A VIRUS (STRAIN A/SWINE/NOW A/1970							L
WASI DAZII	NONSTRUCTION OF THE PROPERTY O	INTLUENZA B VIRUS (STRAIN B/PA/79)	100						-
PVISI DOPA	MONSTRUCTURE TROUBLE IN	INTLUENZA C VIRUS (STRAIN CIANN ARBONINS)	ŝ					1	-
PVNSI INCAA	NONSTRUCTURAL PROJEIN PSI	INFLUENZA C VIRUS (STRAIN CCALIFORNIA/18)	333-35					1	1
PVNSI INCCA	NONSTRUCTURAL PROTEIN PS	IIIINIAN BESPEATORY SYNCYTIAL VIRUS (SUBGROUP BY STRAIN 18517)	70.49						1
PVNS2 IIRSVI		THE STATE OF COMPATORY SYNCYTIAL VIRUS (STRAIN A2)	10-49						\downarrow
PVNS1 IGASVA	_	DATE HENZA B VIRUS (STRADA BALEZA)	48-17						1
PVNS1 INBLE	NOWSTRUCTURAL PROTEIN NA	INCLIENZA B VIRUS (STRAIN BY AMAGATAIN))	48.17						
VYBYI THBYA	MONSTRUCTURAL PROTEIN POS	LOBONA VIRUS LINV (STRAIN S)	17.45						4
VHS4 CVMS		PROSCINE TRANSLISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN FS77	4.34						1
PVNS1 CVPFS		CONCINC TRANSMISSING CASTROENTERITIS CORONAVIRUS (STRAIN PUR	5.5				_		1
PVNS4 CVPPU		FUNCTION AND AND AND AND AND AND AND AND AND AN	6.30				1		
VINSA CVPRM	_	TORUME MESTINATION CONTRACTOR A 191	8						4
VINST CVIAS	1	MICHIGA CONCANT AND	20.00						4
VAST CVAR	ī	MONTHS CONCINCTON TO CONTRACT AND CONTRACT A	222-255						4
WAST INCOL	T	INTEGERS C VINCE (4) PAIN CONTAINE (4) BOUNDS	333.335						4
HONET DATE	HOWSTRUCTURAL PROTECUS MSI-MSZ	INTELLIGENCE OF CORTS AND PARTICULAR CONTRACTOR CONTRACTOR AND CONTRACTOR CONTRACTOR AND CONTRACTOR CONTRACTOR CONTRACTOR AND CONTRACTOR CONTRACTOR AND CONT	222-255						4
PVNST PROMI	Г	WILLIAMS CUBIC LETT AND CHANACATA/IOTI	133-333					_	4
VINST DICYA	NONSTRUCTURAL PROTEINS INST-NS2	PATION AND STREET AND	24.25			!	:	:	1
	i								

MACE MACE	PCGENE	PLICTICAL	ites (na batteriophager)	AREAI	ARCAI	AREAS	ARCAS	AREAS AR	AREA 4	ANTAI
	ILE MANE	ROIGIN	ENZA A VIBLIS (STRADA ACHICKEN/FENSYLVANIA)	Γ	П	П				
	VIRUC DACKP	AUCL EOPROTEIN		\$4.388						
The profit is a contribution of the profit is a contribution	VAUC IAHLO	JUCIEOPROTEIN		24.33						
ACCIDENTIFIED ACCIDENT TO	WALL INITIA	ALCLEOPROTEIN		1117				-	_	
	WHILE IN ITE	UCLEOPROTEIN		1				-		
MACRIER OF	WALC MABYN	UCLEOFACTEIN	RE)							
	VINUE MABYP	NCLEOPROTEIN		Т	10.00			-		
	-	PROTEINO		Τ				-		
INTERPOLIED AUGUSTATION	_	ROTEINOI		Ţ	16915			-		
INTERPRETED STATEMENT ST	T	SE KO PROTEIN		T.			İ		\mid	
STANDARIES STANDARIO STA	Τ	23 KD PROTEDN	Ī		Ī		Ť			
	Ţ	SECTION SECTION		66.17					T	
AUTOCATE	7	SOME ELEKTRIANE ANTIGEN 3	~				1			
FOURTRY PROPERTY AND PART AND PARTIES	Т	IN DEPOTED.		=					\dagger	
FOUR ASSESSMENT YND DRYAMAUDATION FOLEN FOUR ASSESSMENT YND STATEMENT FOUR ASSESSMENT YND DRYAMAUDATION FOUR ASSESSMENT YND DRYAMAUDATION FOUR ASSESSMENT YND STATEMENT FOUR ASSESSMEN	Т	IN PROTEIN		7			1		Ì	
COURT AND DRA MAY TO ANY DATA MAY TO ANY DESTA MAY TO ANY DESTA MAY TO ANY ANY DATA	Т	STATE OF THE PARTY	_	Ī				1		
TOTALE CASID PROTEST VITE TOTALE CASID PROTEST VITE	Т	TACID ASSESSMENT AND DAY MATINEATION PROTEIN		٦	117-323		1	1	1	
THE CASE OF THE	Т	A SUL ASSEMBLI AND DAY DAY OF THE COLUMN TO SERVICE OF THE COLUMN TO SE						1		
	J	ROBABLE CASIO PROJECT VILL			706-238					
MAGABLE CASID PROTEIN V22 VALCELLA TOSTER VIRUS GERANTE UT STAND VACCINE) 121-211	٦	MORABLE CAPSID PROJEIN V7.3		7						
	٦	ROBABLE CAPSID PROTEIN VP23		124-253						
ACTION COLOR ACTI		ROBABLE CAPSID PROTEIN VEZ	RAIN VACCINE)	106.441		1				
Inter CASID PROTEIN V72 ILLE TOWGE VILLS SEROITYEE 11 STOCK AUGUSTALLA) 191-319 545-491		DUTER CAPSID PROTEIN VP2		149-643						
OUTE CASID PROTEIN V71 DELEG IONGIE VIBED SEGUITE LASID FROETH V72 DELEG IONGIE VIBED SEGUITE CASID PROTEIN V72 DELEG IONGIE VIBED SEGUITE CASID PROTEIN V72 DELEG IONGIE V12 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13 DELG IONGIE V13		SUTER CAPSID PROTEIN VP3		Т	13.5					
OUTIE CASID PROTEIN V77 BLUE (DWGUE WING SERGITYE 115GA/READS) 515-681		SUTER CAPSID PROTEIN VP2		Ī	564.593					
GUITE CASID PROTEIN V7		SUTER CAPSID PROTEIN VP?		T				-		
OUTER CAND POLITIN V7		JUTER CAPSID PROTEIN VP2		24.640						
The CASID FROITEN V2 BOVINE BOLIVER 2 BOLIVER V2 BOLI		DUTER CAPSID PROTEIN VP3		310.01					-	
19.151 1	Ш	SUTER CAPSID PROTEIN VP2		Τ						
INAL BRODING PROTEIN VP2		INA-BINDING PROTEIN VP2		Τ	133-558			-		
HAN AND PROTECTION 127 199	П	INA-BINDING PROTEIN VP2	CTRAIN (VA)	Τ	13:567		Ī			
13-359		INA BINDING PROTEIN VP2		Т	119-613	198-119				
MAN-BADDING AND END TEAT MAN-BADDING AND		KWA-BIXINKO PROTEIN CP2		Т	33.55					
INTERPREDICTABLE CONTINUED AND STREET C		AMA-BINDING PROTEIN VP2		T						
INTERPRETATION TANKED PROTEIN 198-119								-		
INTERPRETATION INVESTITION	VACCV			=						
THE CASE FROITEN FOR THE FROITEN FOR THE FROM THE FROM THE FROITEN FOR THE FROITEN FROM THE F	VARV		VICTORIAL AND THE APPLICACES VIRUS COPRISION VI	10.10	Ī					
VPT CORE FROIDEN VPT CORE FR		MAKIN (APKIN PROJETA	-	T	21.710					
STATE STAT	٦	VT) CORE PROJEIN	Ì	Τ	734.770			-	T	
STATE STAT	ا ا	VP) CORI, PROTEIN		197.130						
CASSED FROTEIN FOR PSTETIN BARR VIRUS (STRAIN DRY A) (10 ALAN TERPESVIRUS 4) 19-419	i	MANNETT AND STRIKE TOTALS TRUNCED IN	TAIN SAID	533.688						
	١	INNER CORE PROTEIN VE		139.453						֓֝֟֜֜֜֜֜֓֓֓֓֓֓֓֓֜֟֜֜֓֓֓֓֓֓֓֓֓֡֓֜֡֓֓֓֓֓֡֓֡֓֡֓֡
CAPSID PROTEIN PORTOR VARIETIA VIRUS STRAND DIAASSTRAND TIDDAVE VAR3) (IL.19 16-119	ļ	CAPSID PROTEIN PRO		19.15	ĺ					
CASE PROFESS VARICEELA TOR FOR VARICEELA POUNTS 181-516		ļ	Т	1						
VICTAL TANISCRIPTION REGULATOR PAT PROCESSING PROCESSING PROCESSING PAGE PROCESSING PATEGRANDS VICTAL TANISCRIPTION REGULATOR PATEGRANDS VICTINAL VICTOR PATEGRANDS VISTOR PATEGRANDS	ī	CARSIN PROTEIN PAR		18:316						
MAJOR CORE PROTEIN PAA PRECURSOR VACCINIA VIRUS (STRAIN WR) 191-391	Т	CIENT TEAMCORPHISM BEGIL ATOR PA		119-270					1	
MARINE CORE PROTEIN PAA PRECURSOR		LA MARCORE PROTEIN PAA PRECURSOR A		183.881					1	
MANAGE CORE PROTEIN FAA FRECURSOR VARIETY		LIAND CORE PROTEIN PAA PRECURSOR		551-591						
DOTTEL CASED PROTEIN VP4	$\overline{}$	MAINE CORP PROTEIN PAR PRECUASOR		554-592						
MONSTRUCTURAL PROTEIN PRIST WORSTRUCTURAL PROTEIN PRIST OUTER CAPSID PROTEIN VP3 WILD HOUSE (WILD SERVICE AUGUSTALLIA) 1219-109		CATER TAPCID PROTEIN VP4		11116	468-479			-	1	
OUTER CASSID PROTEIN VF1 SEGNISHA VF2 SEGNISH VF2 TISOLATE AUSTRALIA) P4-131	NAME OF TAXABLE PARTY.	NOWSTREETING A PROTEIN PASS		178.308	624.659				1	
A OUTER CAPSID PROTEIN VPS IN THE FOWCHE VIRILY ELISTANTALY IN THE THORAT VIRILY CAPSID PROTEIN VPS IN THORAT VIRILY ELISTANTE SYCHILATRICA) IN THE THORAT VPS IN THORAT VPS IN THORAT V SHIRT (STRUTYTE SYCHILATRICA) IN THE CAPSID PROTEIN VPS IN THORAT VPS IN THORS VPS IN THORAT		¥-13	32.30			1	1			
ALTHER CAPSID PROTEIN VPS INTER CAPSID PROTEIN	101	CHITER CAPSID PROTEIN VPS		201-334						
HIGH THAT CASHD FRUITEN VFS INTO THE CASHD FRUIT (STRUIT FOR THE USA) OUTER CASTD PROTEIN VFS IND THAT STRUIT (STRUIT FOR THE USA) OUTER CASTD PROTEIN VFS IND THAT STRUIT (STRUIT FOR THE USA)		CALLER CAPSID PROTEIN VPS	(۷)	295-124						
OUTER CAPSID PROTEIN VPS Leader Helphonic COSCASE VIRUS (SENOTYRE 1) [ENDV-1) OUTER COAT PROTEIN IS CONTER COAT PROTEIN IS	PVP1 niv/A	CALLE CAPSED FROM NYS		195.334						
CUTER COAT PROTEIN PS	PVPS EIIDVI	OUTER CAPSID PROTEIN VPS		200					1	
This is the state of the state	VIW GV	DUTER COAT PROTEIN PS		41.18				\dagger	1	
N. S. C.	PVPAI RIVIO	VP4 PROTEIN	weig in active io ischafe USA)	138-117				1	1	

110 100 100 100 100 100 100 100 100 100	PINCT LAIP REGISTRATE IN PROBABILE HONSTRUCTURAL 16 3 KD PROTEIN		П	110-145			1		
	DASTRUCTURAL 36 3 KD PROT		П	in a					
	DASTRUCTURAL 36 3 KD PROT		I						
	DASTRUCTURAL 36 3 KD PROT				Ī	+	T		
			205-313	1			1	Ī	
	OR ENVELOPE GLYCOPROTEIN PRECURSOR	ORCATA PSEUDI SUCATA PRETEAS BOT MEDITOLIS VIRUS (ACMINPV)	311.182					Ī	١
	LIA WAR ENVELOPE OF YCOPROTEIN PRECURSOR		198-233						١
	NA PAINE OF CLANDED FIN		155.10						١
	UR ENVELOR OF THE STATE OF THE								
	VI PROJEIN			†					
	VI TOTAL					1	Ì		
	VPS PROTECT	BLUE LORGUE VIANO (PEROTVEC 9 JICOLATE USA)	131-159	١					
WIVAL WIVAC WIV WIV WIV WIV WIV WIV WIV WIV WIV WIV	10 to 10 to		100.300						
WIVEL WIVE WIV WIV MIVE MIVE MIVEL MIV MIV MIV MIV MIV MIV MIV MIV MIV MIV MIV MIV MIV MIV MIV MIV	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		20.30						
WIVAL WIV WIV NPVOP BIVIO	STRUCTURAL PROTEIN PE	Т	<u> </u>						
MTV WTV MPVOP BTV10 BTV11	STRUCTURAL PROTEIN PS	LVIIEDROSIS VIRUS (ACNINFV)	403-467						
WTV MPVOP BTV10	WKD PROTEIN	Ť	0474SI						١
MPVOP BTVIO	CONSTRUCTION AT PROTEIN PAST		23.412						
BTV10	SIRAC ORAC I	ACSIS VINCS (S)	971.79						
BTVII	CAPSID PROTEIN FIL								١.
BIVII	STRUCTURAL PROTEIN FE		A(1.8)				Ī		
	NONSTRUCTURAL PROTEIN PO	PLOCI UNIOS VINCE IN TICOL ATE IN AN	66-59						
	CHAIN THEAT PROJETY PO	BLUE TONGOR VIRUS (SERVI) THE THIRD STATES	96.19						
	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COLUMN TWO IS NAMED IN COL	DI LE TONGLE VIRUS (SEROTYPE 1771SALA 12 USA)							
	NOWSTRUCTURAL PROTEIN TO	IN THE TOWALTE VIRUS (SCROTYPE I / ISOLATE AUSTRALIA)		İ					
Ĺ	ISTRUCTURAL PROTEIN PU	STITE TOWER CIPILS ASPENTABLE I ISOLATE SOUTH AFRICA	3	1			Ī		
Ţ	CINICIPAL PROTEIN PO	BLUE LONGOE VINOS (SERVICE)	8						
	26 N. 31 Cas of State (1975)	BLUETONGUE VIRUS (SERVITVE ATTSCHALLE SON)	6						
PUTE BTV2A	SI MUCIONAL PROTECTION	MICH DWANT VIRUS (MDV)	Ĩ						
FVFB ROV COUR	OUTER CAPSID PROTEIN FE	INTERIOR CONTRACTOR	Ì						
	MILER CATSID PROTEIN TO	WOUND TOTAL TOTAL TOTAL EAR POR VIETBROSIS VIRUS (ACAIMPV)	145-173						
Ì	TANK VIENDAL SHVELOPE PROTEIN	AUTOCKATIIA CALIFORNICA I COLORIA DI COLORIA MANAPANI	133.151						
.1	THE PROPERTY OF THE PROPERTY	ORGVIA PSEUDOTSUCATA MULTIK AFSID FULTIERING							
VPHE NOVOF 12 K	O POL TIEDIAL CATALON	HENAN BARTHODEFICIENCY VIRUS TYPE I (ARVISEZ ISOLATE) (FITY 1)							
	VPR PROTEIN	THE WAY IN THE WAY THE WAY VIEWS TYPE 3 (SCH. ATCHOUNCE)	-					:	:
PVPR IIVING VPR	VIT PROTEIN	CONTRACTOR AND AND VIEW AND	1.1						
	X = = = = = = = = = = = = = = = = = = =	HINDER THE THE TANK THE TANK THE TANK A THE DISCOULT OF THE THE TANK THE THE TANK TH	11:13						
		III MAN INDICATOR CONTRACTOR CONT	1.11						
Ī.	MINIOTO SECTION	HUNIAN INDICACOL TOTAL AND A COLOR AND A COLOR	15:17						
Ì	7.5	HUMAN IMMUNODERCIENCY VINUS 1775 4 HACK							
Ī	VVR PROTEIN	THINIAM INDICIONCHERICIENCY VIRUS TYPE & (1SOLATE ROD) (IIIV-2)		:	!	-			L
PUPE HVIRO VPR	VPR PRUTEIN	C. VIDANIBLE IN THE STATE OF THE SERVICE STATE OF THE STA		-	1				<u> </u>
1	NI-ICHA E	CONTRACTOR AND CHARLEST AND	\$ ~						
	THOUGHT.	HINNING THE PROPERTY OF THE PERSON OF THE PE	37.74						
	7.316	CHINIPANZEE DENIGRODE ICHEMA TANGO (SINCE)							
SIVCZ	N PROJECT	SINITAN INDICADDEFICIENCY VIRUS (ADVI-43-03 ISOLATE) ISOVALIAL							L
PUPE SIVILII UPE	VPR PROTEIN	CALITAN IAMINIMUM FIFTH MEY VIRITS IKOW ISOCATE) (SIV. MAC)	•	;					
PUPE SIVINK VP	VIE PROTEIN	TOTAL STATE OF THE	5=					:	,
	National State of the Party of		27.55						
		CINTIAN INTERIOR OF THE WAY OF THE STANDARD OF							L
-XXX EX		CHAILAN INIMIDICADE HOLENCY VIRUS (PULDCL) ISOCATE) (SOOTY MANGALIU							
VFR SIVSF VIT	VIR PROBLIN	INTITION INTERPROPERCIENCY VIRUS TYPE I (BHID ISOLATE, HXD) ISOLATE	1.1						l
PVPU BIVIDI	VPU PROTEIN	THE TANK AND THE PROPERTY VIRUS TYPE I (BILL ISOLATE) (HIV-1)	-13						
	VPU PROTEIN	THE THE PART OF TH	==						
Ī,	WILLIAM STATES		= = =						
	XI	THE PLAN IN THE PARTY OF THE PA							
		HILIPIAN INICIPACITIC COLORS TYPE I (HXDZ INCLATE) (HTV)							L
į	William William	HINDIAN INDICIONAL ICH NCV VIRUS TYPE I (IACSF ISOLATE) (IIIV-1)					-		ļ
PVPU IIVIR VP	Uranten	CONTRACTOR AND VIEW TYPE - CP - CAN A CONTRACTOR - CONTRA	1.0						1
Ì.	NI LIGHT	THE PROPERTY OF THE PROPERTY O	16-634						
	71.00m.iv	SHELF FULNIONARY AUCTOMIA 1023 TINGS	100				1 1		
	KINI CHA XON	LACTATE DEMYDROCENASE-ELEVATING VINGS (EM.)	5						
	OBS. Y PROTEIN	10.A1C 1477	1	474.705					
T.	ALECT A PROPERTY	BALLEY STRIPE MOSAIC VIRUS (DSMV)							
Т	CALLY OF THE PROPERTY NO. VET.	HUDIAN ROTAVIRUS (STRAIN ICV-10-1)							L
PVSOS ROTHE	DASIRUCTORAL PROTEIN NO.	PORCINE ROTAVIAUS (GROUP C / STRAIN COWDEN)		740-161		1			L
٦	HONSTRUCTURAL PROTEIN 1933	SIMIAN II ROTAVIRUS (STRAIN SAII)	35.34						ļ
Ī	NOWSTRUCTURAL PROTEIN PLYF	POUNT BOTAVIRUS (STRAIN RS)							1
	VP6 PROTEIN	CONTRACTOR OF STREET,	(4-4)	313.340					4
Т	VPA PROTEIN	BOVINE ROLAVIAUS (GROOF C. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. DOM S. S. S. DOM OM S. S. DOM S. S. S. S. S. S. S. S. S. S. S. S. S.	(4.6)			L			
200	Car en Car	BOVINE ROTAVIRUS (STILABLUR)							l

				П	П	٦	, , ,
П	Vialis	AREAI	4	4	AND SAME	1	
ELLE WANTE	EQUINE ROTAVIRUS (STRAIN FI-14)	20.5					
	EQUINE ROTAVIRUS (STRAIN H-2)	24.5					
╗	STATE OF AVIETS (SEROTYPE I / STRAIN 1076)	28-65					
٦	HALAN BOTAVIRUS (GROUP C/STRAIN BRISTOL)	H-72	313-340				
╗	HINGAN BOLAVIRUS (SEROTYPE 2 / STRAIN S2)	28-93					
٦	HILLIAN ROTAVIRUS (SEROTYPE I / STRAIN WA)	55-92	313-349				
	PORCHACING ROTAVIRUS (GROUP C. STRAIN COWDEN	64-92					
٦	PORCING ROTAVIRUS (STRAIN COTTFALED)	55-92	2				
	CINIAN II ROTAVIRUS (STRAIN SAII)	55.93	=				
٦	CINIAN 11 ROTAVIRUS (STRAIN SA11)	374-302				1	
7	HINIAN ROTAVIRUS (SEROTYPE 4/ STRAIN ST. THOMAS 3)	131-139				1	
. 1	PORCINE ROTAVIRUS (SEROTYPE 47 STRAIN BEN-144)	131-159				-	
╗	BOVAGE BOTAVIETS (STRAIN NCDV)	23:69					
П	BOOKER BOTA VIBIL CERAIN UKI	25.00					
	LABOUT STOCK STEELS AND AND	23.69					
PVS10 ROTHS NONSTRUCTURAL GLYCOPROTEIN MCVF	TOTAL STATE OF STATE	53.09					
_	THE PROPERTY OF THE PARTY OF TH	53.69					
PVSIG ROTHS NONSTRUCTURAL GLYCOPROTEIN NCVP	SALVANIA MOLINIA MARIA M	52.40			-		
_	TICKING ACTION TO SECTION SECT	20.00					
PVS10 ROTS! NONSTRUCTURAL GLYCOPROTEIN NCVP	SINIAN II ACIAVIROS (SIIMAIN SATI)	2 2					
_	HUMAN KOLAVIROS SEKOLAGOS	74.35					
_	REOVINOS (CITE AT STANING STAN	1919					
Ī.	RICOINGS (FUTE 17 STRAIN LAPPO)	19:102					
Ī	÷	261.290					
TUNIOR NECROSIS FACTOR SOLUBLE RE	=	311.340				L	
TURIOR NECROSIS FACTOR SOLUBLE RE	CEPTOR PRECUM SHOPE FIBROMA VIRUS (STRAIN KASZA) (STV)	181.50					
	CAPILIPOXVIKUS (STRAIM INSTITUTE IN THE BESTURE AT	164.190	105.543			L	
	EPSTEIN-BARK VIRUS (STRAIN BYS-3) (HUMIAN HELD COVINGS 4)	100,000					
PUTER IICMVA PROBABLE DNA PACKAGING PROTEIN .	HIGHAN CYTONECALOVINOS (STRAIN ADIAN)	344.788					
PUTER HSVII PROBABLE DNA PACKAGING PROTEIN	ICTALURID HEIDESVIRUS I (CHAMMEL CATHES) VIRUS) (CLV)						
Γ	SENDAI VIKUS (3) KAIN 674)		l				
	HUMAN ADERGVIAGOS LITTE V	77.					
Г	MAIZE STREAK VINUS (SOUTH-ATRICAN ISOCALE) (MAY)	3.2					
Γ	WHEAT DWALE VIRUS (WDV)	7				_	
Γ	SULFOLOBUS VIXUS-LIKE PAKTILLE 33VI		\downarrow				
V IIYPOTITETICAL II 9 KD PROTEDI (OLF V							
INVESTIGATION NOTED IN SECH	ENT SII SIMBAN II KOTAVIKUS (SIRAIM SAII)	Т					
A INPOTILETICAL II 2 KD PROTEIN	TOBACCO YELLOW DWALE VIRUS (STRAIN AUSTRALIATION)	+					
NEVAC HITPOTHETICAL 13 8 KD PROTEIN DA 39 A	OTEIN SEC	Т					
HYPOTIETICAL 18 0 KD PROTEIN (OR)		139-167		-			
PYZOK SSVI INVESTIETICAL 204 KD PROTEIN (UR) E	MALTE STREAM VIRUS PROFESSIAN ISOLATE: (MSV)	133.155					
J	COVERAN CHARACTE MOTTLE VIRUS	_					
PY3 SOCIA IIIYO HETICAL PROTEIN 2 (UPO 11)	ALTIOCRAPHA CALIFORNICA NUCLEAR POLYMEDADSIS VIRUS (ACMAPA)	112-061 (A DUM)	L				
PYTER ROAD STANDING IN THE PROTEIN OFF	1921 SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	-	\$43-500				
ATTOTICE TO A SAGE OF 11 PROTECT		114.150					
LICENSTITE TO A 2 KD PROTEIN IN DRO		306-344					
TOTAL MANAGEMENT OF A POST OF THE PARTY OF T	-	14-97					
INVESTIGATION OF THE PROTEIN		3					
HIVE TICAL PROTEIN ION!		14-112]	_	
CLEOC	PSID OLD (1015) BOVING CORONAVIRUS (STRAIN F13)	-	37:165				
STORY OF THE PROPERTY IN MICHEST	PSED ORE (IORE)	¥.\$	137-165			1	
THE PROPERTY OF THE PROPERTY O	PSED ONE (TOUR)	41-74	13:165				
PYIOR CYCE HITOIRE PAR FROM MANAGEMENT		997-100					
Т	EPSTEIN-DAXA VIRUS (STIVAN B95-4) (MUNIAN HEAPESVIRUS 4)	230-284					1
3	COSOMETINA YELLOW MOTTLE VIRUS (COYMY)	87-73	<u>=</u>				
_		2 .	4		1	1	
ACCES AVENT HYPOTHETICAL 13 KD PROTEIN (ORF 3)	(PRACINENT) POTATO VIRUS X (STRAIN XC) (PVX)						
TOWN TOWN							

PCT/US95/16733

W	96/19495
---	----------

_		_		_	_	_	_	_	_	1	7	7	7	_	_				П		٦			
	7														L		L	L		_	Ц			
	SPEAS	T																		L				
	1717	1	1	T		T																		
	ALLA	\dagger	\dagger	\dagger	†	+	T						T	T	T	T	1	T						
-	П	+	+	+	+	+	+	+	+	\dagger	+	\dagger	t	\dagger	t	†	1	1	†	1	†	1		
-	AREA	Н		4	1	4	1	+	+	$\frac{1}{1}$	+	+	+	+	+	-	4	$\frac{1}{2}$	+	$\frac{1}{1}$	+	$\frac{1}{2}$		
	AREAL									1								Ц			\dashv	4		
	1 7.50	1000	2.3	111.111	*	233-763	91-134	3	2	=	200	13-43	m.im	304-336	31.5	7	25.55	1	7	35.5	18-51	2		
	H		Ĭ													PENHAC	VACCINIA VIRUS (STRAIN WILL AND VACCINIA VIRUS (31 MAILS	PENHAG	VACCINEA VINUS (STRADS WA), AND VACCINGA VINUS (STRADS 1817)					
	$\ $								AICE TINGRO BACRLIFOUN VIANS (ATE PILL IPPINES) (ATDV)	RICE TUNGRO BACILLIFORM VIKOS (1800 NIFOROSIS VIRUS (ACAIMPV)		689	2	18.0		OJ PUTE		PANACO			STRONG	LYCHOCYTIC CHORLOWSHIPS VIEWS (STEAKUPASTEUR)		
	$\ $		5	5	The Park		Į.		I PPIN	V SISON		Checky	EPSTEEN-BARK VIRUS (STRAIN BY)-U) (HUMAN BARKVIRUS	EPSTEIN BALR VIRUS (STRAIN BPS-1) (RUMAN INC.)	ESCRENIBARA VIRUS (STRAIN 1995-9) (INCANTREM	100 100		100 100	S COM		ARA ARA	LYAPHOCYTIC CHORLOGANING HILLS VIEWS (STEATH FASTEUR)		
			VIEWS FI OVER MOSAIC VIAUS (STEAM M) (WOMY)	WITH CLOVER MOSAIC VIRUS (STRAIN O) (WORV)		THERAIOPROFEUS TENAX VIRUS I (STRAIN RAN) (11)	THERMOPROTEUS TENAX VIRUS I (STRAIN ALALI) (TTV)	THERMOPROTEUS TENAX VIRUS (STRAIN	ATEPI	1914						اء		9	VI DE	2	2	N. P.		
			STEAM	STRAIN		100						3				ENTROPE	X	ENTAGE	2	EXE EXE	ENTAGE			
			VIAUS	VIRUS	1	X VIAU	Y VIRU	Z VIRC			Y Y	SITE	3	STRAIN	STRAIN	A IN COP	AIN WAL	ABM CO	ADI WIL		S NY			
		Cherroph	MOSAIC	MOSAIC	VINUS G	US TEN	EUS TEN	105 TEN	PACIFIC	BACILL	CALIFO	EX VIRU	VIRUS (VINUS	VIRUS	USGIR	LIS CSTR.	LUB (STA	IUS (STR	FES STA	KUS (ST	CCHOR		
		B Virues (ne barteriopuerts)	Ct OVE	O IO	A WAAN A DENOVIRUS GAL!	HOPROT	POPROTI	POPROT	RICE TUNGRO BACILLIFORM VIAUS INC.	LUNGRO	CIAPITA	HERPES SIMPLEX VIRUS (TYPE O / SIXALIN US	144.03	EN-BAL	EN.BAE	SACTOMA VIRUS (STRAIN COPENSIAGEN)	WATA VI	VACCINAL VIELS (STRAIN COPENHAGEN)	TATA VI	VACCORIA VIRUS (STRAIN COPENHAGEN)	VACCINIA VIRLIS (STILAIN COPENHAGEN)	MOCH	2	
		AB Vir			1	THE	1	100	E CE	HEE	1017	235	EX	1543				1		3	X	3	1	
	İ										3				١									
						=					NO.													١
				N (ON)	TH (OFF)	EINCOL	Z	Z	N.	3				핇	2	Z	TEIN	100	TEON	TED	200		CARTA	
				DPROTE	DPROTE	KD PRO	OPROT	KD MO	KD PRO	MOTE	PROTEIN	KDFRO	TEIN IC	J. I PRO	JONA 15	I PRO	X PPRO	KD PRO	KDPRC	KDMC	9 KD PR	6 KD PR	1	
				AL 13 K	7V 13 K	21.13	13	36.13	2 3	CALM	CALPY	CALAIS	3	13	3	17.	17.7	CAL	3	SAL 18	ICAL II	II TY	E 70	ER PRO
				FILE MANIE PROPERTY OF 11 KD PROTEIN (OUT)	PYORL WOAVE THE STREET IS NO PROTEIN (ON 1)	UVPOTHETICAL SI SKD PROTEIN (OR S)	HYPOTHETICAL 1 1 KD PROTEIN	HYPOTIGICAL IN 6 KD PROTEIN	HYPOTHETICAL 20 3 KD PROTEIN	HYPOTHETICAL P14 PROTEIN (ORD	HYPOTHETICAL P24 PROTEIN (OW) 1)	IVPOTIETICAL 4) S KD PROTEIN IN PA	HAPOTHETICAL PROTEIN RES	LYPOTIGETICAL BARS 1 PROTEIN	DATE THE TICAL BERF ! PROTECT	THE STREET AT BIRE ! PROTEIN	VINI EDV MINOTIMETERAL IS 1 ND PROTEIN	YVAE VALLE LIVERING TICAL 99 KD PROTEIN	YVAL VALLY TAYAOTIETICAL 10 BKD PEOTED	TYPEC YALLY LANGING TICAL 10 4 KD PROTEIN	HYPOTHETICAL 119 KD PROTEIN	HYPOTHETICAL 11.6 KD PROTEIN	THE FORCER PROTECT	ZINC FINCER PROTEIN (PRACTICAL
			2				1	Т		Τ	Т	1	1	Ţ	1							18 18	2 V/3	Z) 4X2
			J.	THE PERSON			PYOR'S ALLEUS	A CONTRACTOR	VIT 410V	Vara seav	100			COLUMN TO A COLUMN			PYTRI EBV	X	V	\$	ATTA COMA	PYVIC VACCE	PZNOP LYCVA	VCVP
			PCCENE	3		2			į	ŀ		ξľ	: I		<u> </u>	<u>.</u>	اخ		<u> </u>	<u> </u>	<u> </u>	١٤	.]3	ı

TABLE XV RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG CARBOXY TRUNCATIONS

X-YTS-Z X-YTSV-Z X-YTSVI-Z X-YTSVIT-Z X-YTSVITI-Z X-YTSVITIE-Z X-YTSVITIEL-Z X-YTSVITIELS-Z X-YTSVITIELSN-Z X-YTSVITIELSNI-Z 10 X-YTSVITIELSNIK-Z X-YTSVITIELSNIKE-Z X-YTSVITIELSNIKEN-Z X-YTSVITIELSNIKENK-Z X-YTSVITIELSNIKENKC-Z X-YTSVITIELSNIKENKCN-Z X-YTSVITIELSNIKENKCNG-Z 15 X-YTSVITIELSNIKENKCNGT-Z X-YTSVITIELSNIKENKCNGTD-Z X-YTSVITIELSNIKENKCNGTDA-Z X-YTSVITIELSNIKENKCNGTDAK-Z X-YTSVITIELSNIKENKCNGTDAKV-Z X-YTSVITIELSNIKENKCNGTDAKVK-Z X-YTSVITIELSNIKENKCNGTDAKVKL-Z X-YTSVITIELSNIKENKCNGTDAKVKLI-Z X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQEL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELD-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVT-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-2 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLM-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z

The ne lett r amin acid code is used.

Additi nally,

"X" may r present an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

10

15

20

25

30

35

TABLE XVI RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG AMINO TRUNCATIONS

```
X-QST-Z
                                                X-MQST-Z
                                               X-LMQST-Z
5
                                              X-LLMQST-Z
                                             X-OLLMOST-Z
                                            X-LOLLMOST-Z
                                           X-ELOLLMOST-Z
                                          X-TELQLLMQST-Z
                                         X-VTELOLLMOST-Z
                                        X-AVTELQLLMQST-Z
10
                                      X-NAVTELQLLMQST-Z
                                      X-KNAVTELQLLMQST-Z
                                    X-YKNAVTELQLLMQST-Z
                                    X-KYKNAVTELQLLMQST-Z
                                  X-DKYKNAVTELQLLMQST-Z
                                 X-LDKYKNAVTELQLLMQST-Z
                                X-ELDKYKNAVTELQLLMQST-Z
                               X-QELDKYKNAVTELQLLMQST-Z
15
                              X-KQELDKYKNAVTELQLLMQST-Z
                             X-IKQELDKYKNAVTELQLLMQST-Z
                             X-LIKQELDKYKNAVTELQLLMQST-Z
                            X-KLIKQELDKYKNAVTELQLLMQST-Z
                          X-VKLIKQELDKYKNAVTELQLLMQST-Z
                         X-KVKLIKQELDKYKNAVTELQLLMQST-Z
                        X-AKVKLIKQELDKYKNAVTELQLLMQST-Z
20
                       X-DAKVKLIKQELDKYKNAVTELQLLMQST-Z
                      X-TDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                      X-GTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                    X-NGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                    X-CNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                  X-KCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                  X-NKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                X-KENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
25
              X-IKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
             X-NIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
            X-SNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
           X-LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
          X-ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
         X-IELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
        X-TIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
       X-ITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
30
      X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
     X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-2
    X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
    The one letter amino acid code is used.
```

35 Additionally,

"X" may r present an amino group, a hydrophobic group, including but not limited to carbob nzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl gr up; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

10

15

20

25

30

TABLE XVII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG CARBOXY TRUNCATIONS

X-FYD-Z X-FYDP-Z X-FYDPL-Z 5 X-FYDPLV-Z X-FYDPLVF-Z X-FYDPLVFP-Z X-FYDPLVFPS-Z X-FYDPLVFPSD-Z X-FYDPLVFPSDE-Z X-FYDPLVFPSDEF-Z X-FYDPLVFPSDEFD-Z X-FYDPLVFPSDEFDA-Z X-FYDPLVFPSDEFDAS-Z X-FYDPLVFPSDEFDASI-Z X-FYDPLVFPSDEFDASIS-Z X-FYDPLVFPSDEFDASISQ-Z X-FYDPLVFPSDEFDASISQV-Z X-FYDPLVFPSDEFDASISQVN-Z X-FYDPLVFPSDEFDASISQVNE-Z X-FYDPLVFPSDEFDASISQVNEK-Z X-FYDPLVFPSDEFDASISQVNEKI-Z X-FYDPLVFPSDEFDASISQVNEKIN-Z X-FYDPLVFPSDEFDASISQVNEKINQ-Z X-FYDPLVFPSDEFDASISQVNEKINQS-Z X-FYDPLVFPSDEFDASISQVNEKINQSL-Z X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z 25 X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z

The one letter amino acid code is used.

X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a 35 T-butyloxycarbonyl group; a macromolecular carrier

group including but not limit d to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrat s.

TABLE XVIII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG AMINO TRUNCATIONS

X-DELL-Z X-SDELL-Z X-KSDELL-Z 5 X-RKSDELL-Z X-IRKSDELL-Z X-FIRKSDELL-Z X-AFIRKSDELL-Z X-LAFIRKSDELL-Z X-SLAFIRKSDELL-Z X-QSLAFIRKSDELL-Z 10 X-NQSLAFIRKSDELL-Z X-INQSLAFIRKSDELL-Z X-KINOSLAFIRKSDELL-Z X-EKINQSLAFIRKSDELL-Z X-NEKINQSLAFIRKSDELL-Z X-VNEKINQSLAFIRKSDELL-Z X-QVNEKINQSLAFIRKSDELL-Z X-SQVNEKINQSLAFIRKSDELL-Z 15 X-ISQVNEKINQSLAFIRKSDELL-Z X-SISQVNEKINQSLAFIRKSDELL-Z X-ASISQVNEKINQSLAFIRKSDELL-Z X-DASISQVNEKINQSLAFIRKSDELL-Z X-FDASISQVNEKINQSLAFIRKSDELL-Z X-EFDASISQVNEKINQSLAFIRKSDELL-Z X-DEFDASISQVNEKINQSLAFIRKSDELL-Z 20 X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-LVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-DPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-YDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, p lyethylene glycol, or carbohydrates.

TABLE XIX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG CARBOXY TRUNCATIONS

X-ITL-Z X-ITLN-Z X-ITLNN-Z X-ITLNNS-Z X-ITLNNSV-Z X-ITLNNSVA-Z X-ITLNNSVAL-Z X-ITLNNSVALD-Z X-ITLNNSVALDP-Z X-ITLNNSVALDPI-Z X-ITLNNSVALDPID-Z 10 X-ITLNNSVALDPIDI-Z X-ITLNNSVALDPIDIS-Z X-ITLNNSVALDPIDISI-2 X-ITLNNSVALDPIDISIE-Z X-ITLNNSVALDPIDISIEL-Z X-ITLNNSVALDPIDISIELN-2 X-ITLNNSVALDPIDISIELNK-Z X-ITLNNSVALDPIDISIELNKA-Z X-ITLNNSVALDPIDISIELNKAK-Z X-ITLNNSVALDPIDISIELNKAKS-Z X-ITLNNSVALDPIDISIELNKAKSD-Z X-ITLNNSVALDPIDISIELNKAKSDL-Z X-ITLNNSVALDPIDISIELNKAKSDLE-Z X-ITLNNSVALDPIDISIELNKAKSDLEE-Z X-ITLNNSVALDPIDISIELNKAKSDLEES-Z 20 X-ITLNNSVALDPIDISIELNKAKSDLEESK-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKE-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEW-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWI-Z

The one letter amino acid code is used.

or carbohydrates.

X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIR-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG AMINO TRUNCATIONS

```
X-RRS-Z
                                   X-IRRS-Z
                                  X-WIRRS-Z
5
                                 X-EWIRRS-Z
                                X-KEWIRRS-Z
                               X-SKEWIRRS-Z
                              X-ESKEWIRRS-Z
                            X-EESKEWIRRS-Z
                           X-LEESKEWIRRS-Z
                          X-DLEESKEWIRRS-Z
10
                         X-SDLEESKEWIRRS-Z
                         X-KSDLEESKEWIRRS-Z
                       X-AKSDLEESKEWIRRS-Z
                      X-KAKSDLEESKEWIRRS-Z
                     X-NKAKSDLEESKEWIRRS-Z
                    X-LNKAKSDLEESKEWIRRS-Z
                   X-ELNKAKSDLEESKEWIRRS-Z
                  X-IELNKAKSDLEESKEWIRRS-Z
15
                 X-SIELNKAKSDLEESKEWIRRS-2
                X-ISIELNKAKSDLEESKEWIRRS-Z
               X-DISIELNKAKSDLEESKEWIRRS-Z
              X-IDISIELNKAKSDLEESKEWIRRS-Z
             X-PIDISIELNKAKSDLEESKEWIRRS-Z
            X-DPIDISIELNKAKSDLEESKEWIRRS-Z
           X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
20
          X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
         X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
        X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
       X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
      X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
     X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
    X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
```

The one letter amino acid code is used.

25

35

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXI HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG CARBOXY TRUNCATIONS

X-ALG-Z X-ALGV-Z X-ALGVA-Z 5 X-ALGVAT-Z X-ALGVATS-Z X-ALGVATSA-Z X-ALGVATSAQ-Z X-ALGVATSAQI-Z X-ALGVATSAQIT-Z X-ALGVATSAQITA-Z X-ALGVATSAQITAA-Z 10 X-ALGVATSAQITAAV-Z X-ALGVATSAQITAAVA-Z X-ALGVATSAQITAAVAL-Z X-ALGVATSAQITAAVALV-Z X-ALGVATSAQITAAVALVE-Z X-ALGVATSAQITAAVALVEA-Z X-ALGVATSAQITAAVALVEAK-2 15 X-ALGVATSAQITAAVALVEAKQ-Z X-ALGVATSAQITAAVALVEAKQA-Z X-ALGVATSAQITAAVALVEAKQAR-Z X-ALGVATSAQITAAVALVEAKQARS-Z X-ALGVATSAQITAAVALVEAKQARSD-Z X-ALGVATSAQITAAVALVEAKQARSDI-Z X-ALGVATSAQITAAVALVEAKQARSDIE-Z X-ALGVATSAQITAAVALVEAKQARSDIEK-Z X-ALGVATSAQITAAVALVEAKQARSDIEKL-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLK-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKE-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKEA-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAI-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAIR-Z

25 The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXII HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG AMINO TRUNCATIONS

```
X-IRD-Z
                                   X-AIRD-Z
5
                                  X-EAIRD-Z
                                 X-KEAIRD-Z
                                X-LKEAIRD-Z
                              X-KLKEAIRD-Z
                             X-EKLKEAIRD-Z
                            X-IEKLKEAIRD-Z
                           X-DIEKLKEAIRD-Z
                          X-SDIEKLKEAIRD-Z
10
                         X-RSDIEKLKEAIRD-Z
                        X-ARSDIEKLKEAIRD-Z
                       X-QARSDIEKLKEAIRD-Z
                      X-KQARSDIEKLKEAIRD-Z
                     X-AKQARSDIEKLKEAIRD-Z
                    X-EAKQARSDIEKLKEAIRD-Z
                   X-VEAKQARSDIEKLKEAIRD-Z
15
                  X-LVEAKOARSDIEKLKEAIRD-Z
                 X-ALVEAKQARSDIEKLKEAIRD-Z
                X-VALVEAKQARSDIEKLKEAIRD-Z
               X-AVALVEAKQARSDIEKLKEAIRD-Z
              X-AAVALVEAKQARSDIEKLKEAIRD-Z
             X-TAAVALVEAKQARSDIEKLKEAIRD-Z
            X-ITAAVALVEAKQARSDIEKLKEAIRD-Z
           X-QITAAVALVEAKQARSDIEKLKEAIRD-Z
20
          X-AQITAAVALVEAKQARSDIEKLKEAIRD-Z
         X-SAQITAAVALVEAKQARSDIEKLKEAIRD-Z
        X-TSAOITAAVALVEAKOARSDIEKLKEAIRD-Z
       X-ATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
      X-VATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
     X-GVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
    X-LGVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
```

The one letter amino acid code is used.

25

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXIII REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

- X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-Z X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-Z X-VNKIALLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-2 X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z
- X-VNKIALLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z
 X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
 X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
 X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
 X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z

X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-Z

Anti-human parainfluenza virus 3 peptides

X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRSN-Z X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRSNQ-Z X-NNSVALDPIDISIELNKAKSDLEESKEWIRRSNQK-Z X-NSVALDPIDISIELNKAKSDLEESKEWIRRSNQKL-Z X-SVALDPIDISIELNKAKSDLEESKEWIRRSNQKLD-Z X-VALDPIDISIELNKAKSDLEESKEWIRRSNQKLDS-Z X-ALDPIDISIELNKAKSDLEESKEWIRRSNQKLDSI-Z X-LDPIDISIELNKAKSDLEESKEWIRRSNOKLDSIG-Z X-DPIDISIELNKAKSDLEESKEWIRRSNQKLDSIGN-Z X-PIDISIELNKAKSDLEESKEWIRRSNQKLDSIGNW-Z X-IDISIELNKAKSDLEESKEWIRRSNQKLDSIGNWH-Z X-DISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQ-Z X-ISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQS-Z X-SIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSS-Z X-IELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSST-Z 35 X-ELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSSTT-Z X-TAAVALVEAKQARSDIEKLKEAIRDTNKAVQSVQS-Z

```
X-AVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSSI-Z
X-LVEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNL-Z
X-VEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIV-Z
X-EAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIV-Z
X-AKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVA-Z
X-QARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIK-Z
X-ARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKS-Z
X-RSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSV-Z
X-SDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQ-Z
X-KLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVN-Z
X-LKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
X-AIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
```

10 Anti-simian immunodeficiency virus peptides

```
X-WQEWERKVDFLEENITALLEEAQIQQEKNMYELQK-Z
X-QEWERKVDFLEENITALLEEAQIQQEKNMYELQKL-Z
X-EWERKVDFLEENITALLEEAQIQQEKNMYELQKLN-Z
X-WERKVDFLEENITALLEEAQIQQEKNMYELQKLNS-Z
X-ERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWD-Z
X-RKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDV-Z
X-VDFLEENITALLEEAQIQQEKNMYELQKLNSWDVF-Z
X-DFLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z
X-FLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z
```

Anti-measles virus peptides

X-LHRIDLGPPISLERLDVGTNLGNAIAKLEAKELL-Z
X-HRIDLGPPISLERLDVGTNLGNAIAKLEAKELLE-Z
X-RIDLGPPISLERLDVGTNLGNAIAKLEAKELLES-Z
X-IDLGPPISLERLDVGTNLGNAIAKLEAKELLESS-Z
X-DLGPPISLERLDVGTNLGNAIAKLEAKELLESSD-Z
X-LGPPISLERLDVGTNLGNAIAKLEAKELLESSDQ-Z
X-GPPISLERLDVGTNLGNAIAKLEAKELLESSDQI-Z
X-PPISLERLDVGTNLGNAIAKLEAKELLESSDQIL-Z
X-PISLERLDVGTNLGNAIAKLEAKELLESSDQILR-Z
X-SLERLDVGTNLGNAIAKLEAKELLESSDQILRSM-Z
X-LERLDVGTNLGNAIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carb xyl group; an amido group; a T-butyloxycarbonyl group; a macr molecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques. Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, sambrook, et al., 1989, Molecular Cloning, A Laboratory Manual, Vols. 1-3, Cold Spring Harbor Press, NY.

10

15

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are non-peptide bonds. These alternative non-peptide 20 bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another embodiment of the invention, peptides comprising the 25 sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity of the peptides is enhanced. For example, hydrophobic 30 groups such as carbobenzoxyl, dansyl, or tbutyloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. (See "X" in Tables I to IV,

above.) Additionally, the hydrophobic group, tbutyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a

compound, such as the peptides of the invention, to

inhibit membrane fusion events. Specifically, assays

for cell fusion events are described in Section 5.5.1,

bel w, and assays for antiviral activity are described in Section 5.5.2, bel w.

5.5.1 ASSAYS FOR CELL FUSION EVENTS

Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides antifusogenic capabilities.

vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

20

known to those of ordinary skill in the art, are used.

After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as crystal violet stain, may be used to facilitate the visualization of syncytial formation.

5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

The antiviral activity exhibited by the peptides of the invention may be measured, for example, by

asily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an 10 assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for 20 the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4+ cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4* cells by cell-free HIV. Such an assay may comprise culturing an appropriate

concentration (i.e., TCID₅₀) f virus and CD-4+ cells in the presence f the peptide t be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the present of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those 10 described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference 15 in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying non-retroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.

30

Additionally, anti-RSV activity can be assayed in vivo via well known mouse mod ls. Fr exampl, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of 10⁴ to 10⁵ pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known.

Virus replicates to high titer in the nose and lungs
of the cotton rat but produces few if any signs of
inflammation.

5.6. USES OF THE PEPTIDES OF THE INVENTION

10

25

35

The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral

structure with a cell membrane. Among th intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

with respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

10

15

These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

Non retroviral viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides f the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective 10 in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the 15 antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4 cells may be co-infected 20 with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose 25 retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific 35

peptide sequence is found. A diagnostic procedure as described, above, for DP178, may b used in conjunction with the DP107/DP178 analog of interest.

5.5.1. SCREENING ASSAYS

15

20

As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described, above, in Sections 5.1 through 5.3 may also be

compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and

small organic or inorganic molecules. Synthetic compounds, natural products, and other sources of

potentially effective materials may be screen d in a vari ty of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing, for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP107 peptide for a time sufficient to allow binding of the compound to the DP107 peptide;
 - (b) removing non-bound compounds; and
 - (c) determining the presence of the compound bound to the DP107 peptide,
- thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;
 - (b) removing non-bound compounds; and

35

30

(c) d termining the presence of the c mpound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

One method utilizing these types of approaches that may be pursued in the isolation of such DP107binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface 20 with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

25

30

In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of label immobilized on the surface indicates that

compl xes were formed. Where the labeled comp nent is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or DP178, whichever is appropriate for the given assay, or ab antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored complexes.

10

15

30

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two peptides to interact and bind, thus forming a complex.

In ord r to test a compound for disruptive activity, th reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted 15 in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either 20 approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have

PCT/US95/16733 WO 96/19495

been f rm d. The vari us formats are described briefly bel W.

In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with 10 a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the 25 binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled 30 anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alt rnatively, the reacti n can b conducted in a liquid phas in the pr sence or absence f the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

10

15

20

25

30

35

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for the their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41 Δ 178 peptides and by assaying test

comp unds for the disruption of the c mplexes formed by thes two peptides by immun metrically visualizing DP178/M41\(\Delta\)178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41\(\Delta\)178 is a maltose binding fusion protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41∆178 may be immobilized onto solid supports such as microtiter wells. A series of dilutions of a test compound may 10 then be added to each M41 Δ 178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test compound are removed from the wells and wells are then incubated with the DP178/M41\Delta178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be conducted. Test compounds showing an ability to 20 disrupt DP178/M41∆178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41\Delta178 for the determination of binding constants of the ligand of inhibitory constants for competitors of DP178 binding.

30

35

Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41\(\Delta\)178 is immobilized onto a solid support such as a microtiter well. DP178

binding to M41 Δ 178 is then quantitated by measuring the fraction of DP178 that is bound as ¹²⁵I-DP178 and calculating the total amount bound using a value for specific activity (dpm/ μ g peptide) determined for each labeled DP178 preparation. Specific binding to M41 Δ 178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).

10

5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art. 15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may 20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal, 25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline 30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration of the peptides of the invention or other inhibitory

ag nts is pr f rred, techniques well known to th se f rdinary skill in the art may be utilized. F r example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-20 associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley 30 Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure

to an HIV virus. Examples of such pr phylactic us of the peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

10

20

A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LDso (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with

r no toxicity. The dosage may vary within this rang dep nding upon the d sage form empl yed and the route of administration utilized. Fr any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the ICm (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels 15 in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

25

The peptides may be formulated with a suitable adjuvant in order to enhance the immunological

PCT/US95/16733 W 96/19495

r sponse. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydr xide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

10

25

30

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by 15 The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art. Administration of the antibodies may be accomplished 20 using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administrated dose in 35 the management of the oncogenic disorder of interest

will vary with the severity f th condition t be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the 10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be 15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, 20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated

35

f r oral administration may be in the form f tablets, drag s, capsules, r solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active 10 compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain 20 suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

25

30

add d, such as the cr ss-linked polyvinyl pyrr lidone, agar, or alginic acid or a salt there f such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4⁺ cell-cell fusion and infection by cell free virus. In the fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1) shows that the antiviral activity of DP178 (SEQ ID:1)

is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-deriv d DP178 homol g is also found to block HIV-1-mediated syncytia formation.

6.1. MATERIALS AND METHODS

6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide 10 synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were 15 synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the 20 resin by treatment with trifluoracetic acid (TFA) (10ml), H_2O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were 25 chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15µ spherical) with a linear gradient; H₂O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry 30 yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

35

6.1.2. <u>VIRUS</u>

The HIV-1, virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 µm filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25µl of 10 serial diluted virus was added to 75µl AA5 cells at a concentration of 2 x 10⁵/ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post 15 infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497). 20 The titer of the HIV-1_{LAI} and HIV-1_{MN} stocks used for these studies, as measured on the AA5 cell line, was approximately 1.4 x 10^6 and 3.8 x 10^4 TCID₅₀/ml, respectively.

6.1.3. CELL FUSION ASSAY

Approximately 7 x 10⁴ Molt cells were incubated with 1 x 10⁴ CEM cells chronically infected with the HIV-1_{IAI} virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of 100µl culture medium as previously described (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10µl and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the ntire well in a single field.

6.1.4. CELL FREE VIRUS INFECTION ASSAY

synthetic peptides were incubated at 37°C with either 247 TCID₅₀ (for experiment depicted in FIG. 2), or 62 TCID₅₀ (for experiment depicted in FIG.3) units of HIV-1_{LAI} virus or 25 TCID₅₀ units of HIV-2_{NHZ} and CEM CD4⁺ cells at peptide concentrations of 0, 0.04, 0.4, 4.0, and 40µg/ml for 7 days. The resulting reverse transcriptase (RT) activity in counts per minute was determined using the assay described, below, in Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J. Hyg. 27: 493-497 for an explanation of TCID₅₀ calculations.

15

25

30

35

6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was adapted from Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). Supernatants from virus/cell cultures are adjusted to 1% Triton-X100. A 10µl sample of supernatant was added to 50µl of RT cocktail in a 96-well U-bottom microtitre plate and the samples incubated at 37°C for 90 min. The RT cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM MgCl₂, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01), 0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-radioactive dTTP, and 10µCi/ml ³²P-dTTP (Amersham, cat. No. PB.10167).

After the incubation period, $40\mu l$ of reaction mixture was applied to a Schleicher and Schuell (S+S) NA45 membrane (or DE81 paper) saturated in 2 x SSC buffer (0.3M NaCl and 0.003M sodium citrate) held in a S+S Minifold over one sheet of GB003 (S+S) filter

paper, with partial vacuum appli d. Each well of the minifold was washed f ur tim s with 200µl 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

6.2. RESULTS

10

6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells 15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between $10\mu g/ml$ and 12.5ng/ml were tested for blockade of the 20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1LAI, HIV-1MN, HIV- 1_{RF} , or HIV- 1_{SF2} virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection 25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For $\mbox{HIV}_{\mbox{\scriptsize LAI}}$ inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study 30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of $40\mu g/ml$ (FIG. 4). These observations 35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not relat d to non-specific peptid /protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1_{SF2} isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as $10\mu g/ml$. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 25 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1mediated cell fusion, but the peptide's inability to inhibit HIV-2 medicated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested f r its ability to block CD-4+ CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an 5 experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1LAI isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) 10 represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. et al., 1992, Proc. Natl. Acad, Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each 15 concentration (0, 0.04, 0.4, 4, and $40\mu g/ml$) of peptide was incubated with 247 TCID₅₀ units of HIV-1_{LAI} virus and CEM cells. After 7 days of culture, cellfree supernatant was tested for the presence of RT activity as a measure of successful infection. 20 results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC50=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ: ID:8) and DP-118 (SEQ 25 ID:10), had over 60-fold higher IC50 concentrations of approximately $5\mu g/ml$.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1_{IAI} or HIV-2_{NIHZ}. 62 TCID₅₀

30 HIV-1_{IAI} or 25 GCID₅₀ HIV-2_{NIHZ} were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC50 of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC50 for HIV-35 2_{NIHZ}, thus making DP178 (SEQ ID:1) two logs more potent

as a HIV-1 inhibitor than a HIV-2 inhibit r. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEO ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

15 Approximately 3.8x10⁵ CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40μg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

7.2. RESULTS

ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

The results of the cyt toxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects n cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40µg/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the 10 Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

20

25

30

TABLE XXIV

% Viability
at time (hours)

5	<u>Peptide</u>	Peptide Concentration ug/ml	0	24	48	72
	DP178 (SEQ ID:1)	40	98	97	95	97
10		10	98	97	98	98
TO		2.5	98	93	96	96
	DP116 (SEQ ID:9)	40	98	95	98	97
15		10	98	95	93	98
		2.5	98	96	98	99
20	No Peptide	0	98	97	99	98

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107
Soluble recombinant forms of gp41 used in the

25 example described below provide evidence that the
DP178 peptide associates with a distal site on gp41
whose interactive structure is influenced by the DP107
leucine zipper motif. A single mutation disrupting
the coiled-coil structure of the leucine zipper domain
transformed the soluble recombinant gp41 protein from
an inactive to an active inhibitor of HIV-1 fusion.
This transformation may result from liberation of the
potent DP178 domain from a molecular clasp with the
leucine zipper, DP107, determinant. The results also
indicate that the anti-HIV activity of various gp41
derivativ s (p ptid s and recombinant proteins) may be

PCT/US95/16733 W 96/19495

5

due t their ability to form c mplexes with viral gp41 and interfere with its fusogenic process.

8.1. MATERIALS AND METHODS

8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of 10 gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 15 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 20 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41 Δ 107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'-

- 25 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41\Delta178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the
- 30 Xmn I site of pMal-p2. Primer A and 5'-ATAGCTTCTAGATTAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M41-
- 35 PA178. All inserted sequences and mutated residues

wer checked by restriction enzyme analysis and confirmed by DNA sequencing.

8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide 10 gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold, 15 or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed 20 protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

25 8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY
Cell fusion assays were performed as previously
described (Matthews et al., 1987, Proc. Natl. Acad.
Sci. USA 84: 5424-5481). CEM cells (7 X 10⁴) were
incubated with HIV-1_{HIB} chronically infected CEM cells
30 (10⁴) in 96-well flat-bottomed half-area plates
(Costar) in 100 μl culture medium. Peptide and fusion
proteins at various concentrations in 10 μl culture
medium were incubated with the cell mixtures at 37°C
for 24 hours. Multinucleated syncytia were estimated
35 with microscopic examination. Both M41 and M41-P did

n t sh w cytot xicity at the concentrations t sted and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41\textit{\Delta}178 or M41-P\textit{\Delta}178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

10

8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41 Δ 178 or M41-P Δ 178 (5 μ g/ml) in 0.1M NaHCO₃, pH 8.6, were coated on 96 wells 15 Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) 20 were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room 25 temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. 30 peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H2O2 were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H₂SO₄ after incubation at room temperature for 10 minutes. The optical density of the stopped reaction 35 mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

5

8.2. RESULTS

8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF qp41

As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic 10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because 15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (i.e., the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely 20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind 25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant 30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HTV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix 35 motif, i.e., DP107 or DP178, of the M41 fusion protein

liminated reactivity with Fab-d. These results indicate that both helical regions, separat d by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

5

8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, <u>supra</u>, synthetic peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as high as 50 µM (Table XXV, below).

TABLE XXV							
		LEUCINE ZIPPER OF ANTI-HIV MOTIF					

20		DP107	DP178	<u>M41</u>	<u>M41-P</u>	<u>Μ41-ΡΔ178</u>
	Cell fusion (IC ₅₀)	1 μΜ	1 nM	>50 μM	83 nM	> 50 μM
25	Fab-D binding (k _D)	-	-	3.5x10°	2.5x10*	•
	HIV infectivity (IC ₂₀)	1 μΜ	80 nM	> 16 μM	66 nM	>8 µM

The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

^{- =} No detectable binding of Fab-d to the fusion proteins.

³⁵Antiviral Infectivity Assays. 20 μ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20 μ l of the indicated

concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20 µl of CEM4 cells at 6 x 10³ cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO₂ incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID₃₀) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

10

5

Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1mm infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PΔ178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41\Delta178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-P△178, was not active in similar competition experiments (FIG. The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

PCT/US95/16733 WO 96/19495

th DP178 r gi n, making it unavailable for anti-viral activity.

A specific association between thes two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the 5 pp178 peptide or the fusion protein M41 Δ 178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-P∆178, failed to reconstitute the epitope in similar mixing experiments.

10

EXAMPLE: METHOD FOR COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES

A number of known coiled-coil sequences have been 15 well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D 20 tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form 25 di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes 30 c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs 35 were tailored to the DP107 and DP178 sequences by

deducing the m st likely possibilities for heptad
p sitioning f the amino acids of HIV-1 Bru DP-107,
which is kn wn to have coiled-coil structure, and HIV1 Bru DP178, which is still structurally undefined.
The analysis of each of the sequences is contained in
FIG. 12. For example, the motif for GCN4 was designed
as follows:

- The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 2. All amino acids were found at B, C, E, F, and G positions except (CFGIMPTW).
 - 3. The PESEARCH motif would, therefore, be written as follows:

 $[LMNV] - \{CFGIMPTW\} (2) - [LMNV] - \{CFGIMPTW\} (3) -$

15 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-

 $[LMNV] - \{CFGIMPTW\} (2) - [LMNV] - \{CFGIMPTW\} (3) -$

[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

position either L, M, N, or V must occur; at positions
B and C (the next two positions) accept everything
except C, F, G, I, M, P, T, or W; at the D position
either L, M, N, or V must occur; at positions E, F,
and G (the next 3 positions) accept everything except
C, F, G, I, M, P, T, or W." This statement is
contained four times in a 28-mer motif and five times
in a 35-mer motif. The basic motif key then would be:
[IMNV]-{CFGIMPTW}. The motif keys for the remaining
well described coiled-coil sequences are summarized in
FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and als includes motif d signs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also 10 possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the 15 other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is [ILMNQTV] {CFIMPT}. Notice that now only two basic 25 hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. 30 It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

Hybridizations can be p rform d n any c mbination f two or m re motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with 10 only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the fact that DP-178 is located only approximately ten 20 amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper 30 motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped r glycopr t in sequences (library file PVIRUSE1).

Tables V through XIV c ntain lists of prot in sequ nce names and motif hit locations for all the motifs searched.

5

10. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107 AND DP178-LIKE SEQUENCES IN HUMAN IMMUNODEFICIENCY VIRUS

FIG. 20 represents search results for HIV-1 BRU 10 isolate gp41 (PC/Gene protein sequence PENV_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 15 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, 20 for which the key is found in FIG. 17 ({CDGHP} {CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable 25 additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTIS hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies 30 the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave 35 several hits in HIV-1 BRU including 503-525 which is

at the v ry C-t rminus of gp120, just upstream f the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic d main of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN RESPIRATORY SYNCYTIAL VIRUS

FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF_ 20 HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with similarities to DP-178, one just downstream of what 25 would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids 116-202, 267-302, and 506-549. The proline-leucine 30 zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions which share location similarities with DP-178 of HIV-35 1.

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41 (AGM3 isolate; PC/Gene protein sequence name 5 PENV_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would 10 represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV 15 also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178 LIKE SEQUENCES IN CANINE DISTEMPER VIRUS

25

fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23).

Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residu s 340-367. ALLMOTI5 highlights three areas of

interest including: amino acids 228-297, which completely verlaps both the Lupas predicti n and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

pisease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTI5 finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

30 15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

35

Both motifs 107x178x4 and ALLMOTI5 exhibit
DP107-like hits in the same region, 115-182 and 117182 respectively, of Human Parainfluenza Virus (strain
NIH 47885; PC/Gene protein s quence name PVGLF_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits near rethe transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES OF INFLUENZA A VIRUS

rig. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68)

15 at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated

that several f the identified peptides exhibit pot nt antiviral capability. Additionally, it is shown that several of these peptides xhibit a substantial helical character.

17.1 MATERIALS AND METHODS

5

10

15

25

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from A₂₀₀ using Edlehoch's method (1967, Biochemistry 6:1948).

anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

washed with DPBS (Dulbecco's Phosphate Buffered Saline W/ calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD_{450/690} was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG.

27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;

30

PCT/US95/16733 WO 96/19495

2) peptid s T-120 t T-141 and T-576, as sh wn in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and

3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein 10 DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC data for each peptide represents the average of several experiments conducted utilizing that peptide.

17.2 RESULTS

20 The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like 25 F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purfied peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC, values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-35

131, T-135 and T-137 t T-139, as demonstrat d by their 1 w IC $_{50}$ values. In additi n, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

The results summarized in FIG. 28A-B demonstrate
that a number of DP178-like purified peptides exhibit
a range of potent anti-viral activity. These peptides
include, for example, T-67, T-104, T-105 and T-107 to
T-119, as listed in FIG. 28A, and T-665 to T-669 and
T-671 to T-673, as listed in FIG. 28B. In addition,
some of the DP178-like peptides exhibited some level
of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV antiviral compounds.

15

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS TYPE 3 DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

- In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.
- analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of
- 30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses
35 consisted of circular dichroism (CD) studies. The CD

spectra w re measur d in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at appr ximately 10mM concentrations, using a 1 cm pathlength c ll n a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A_{210} using Edlehoch's method (1967, Biochemistry $\underline{6}$:1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of Hep2 cells chronically infected with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

10

30

35

Uninfected confluent monolayers of CV-1W cells

were grown in microtiter wells in 3% EMEM (Eagle
Minimum Essential Medium w/o L-glutamine [Bio
Whittaker Cat. No. 12-125F], with fetal bovine serum
[FBS; which had been heat inactivated for 30 minutes
at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented
at 3%, antibiotics/antimycotics (Gibco BRL Life
Technologies Cat. No. 15040-017) added at 1%, and
glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected CV-1W cells, then adding peptides (at the

dilutions describ d below) in 3% EMEM, and 500 chr nically HPIV3-infected Hep2 c 11s per well. Wells were then incubated at 37°C for 24 hours.

on day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, avove, in Section 17.1.

Peptides: The peptides characterized in the study presented herein were:

10

20

- Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid resides (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500µg/ml to approximately

500ng/ml. For each f the assays, a w ll containing no peptide was also used.

18.2 RESULTS

The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

As shown in FIG. 29A-B, a number of the HPIV3

DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low IC50 values. In fact, peptides 201 to 205 exhibit IC50 values in the nanogram/ml range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

25

FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were

located at amino acid residues 156-215 and 277-289.

The peptide regions found by ALLMOTI5 were located at

amino acid residues 156-219 and 245-286. Both motifs, ther f re, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm.

Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

30

20. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN EPSTEIN-BARR VIRUS

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB_EBV) glycoprotein gp110 precursor (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

15

20

25

30

35

FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a homodimer.

Search results domonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found between the known DNA binding and dimerization regions of the protein. Specifically, this region is located

at amin acid residues 193-220, as sh wn in FIG. 33. The Lupas program pr dicted no coiled-c il regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN MEASLES VIRUS

FIG. 34 illustrates the motif search results for the fusion protein F1 of measles virus, strain Edmonston (PC Gene® protein sequence PVGLF_MEASE), successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at
amino acid residues 228-262. The ALLMOTI5 search
motif identifies three regions, including amino acid
residues 116-184, 228-269 and 452-500. Three regions
containing proline residues followed by a leucine
zipper-like sequence were found beginning at proline
residues 214, 286 and 451.

The Lupas program identified two regions it predicted had potential for coiled-coil structure, which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN HEPATITIS B VIRUS

FIG. 35 depicts the results of a PZIP motif search conducted on the Hepatitis B virus subtype AYW. Two regions of interest within the major surface antigen precursor S protein were identified. The first lies just C-terminal to the proposed fusion peptide of the major surface antigen (Hbs) which is found at amino acid residues 174-191. The second region is located at amino acid residues 233-267. The Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral activity of these D178/DP107 analog regions, peptides derived from area around the analog regions are synthesized, as shown in FIG. 52A-B. These peptides represent one amino acid peptide "walks" through the

putative DP178/DP107 anal g regi ns. The peptides ar synth sized according to standard Fm c chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Follwing complete synthesis, the peptide aminoterminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antivial peptides are further characterized in model systems such as wood chuck tissue culture and animal sytems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.

24. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN BACTERIAL PROTEINS

The results presented herein demonstrate th identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

FIG. 37 depicts the search motif results for the Pseudomonas aeruginosa fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTIS. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTIS.

10

25

30

35

Pseudomonas gonorrhoeae fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 39 depicts the search motif results for the Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 40 depicts the search motif results for the Staphylococcus aureus toxic shock syndrome Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

r gion located at amino acid residues 102-148 w re identified by the ALLMOTI5 search motif. No c iled-c il regions were predict d by the Lupas pr gram.

FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTIS motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5 motif, with the first residing at amino acid residues

55-115, and the s cond residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

5 25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS WITHIN VARIOUS HUMAN PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

conducted on the human lupus KU autoantigen protein prot. The ALLMOTIS motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

35

30

10

15

26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107
ANALOGS: CD AND ANTIVIRAL
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A₂₈₀ using Edlehoch's method (1967, Biochemistry 6:1948).

15

20

35

assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (i.e., cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum

PCT/US95/16733 WO 96/19495

[FBS; which had been heat inactivated for 30 minut s at 56°C; Bi Whittaker Cat. No. 14-501F) supplement d at 10%, antibiotics/antimyc tics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E). Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope. 25

20

Anti-MeV antiviral activity plague reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as described above.

The antiviral assay was c nducted by, first, rem ving all media from the wells containing uninfected Vero cells, then adding peptid s (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

on day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

10

20

25

30

<u>Peptides</u>: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC₅₀ values for such peptides were d termined, as shown in FIG. 47, and ranged from $1.35\mu g/ml$ (T-257B1/C1) to $0.072\mu g/ml$ (T-265B1). None of th DP178-like peptides showed, by CD analysis, a detectable level of helicity.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

10

5

27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides

15 identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis, A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk through the DP178-like region of the SIV TM protein.

Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

35

27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-SIV antiviral compounds.

28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP178 PEPTIDE TRUNCATIONS AND MUTATIONS

The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

20

15

28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed
were as those described, above, in Section 6.1.
Assays utilized HIV-1/IIIb and/or HIV-2 NIHZ isolates.
Purified peptides were used, unless otherwise noted in
FIGS. 49A-C.

<u>Peptides</u>: The peptides characterized in the study presented herein were:

1) FIGS. 49A-C present peptides derived from
the region around and containing the DP178
region of the HIV-1 BRU isolate.
Specifically, this region spanned from gp41
amino acid residue 615 to amino acid residue
717. The peptides listed contain
truncations of this region and/or mutations

PCT/US95/16733 WO 96/19495

> which vary from the DP178 sequence amino acid sequ nc . Further, c rtain of the peptides hav had amino- and/ r carb xyterminal groups either added or removed. as indicated in the figures; and

FIG. 50. presents peptides which represent 2) truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

28.2 RESULTS

Anti-HIV antiviral data was obtained with the 15 group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low IC50 values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50 represents a test peptide which contains a point mutation, as indicated by the residue's shaded 25 background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIHZ isolate demonstrated appreciable antti-HIV-2 antiviral

30 activity.

35

5

10

20

Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ($IC_{50}>400\mu g/ml$) whereas the carboxy terminal peptide showed potent antiviral

activity (IC₅₀= 3μ g/ml). A number of additional test peptides also exhibited a high level of antiviral activity. These included, fr xample, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

Truncations of the DP107 peptide (referred to in IG. 50 as T21) were also produced and tested, as shown in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by their low IC50 values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

25

In the Example presented herein, peptides derived
from the Epstein-Barr (EBV) DP-178/DP107 analog region
of the Zebra protein identified, above, in the Example
presented in Section 20 are described and tested for
anti-EBV activity. It is demonstrated that among
these peptides are ones which exhibit potential antiviral activity.

29.1 MATERIALS AND METHODS

Electrophoretic Mobility Shift Assays (EMSA): Briefly, an EBV Zebra protein was synth sized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a 32P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-15 shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-20 bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

25

29.2 RESULTS

Th EBV Zebra pr tein transcription fact r contains a DP178/DP107 anal g region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

10

30

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays 15 described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the 20 DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of 25 the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

scope by the specific embodiments described which are intended as single illustrations of individual aspects

f th inv ntion, and functionally equivalent methods and comp nents are within the sc pe of the invention. Indeed, various modificati ns f the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

 An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.

2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.

- The peptide of Claim 2 in which the virus is HIV-1 or HIV-2.
 - 4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
- 5. The peptide of Claim 2 in which the virus is a human parainfluenza virus.
- 6. The peptide of Claim 2 in which the virus is an influenza virus.
 - 7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
- 8. The peptide of Claim 2 wherein the virus is an Epstein-Barr virus.
 - 9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
- 10. The method of Claim 9 wherein the virus is HIV-1 or HIV-2.

11. The method f Claim 9 wherein the virus is a respiratory syncytial virus.

- 12. The method of Claim 9 wherein the virus is a human parainfluenza virus.
- 13. The method of Claim 9 wherein the virus is an influenza virus.
- 14. The method of Claim 9 in which the virus is a hepatitis B virus.
 - 15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

15

20

25

30

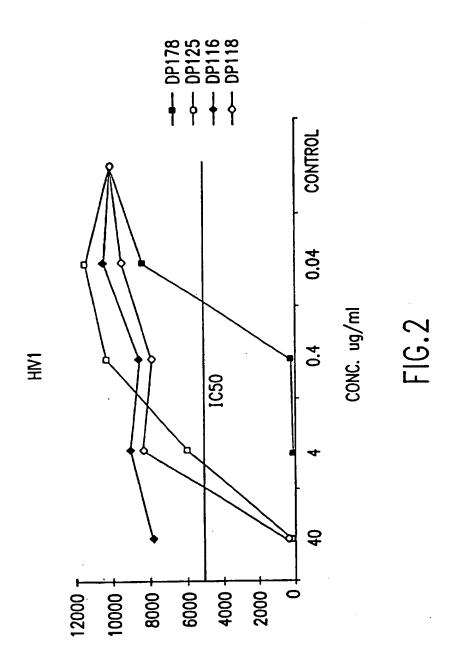
35

7872-020 (SHEET | OF 63)

LOARILAVERYLKI	DP116 (SEQ 10:9)
CGGNNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKI	DP125 (SEQ ID:8)
QQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKYLKDQ	DP118 (SEQ ID:10)
SSESFTLLEQMINIMKLQLAEQMLEQINEKHYLEDIS	0P180 (SEQ 10:2)
LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL	HIV2NIHZ (SEQ ID:7)
LEANISKSLEQAQIQQEKNAMYELQKLNSWDIFGNWF	HIV2ROD (SEQ 10:6)
YTSL1YSLLEKSQTQQEKNEQELLELDKWASLWNWF	HIV1MN (SEQ ID:5)
YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF	HIV1RF (SEQ ID:4)
YTNTIYNLLEESQNQQEKNEQELLELDKWASLWNWF	HIV1SF2 (DP-185; SEQ 10:3)
YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF	HIV1LAI (DP-178; SEQ ID:1)

. اک

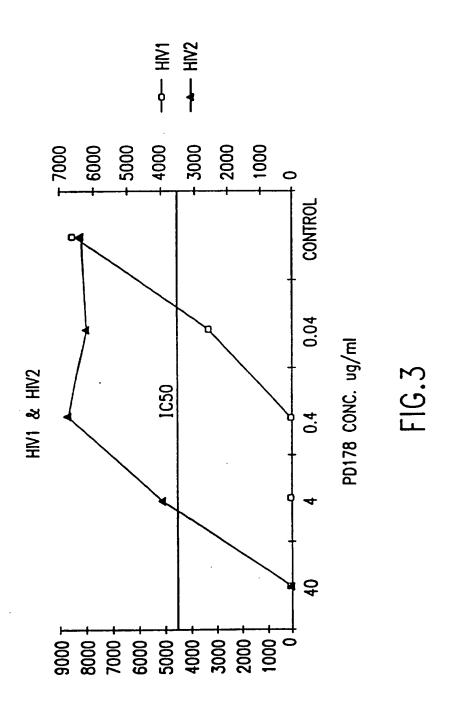
7872-020 (SHEET 2 OF 63)



REVERSE TRAUSCRIPTASE UNITS

PCT/US95/16733

7872-020 (SHEET 3 OF 63)



7872-020 (SHEET 4 OF 63)

Syncylia										
HIVILAI	0P178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
HIVIMN 0 0 0 0 0 0 ND ND ND ND HIVISF2 0 0 0 0 0 0 ND ND ND ND ND ND ND ND ND ND ND ND ND	Syncylia			_	_	_	•	0	^	67
HIVINN	HIVILAL						_		-	34
ND ND ND ND ND ND ND ND	HIVIM			-	-				-	65
DP125 10 5 1 0.2 0.1 0.05 0.025 0.0125	HIVIRF	0							· · -	58
Syncylia HIVILAI O O 54 69 80 75 79 82 HIVIMN O O 30 36 ND ND ND ND ND ND HIVIRF O O 67 63 ND ND ND ND ND ND ND ND ND ND ND ND ND	HIV1SF2	0	0	0	0	0	NU	NU	NU	3 0
HIVILAI	DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
HIVILAI	Syncylia									63
HIVING 0 0 67 63 ND		0	0	54						67
HIV1RF 0 0 67 63 ND	HIVIMN	0	0	30	36					34
HIVISF2 0 0 9 66 ND ND ND ND ND ND ND ND ND ND ND ND ND		0	0	67	63	ND				65
Syncylia		0	0	9	66	ND	ND	МО	ND	58
Syncylia	DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Contro
HIVILAL 75 NO NO NO NO NO NO		75	МD	ND	ND	ND	ND	ND	ND	67
HIVININ 35 ND ND ND ND ND ND ND	-		ND	ND	ND	ND	ND			34
HIVIRE 81 ND			ND	ND	ND	ND	MD	МD		65 58

FIG.4A

DP180	40	20	10	5_	2.5	1.25	0.625	0.3125	Control
Syncylia HIV1LA1	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylio HIVILAI	0	0	0	0	0	0	0	ND	60

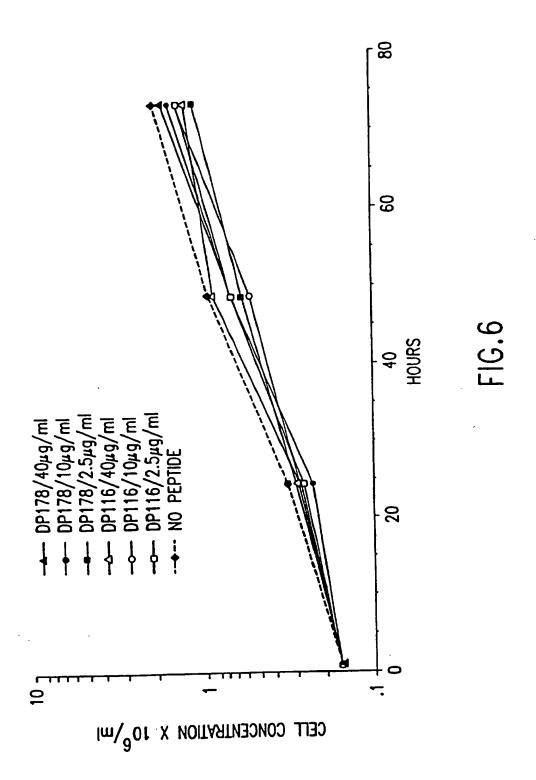
FIG.4B

7872-020 (SHEET 5 OF 63)

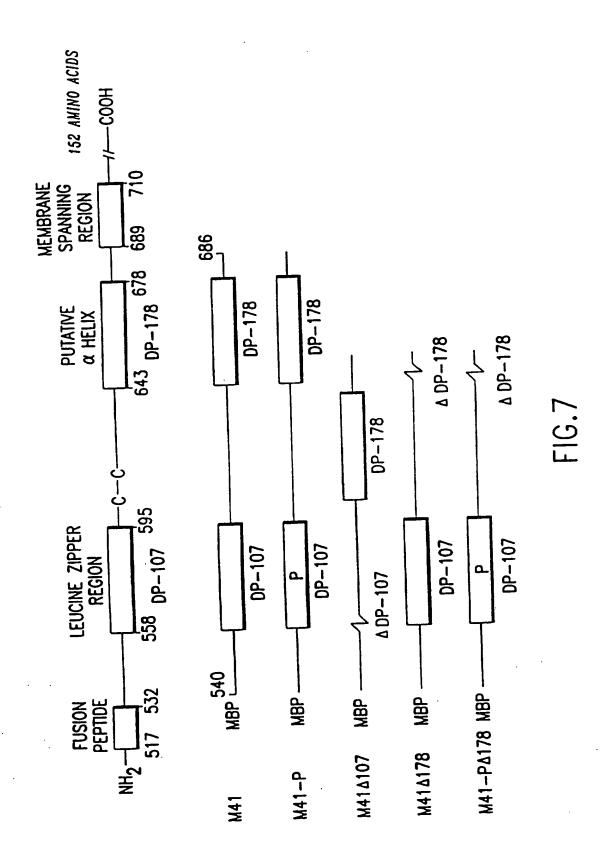
				HIVI	_			
	Number	of	Syncyli	o/well:	concer	itration	in ng/ml	(nanograms/ml)
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylia HIV1	0	0	0	0	0	14	20	48
DP116	20	10	5_	2.5	1.25	0.625	0.3125	Control
Syncylia HIVI	ND	48	ND	ND	ND	ND	ND	ND
				HIV			· /ml	(niorograms/ml)
	Number	r of	Syncyl	io/well	conce	ntration	in μg/mi	(micrograms/ml)
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylio HIV2	50	54	55	57	63	77	78	76
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylio HIV2	ND	58	B ND	ND	ND	ND	ND	ND

FIG.5

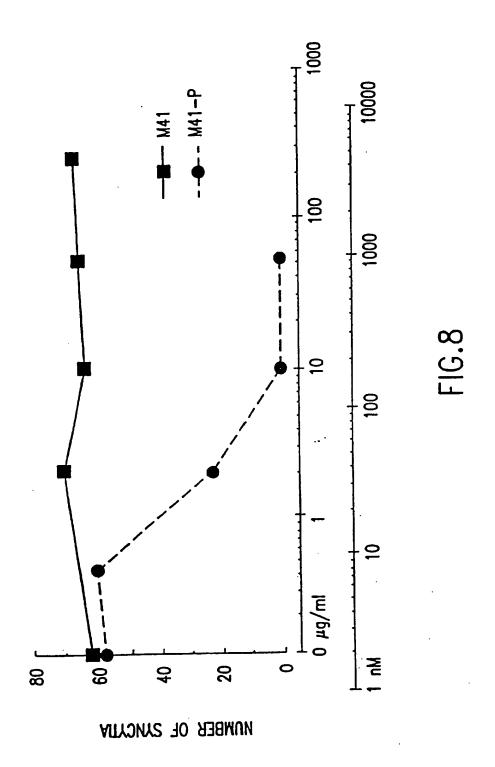
7872-020 (SHEET 6 OF 63)



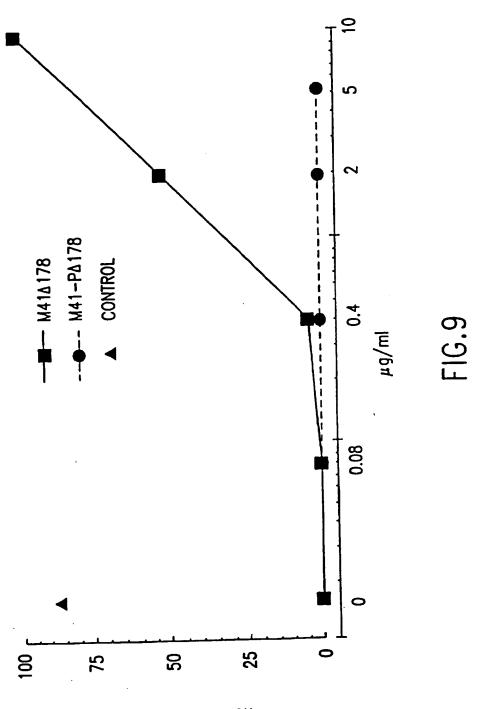
7872-020 (SHEET 7 OF 63)



7872-020 (SHEET & OF 63)

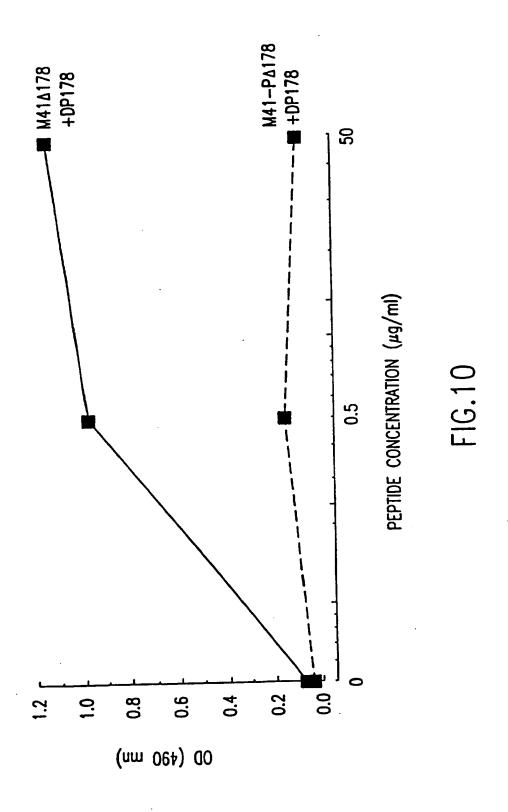


7872-020 (SHEET 9 OF 63)

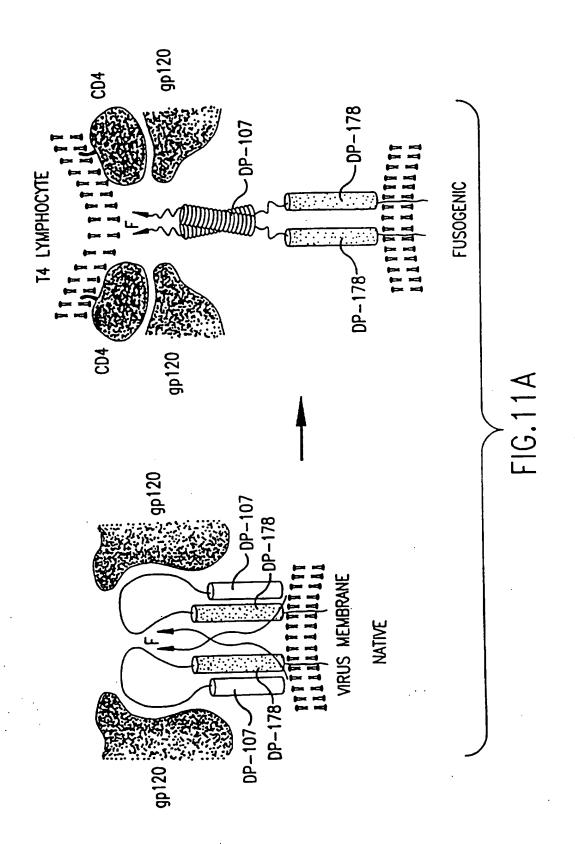


NUMBER OF SYNCYTA

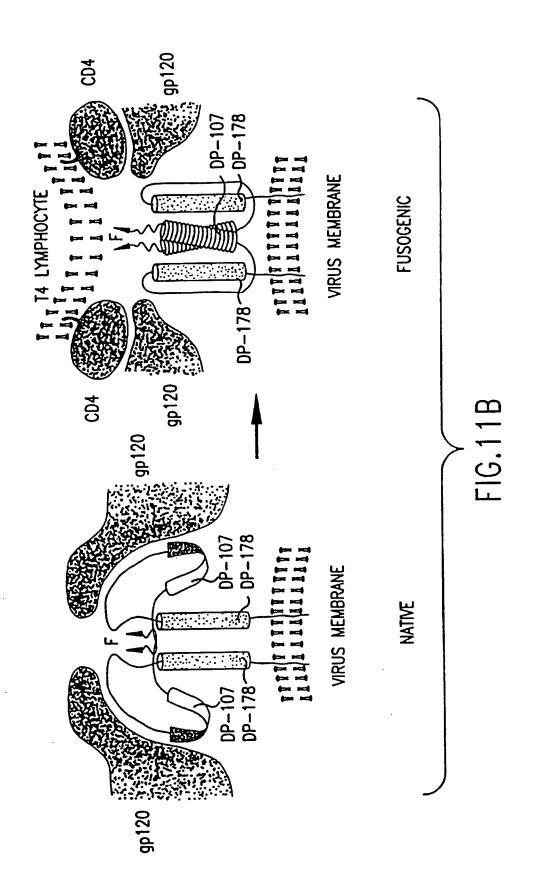
7872-020 (SHEET 10 OF 63)



7872-020 (SHEET II OF 63)



7872-020 (SHEET 12 OF 63)



7872-020 (SHEET 13 OF 63)

WOLLIS		LMNV) {CFGIMPTW} {IKLT} {CFGHIMPRYMY} {AILNV] {CDFGHILPYWY} {ELR] {ACFGMPYWY}	[FILÍV] {ACFLMPTÝM}
[의		
Į	V		
(0		
1	V	_ <u> </u>	-
1	0	V E E L L S K N Y H L E N E V A R L K K L T O O L E D E K S A L O T E I A N L L K E V K T L K A O N S E L A S T A N M L R E O F O L K H K L F O L R N S	HOILE KEFSEVEGRIODLEKY
Posilions	A	E N E V O T E E V V A S T A N E	E G R I
-	و	SAL	SEL
	⋖	Z X Z 0	
	<u> </u>	X O C C C C C C C C C C C C C C C C C C	0 1 E K
	⋖	TO TO TO TO TO TO TO TO TO TO TO TO TO T	R R
	<u>_</u>	R T C C C C C C C C C C C C C C C C C C	KTN
	⋖	XO Y C	. U
	Sequence	GCN4 (gcn4 yeast) C-FOS (fos_human) C-JUN (top1_human)	FLU LOOP 36

FIG. 12

7872-020 (SHEET 14 OF 63)

Wolifs		11.017 GT 11.0PS 17 11.017 GOF 11.0PS 1 11.017 GOF 11.0PS 1	[EKLNOV] {CDFKAPSVY} {EKLNOV} {CFKAPS} [EKLNOV] {CFKAPS}	[EKLOY] {ACFGAPRWY} [EKLOMY] {CFGAPRVY} [EFKLOMY] {CFGAPRVY}	[EILNOSY] {ACFGAPRWY} {EILNOSWY} {CFGAPRVY} {CFGAPRVY}
ſ	<u></u>	0			<u>u</u>
•	\neg	LAVERYL LAVERYLKD0	L A V E R Y L L A V E R Y L K D 0		LELDKWASLWNW LELDKWASLWNW
ſ	ᅪ	<u></u>	X	٠ احــ	3 ₹
l	4	- = = -		* * Z Z * *	
	ı	$\propto \propto$	>- >-	ZZ	SI
•	_	<u> </u>	<u> </u>	<u> </u>	₹ ₹
I	回	->>	>>	SS	XXX
		<u>۔</u> ۔	44	LELDK WASLW LELDKWASLW	000 XXX
	V			≱	
	_	X 0 L 0 A R 0 L 0 A R 1 L		×××	<u> </u>
	- 1	A A A	A 0 0 H L L 0 L T V W G 1 K 0 L 0 A R 1 A 0 0 H L L 0 L T V W G 1 K 0 L 0 A R 1 A 0 0 H L L 0 L T V W G 1 K 0 L 0 A R 1		E S O N O O E K N E O E L L E S O N O O E K N E O E L L E S O N O O E K N E O E L L
1		000	000	<u> </u>	w w w
	۳	000			000
		\times \times	000		யயய
S	lacksquare		X X X	EES ON O O E E E E E E E E E E E E E E E E	ZZZ
. <u>ō</u>		ပပပ		000	~ ~ ×
==		***	3 3 3 3	ZZZ	000
Posilions	6	1 0 W C 1 1 2 W C 1 1 2 W C 1 1 2 W C 1 1 2 W C 1 1 2 W C 1 1 2 W C 1 1 2 W C 1 1 2 W C 1 2 W	>>>	***	000
				ווו נוו נוו	ZZZ
	_	1001	<u></u>	<u> </u>	10 10 10
	⋖	<u></u>	000	777	W W W
		1 H H O O		000	
		E E A O O A A O O O A A A O O O A A A A	= = =	S S S S	
	0	000	000	பயய	<u></u>
		444	000	<u></u>	T T T
		m m m	 		
	צו	444		SSS	
		∞ ∞ ∞	444	x = x	SSS
		N N N N N L L L L R A A L L R A A A	N N N N N L L L L L R R A A A A	Y T S L L H S L X T S L X X X X X X X X X X X X X X X X X X	√ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑ ↑
		<u> </u>	<u> </u>	<u> </u>	
		ZZZ			· }
	\blacksquare	22-	ZZZ	>->-	
	_				
		유유		A= A=	
			222		エエニ
		555	֓֞֞֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	222	2 2 2
		عَ مِ مِ	~~ ~	7 th	777
		1222	خ خ خ	خخذ	들들들
		2 2 2	2 2 2	2 2 2	6 6 6
	٩	و و و	೨೨೨	ڪٽ	
	700	888	94	82 82 82	888
	Sections		777	<u> </u>	OP-178 (env_hv1bru)Y1=0 OP-178 (env_hv1bru)Y1=0 OP-178 (env_hv1bru)Y1=0
	ð	OP-107 (env_hv1bru)L1=0 OP-107 (env_hv1bru)L1=0 OP-107 (env_hv1bru)L1=0	OP-107 (env_hv1bru)L2=D OP-107 (env_hv1bru)L2=D OP-107 (env_hv1bru)L2=D	0P-178 (env_hv1bru)Y1=A 0P-178 (env_hv1bru)Y1=A 0P-178 (env_hv1bru)Y1=A	

FIG. 1

7872-020 (SHEET 15 OF 63)

	A D A D A D Porent Wolif Hybrid Wolff	L SKINTHIENEVARICKKI [LMNV] (CFCIMPTW)	O HILLOLITV W CIIK OLO A RIIL AVERYL (ILOT) (CFINPSTY) (ILMNOTV) (CFINPT) O HILLOLITV W CIIK OLO A RIIL AVERYL (ILOTV) (COFINPST) (ILMNOTV) (CFINPT) O HILLOLITV W CIIK OLO A RIIL AVERYLKOO (ILOTV) (COFINPST) (ILMNOTV) (CFINPT)	OHILOLIVECKOPSVY EKLMOV COMPONENT EKLMOV COMPSVY EKLMOV COMPSVY COMPSV
Positions	D A	THLENEVAR	1	L T V W G T K O L L T V W G T K O L
	<u> </u>	1	E A 0 0 H L L E A 0 0 H L L L	A 0 0 H L L 0 A 0 0 H L L 0 A 0 0 H L L 0
	A O A	×	NNLLRA NNLLRA LLRA	NN LLL NN LLL NN LLRA LE
	Centions	14 yeast)	DP-107 (env_hvibru)L1=0 N N L L R A I E A C C C C C C C C C C C C C C C C C C	DP-107 (env_hvibru)[2=0 N L R A E A Q C DP-107 (env_hvibru)[2=0 N DP-107 (env_hvibru)[2=0 N DP-1

FIG. 12

7872-020 (SHEET 16 OF 63)

Sequence A D<	Hybrid Holil			[eklimovy] {cfgap#} [eklimovm] {cfgap} [efklimovm] {cfgap}	EILNOSY] {ACFGWPRVMY} [EILMNOSYY] {CFGWPW} EILNOSWY] {CFGWPRVY} [EILMNOSVMY] {CFGWP} EFILNOSWY] {CFGWPRVY} [EFILMNOSVMY] {CFGWP}
N	Parent Molif		[LMN] {CFCIMPTH}	[EKLOY] {ACFGAPRYMY} [EKLOMY] {CFGAPRYY} [EFKLOMY] {CFGAPRYY}	
N	C				<u> </u>
N	,				<u> </u>
N	ì	≝		3= 3=	- 5-5
N			:	2 Z 3= 3=	AS
N	[<u> </u>			≆ ≆
N		1		X X	000
N	- {	⋖		* *	<u></u>
A			×	000	
M K O L E D K V E E L L S K N Y H L V S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O O O O O O O O O O O O O O O O	1		<u>-</u> -	<u> </u>	
M K O L E D K V E E L L S K N Y H L V S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O O O O O O O O O O O O O O O O		=	~		000
M K O L E D K V E E L L S K N Y H L V S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O O O O O O O O O O O O O O O O	S	<u> </u>	-	<u></u>	2 2 2
M K O L E D K V E E L L S K N Y H L V S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O E K Y T S L I H S L I E E S O N O O O O O O O O O O O O O O O O O	<u>.</u> 5	Г	<u></u>	000	***
MKOLEOKVEELLS Y T SL I H SL I EES I I SL I SL	sit	1	w.	222	000
MKOLEOKVEELLS Y T SL I H SL I EES SL I I SL I SL	٣		=	* * *	222
MKOLEOKVEELLS Y T SL I H SL I EES SL I I SL I SL			Ξ	000	000
MKOLEOKVEELLS Y T SL I H SL I EES SL I I SL I SL		_	등	222	- 27 27 27
DP-178 (env_hv1bru)Y1=0 DP-178 (env_hv1bru)Y1=0 DP-178 (env_hv1bru)Y1=0 DP-178 (env_hv1bru)Y1=0 DP-178 (env_hv1bru)Y1=0 CP-178 (env_hv1bru)Y1=0 Y T S L I H S L I E E E E E E E E E E E E E E E E E E			1	000	
Sequence GCN4 (gcn4 yeast) MK 0 E D K V E E DP-178 (env_hvibru)Yi=A Y I S I H S I E DP-178 (env_hvibru)Yi=A Y I S I H S I E DP-178 (env_hvibru)Yi=D Y I S I H S I E DP-178 (env_hvibru)Yi=D Y I S I H S DP-178 (env_hvibru)Yi=D Y I S I H S DP-178 (env_hvibru)Yi=D Y I S I H S			1	<u> </u>	
Sequence CCN4 (gcn4 yeast) DP-178 (env_hv1bru)Y1=A Y I S L I H S L DP-178 (env_hv1bru)Y1=A Y I S L I H S L DP-178 (env_hv1bru)Y1=D Y I S L I H S L DP-178 (env_hv1bru)Y1=D Y I S L I H S L DP-178 (env_hv1bru)Y1=D Y I S L I DP-178 (env_hv1bru)Y1=D Y I S L I DP-178 (env_hv1bru)Y1=D Y I S L I			E E	— — <u>—</u>	X X X
Sequence CCN4 (gcn4 yeast) DP-178 (env_hv1bru)Y1=A DP-178 (env_hv1bru)Y1=A CP-178 (env_hv1bru)Y1=B CP-178 (env_hv1bru)Y1=D CP-178 (env_hv1bru)Y1=D Y S I H S I H S I H S I H S I H S I I H S I I H S I I I S I I S I I		\subseteq	>		
Sequence GCN4 (gcn4 yeas1) MK 0 L E DP-178 (env_hv1bru)Y1=A DP-178 (env_hv1bru)Y1=A PP-178 (env_hv1bru)Y1=0 PP-178 (env_hv1bru)Y1=0 Y T DP-178 (env_hv1bru)Y1=0 Y T			Ž	XX X	SSS
Sequence GCN4 (gcn4 yeos1) MK 01 DP-178 (env_hv1bru)Y1=A Y 1 S DP-178 (env_hv1bru)Y1=A Y 1 S DP-178 (env_hv1bru)Y1=0 CP-178 (env_hv1bru)Y1=0 CP-178 (env_hv1bru)Y1=0 CP-178 (env_hv1bru)Y1=0	•	<u></u>	۳	- = = =	
Sequence GCN4 (gcn4 yeast) DP-178 (env_hvlbru)Y1=A Y 1 DP-178 (env_hvlbru)Y1=A Y 1 DP-178 (env_hvlbru)Y1=D DP-178 (env_hvlbru)Y1=D DP-178 (env_hvlbru)Y1=D DP-178 (env_hvlbru)Y1=D			0	SSS	
Sequence GCN4 (gcn4 yeast) GP-178 (env_hvlbru)Y1=A GP-178 (env_hvlbru)Y1=A GP-178 (env_hvlbru)Y1=0 GP-178 (env_hvlbru)Y1=0 GP-178 (env_hvlbru)Y1=0 GP-178 (env_hvlbru)Y1=0		4	, ≚		
		9	CON (gent yeast)	DP-178 (env_hvlbru)Y1=A DP-178 (env_hvlbru)Y1=A DP-178 (env_hvlbru)Y1=A	DP-178 (env_hv1bru)Y1=0 DP-178 (env_hv1bru)Y1=0 DP-178 (env_hv1bru)Y1=0

FIG. 15

7872-020 (SHEET 17 OF 63)

Hybrid Molif			
Parent Motif	[1101V] {COF IMPST} [EKLNOV] {CFRAPS} [EFKLOWY] {CFCAPRVY} [EF1LNOSW] {CFCAPRVY}	[FILIV] {ACFLAPTWK}	
Positions Positi	L R A I E A Q O H L L O L T V W G I K O L O A R I L A V E R R A I E A O O H L L O L T V W G I K O L O A R I L A V E R Y I H S L I E E S O N O O E K N E O E L L E L O K W A S L W N T S L I H S L I E E S O N O O E K N E O E L L E L O K W A S L W N T S L I H S L I E E S O N O O E K N E O E L L E L O K W A S	FLU LOOP 36 I E KIT NEKFHOIEKEFSEVEGRIDOLLEKY	

FIG. 16

		7872	-020	(SHEET	18 0	F 63)
Hybrid Molil		[EFIKLIANDIVARY] {GFIJP}	[EFILIMORSTWM] {GFLIP}	[EFKLMOWM] [GFIP]	[efiklimosymy] {cfip}	
Parent Wolif		(LLOTV) {CGCILPOTM} {1LOTV} {CGFILPOST} [EFKLOMY] {GFCLIPRYY}	[LIAN] {CFCIAPTM} [ILOTV] {COFIAPST} [EFILNOSM] {CFCAPRM}	[LIAN] {CCCIMPTW] [EKLNOY] {CFKAPS} [EFKLOMY] {CFCAPRYY}	[LIAN] {GFGIAPT#} [EKLNOV] {GFKAPS} [EFILNOS#Y] {GFGAPRVY}	
(0	0 0 x	0 <u>L</u>	-	U	
1		<u>×</u>	L A V E R Y L K O O	8 0	L A V E R Y L K D O	
,	٧	KOLOARILAVERYL LIELDKWASLWNWF		H L E N E V A R L K K L TVW G I K O L O A R I L A V E R Y L K E K N E O E L L E L D K W A S L W N W F		
		E R W N	<u>~~</u>	∠ ≥ ∝ ≥=	~ ∠	
(٥) \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	> ≥	<u> </u>	<u>× < </u>	
		S V		<u> </u>	∀ 0	
	A	₩		<u> </u>	u	
		X K O	× 4 ¬	× ~ 0	× ~ -	
,		<u> </u>	<u> </u>	<u> </u>	E O L L A K L R K	
	0	201	200	<u> </u>	2 7 9	
		4 7 J	<u> </u>	<u> </u>	40	
ons S	V	2 2 0	<u> </u>	- = = =		
Ξ		Z ¥ W	z≠w	Z 0 W	Z 0 W	
Posilions		H	Y H L E N E V A R L K K L 0 L T V W G I K O L O A R I 0 N O O E K N E O E L L E L	~ > ×	Y H L E N E V A R L K L I V W G I K Q L Q A O N Q O E K N E Q E L	
_		±	エース	± ⊢ ₩	エース	
	ر حج	× 0 0	- 2 - 3 - 5	- 200	200	
	<u> </u>	x z	2 — w	 	2 - u	
		SHOS	2 E E	N H C	<u></u>	
		_ O W			0-	
		<u> </u>	2 U Z	M X O L E D X V E E L L S K N Y N L L R A 1 E A O O H L L O L Y T S L I H S L I E E S O N O O	MKOLEOKVEELLSKNY NNLLRAIEAOOHLLOL YTSLIHSLIEESO	,
	\blacksquare	>	>==	<u> </u>	> = =	
		0 % Z	S / S	OVE	SAO	
		<u>u </u>	<u> </u>	<u> </u>	<u> </u>	
	عا	OZS	- 5 2 5 -	- 3 - 5	8	
	_	× Z F	<u> </u>	×z-	¥ ₹	•
		MKOLEOKVEELLSKNYH NNLLRAIEAOOHLLOL YTSLIMSLIEESONOOE	MKOLEOKVEELLSKNYHU NNLLRAIEAOOHLLOLT YTSLIHSLIEESONG			
	Sequence	n4 yeast) env_hvibru)L1=0 env_hvibru)Y1=A	CCN4 (gand yeast) DP-107 (env_hvibru)L1=D DP-178 (env_hvibru)Y1=D	GCN4 (gcn4 yeast) DP-107 (env_hv1bru)L2=D DP-178 (env_hv1bru)Y1=A	GCN4 (gcn4 yeast) OP-107 (env_hv1bru)L2=0 OP-178 (env_hv1bru)Y1=0	
	3	1388	888	යි සි දි	888	

FIG. 1.

7872-020

(SHEET 19 OF 63) Hybrid Molif **3**E env_hv1bru]Y1=A env_hvlbru)Y1=0

7872-020 (SHEET 20 OF 63)

P[(1)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V] P[(2)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(3)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(3)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(5)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(7)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(8)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(9)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[L V]-[P](6)-[L V]-[P](6)-[L V] P[(1)-[V]-[V]-[V](V]-[V]-[V]-[V]-[V]-[V]-[V]-[V]-[V]-[V]-[
Eggerander - 5
4444444444

-16.19

7872-020 (SHEET 21 OF 63)

Peptide

4107x178x4 4

*.....FLGFLG A AGSTMGARSM TLTVQARQ *LL SGIVOQO DP107-NNL

LRAIEAOOHL LOLTYWGIKO LOARILAYER YLKDO-DP107 OLLGAY I WGC

4107x178x44

YALLMOTISY

LVS Coilcd-Coil

SGKLICT TAVP *WNASWS NKSLEQIWNN MTWM *E *WDREINN DP178-

YTSLIHSL IEESONOOEK NEOELLELDK* WASLWNWT-DP178 NI

◆Transmembrane Region ◆

TNWLWYIK + OF IMIVGGLYGLRIVEAVLSIY NRVRQGYS + PL

+P23LZIPC+

SFOTHLPTPR GPDR +PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRSL+ CL

♥ALLMOTI5♥

4107x178x44

F *SYHRLRDLL LIVTRIVELL GRRGW *EALKY WWNLLOYWSO

ELKNSAVSLL NAT A ALAVAEG TDRVIEVVQG A CRAIRITIPR

RIRQGLERIL L

7872-020 (SHEET 22 OF 63)

Fusion

VALLMOTISY

Peptide

4107x178x44

LGVGSAIAS GVA *YSKVLHL EGEVNICIKSA

+P1&12LZIPC+

LLSTNKAVVS LSNGVSVLTS KVLDLKNYID KQ + V LL +PIVNKQ

4107x178x44

SC ASISNIETY I+ EFOOKNNRLLETTREFSYNAGA VITTYVSTMLTNSELLSL

+P1&12LZIPC+

♥ALLMOTI5♥

INDM →PI →TNDQ KKLMSNNVQI V→ RQQSYSI+ MS IIKEEVLAYV

VQ▼ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

+P7, 12, & 23LZIPC+

4107x178x44

♥ALLMOTI5♥

EPIINFYDPLVF +PSDE +FDASISOVNEKINOSLAF *I+ RKSDELL+

◆ Transmembrane Region ◆

HNYNA * GK STIN *IMITTI IIVIIVILLIS LIAVGLLLY * C+

KARSTPVTLS KDQLSGINNI AFSN

7872-020 (SHEET 23 OF 63)

Fusion

Peptide FLGFLG

♥ALLMOTI5♥ ♦107x178x4◆

♥AAGTA MGAAA ◆TALTYOSOHLLAGILQQOKNLLAAY

4107x178x44

EAQ → QQM → LKLTIWGYKNLNARYTALEKYLEDOARLN → AWG → CA

LVS Coilcd-Coil

♥ALLMOTI5♥ ♦107x178x4♦

WKQVCHTTVP WQWNNRTPDW VNNMT *WLE *WERQISYLEGNTT

4107x178x44

TOLEEARAOEEKNLD* AYOKLSS* WSDFWSW* FDF *SKWLN +ILK

◆ Transmembrane Region ◆

IGFLDYLGIIGLRLLYTY + YS * CIARVRQGYS PLSPQIHIHP WKGQPDNAEG

PGEGGDKRKN SSEPWQKESG TAEWKSNWCK RLTNWCSISS IWLYNS

♥ALLMOTI5♥

♥CLTL LVIILRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL♥

ACRSAYRA IINSPRRVRQ GLEGILN

FIG. 22

7872-020 (SHEET 24 OF 63)

SLRTSLEOSNKAIEEIREATOETVIA* VOGVODY* VNNEL* VP

♦ ALLMOTI5 ♦ 107x178x4 ♦

+P6 & 12LZIPC+

AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD +PISA + EISIQALIYAL

GGEIHKILEKLGYSGSD ← MIAILESRGIKTKI ▼ THVDLPGKF IILSISY

P1 & 12LZIPC
PTLSEVKGVIVHRLEAV SYNIGSQEWYTTVPRYIATNGYLISNFDESSCVFVS

ESAICSQNSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTIINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYP

LVS Coiled-Coil

▼ALLMOTI5 ▼

+P12 & 23LZIPC+

DMVYEGKVAL G +PAISLD +RL+DYGTNLGNALKKLDDAKYLI+

+ Transmembrane Region +
DSS + NOILETVR RS → * SFN + FGSLL SYPILSCTAL ALLLLIYCC →

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

7872-020 (SHEET 25 OF 63)

Fusion ▼∧LLMOTI5▼

Peptide

4107x178x44

▼......FIGAI IGSVALGVA TAAQITAASA LIQANQNAAN ◆ILRLICESITA

TIEAVIIEVTDGLSQLAVA♠ VG KM♥ QQFVNDQFNNTAQELDCIKITQQV

VALLMOTISY

GVELNLYLTELTTV FGPQITSPAL *TQLTIQALYNAGGNMDYLLTKLGVG

+P1 & 12LZIPC+

NNOLSSLIGSGLIT GN♥ *PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET

LSVST TKGFASALVP KVVTQVGSVI EELDTSYCIE TDLDLYCTIU VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGIISQ

♥ALLMOTI5♥

4107x178x44

NYGEAVSLID RHSCN **VLSLD GITLRLSGEF DATYQKNISI LDSQVIVTG

LVS Coiled-Coil

Trans-

N LDISTELGNY NNSISNALDK LEESNSKLDK VNVKLTSTSA +LIT YIA

membrane Region +

LTAISLVCGIJ.SLV * LACYLMY + KQKAQQKTLLWLGNNTLGQMRATTKM

7872-020 (SHEET 26 OF 63)

Fusion

YALLMOTISY

Peptide

107x178x4 *LVS Coiled-Coil*

....FFGGV

*IG *TIALG *VATSAQITAAVALYEAKQARSDIEKLKE

AIRDTNKAVQSVQSSIGNLIVAIKSVQ* DYVNKE** IVPSIARLGCEAAG

YALLMOTI5♥

4107x178x44

LQLGIALTQH *YSELTNIFGDNIGSLOEKGIKLQGIASLYRTNITEY*

+P5 & 12LZIPC+

IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL +PLLTRLLNTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNTNKEGTLAFYTP

∀ALLMOTI5∀

4107x178x44

+P6 & 23LZIPC+

NDITLNNSVALD +PIDI +SIELN YKAKSDLEESKEWI+ RRSNOKL+

+ Transmembrane Region +

DSIGNWHOSSTT +IIIV+ LIMIILFIINVT II+ IIAVKYY+ R

IQKINIRVDQN DKPYVLTNK

7872-020 (SHEET 27 OF 63)

Fusion
Peptide
.....GLFGAI AGFIENGWEGMIDGWYGFRHQNSEGTG

4107x178x44

♥ALLMOTI5♥

LVS Coilcd-Coil

*Q *AADLKST *QAAIDQINGKLNRVIEKTNEKFHQIEKEESEVEGRIQ

DLEKYVEDTKIDL* WSYNAELLVALENOHTI* DLT▼ DSEMNKLFEKTR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

WO 96/19495 PCT/US95/16733

				8	3	1	3	•						•	:	•	;			•
Purlan Array		Pulling	KES CX TIL	(notest)	ŝ	15		40	787	707	354	336	250	116		280	118	253		
				Ą	:	:	ŀ	•	ŀ		ŀ	ŀ	1	1	ŀ	·		ŀ		
				RSV F2	T-443			2.146	7-168	1.147	1767						1	2		
E				ŧ		‡	‡	‡	-		‡	‡	‡	‡	‡	‡	Ī	-	1	
				+	+	+	1	‡	‡	+	‡	‡	#	‡	+	‡	‡	‡	1	
	_	-	ļ	‡	‡			‡	+	#	‡	‡	1	-	1	7	1	ļ		
	_	+	+			7		+	+	+	1					3				
	_				910								0	OIL.	OLL	110	0			
	_				I E L						1 6	1 E L	186	1 3 1	11 E IL	1 8 1	1 1 1	1 6 1		
	_				> V		Z	MM	N A N	Y N	> ¥	A V N	<u> </u>	<u>^</u> ×	> V	NAN	<u> У</u>	> V N	<u> </u>	
	H		1.1		KIYIK	XXX	XXX	X X X	NKY K	N N N	J KIY K	SKY K	N X X	シ ド ド ド	S X Y X	SKY K	DKYK	OKIYIK	DKYK	
	-				<u> </u>	36.70	5610	SEL	3 2 1 0	3 2 5		1 2 2	100	100	_	_	0 E L	061	1 3 3 0	
	-	_	-		×	¥	¥	×	¥	¥	-			1		×	×	X	L K	
	-	_	-	+	200	7			× 2	× >			2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	2		2 2	× >	¥ > ×	×	
		_			* K 12) k 2 2		2 (2 2 2	2 2) C		2	2	2	9 (2)	2 C 2 2) (C) C : ⊇	I	
		_	+	+	Š	<u> </u>	2) 2)	2	<u> </u>	<u> </u>	1	1	¥	¥	Y				2	
		_	+	+		Š	¥	¥	Z Z			=	Ξ Ξ		Σ Σ	<u> </u>				
	İ				_	E1.5	E L S			E 1 3	9	- 3	<u>د</u> 3	E L 8	1.3	8		1	1	1
							1 1 1	=	=	=	1	1						#	1	4
						राधार	Y 1 3 V	VISIT	NS L	_		E	E	E	F					
			:			RSV FE	112	1.143	7:14	T-168	1:141	1957	1.141	1	202	1.151	1.132	1.163	T-154	1.455
				-			+	-	t	1	 	T	\dagger	t	1	t	1		r	

7872-020 (SHEET 28 OF 63)

F16, 27A

7872-020 (SHEET 29 OF 63)

_		. 1		-	_	_		_	_		-	Ī.,	П	Т	- .	П		П
o to so	(XTT) ua/mi		>500	>500	>200	>500	>500	>200	165	8	85,	NOT TESTED	8	Š	8	8	İ	
3	ĮΣ				Ц				Ш	-	<u> </u>	F	╟	4	_	'-	+	Н
H	╀	-	Н	Н	Н		Н		Н				Ħ	#	_	\exists	丰	日
H	╁	1	\vdash	Н	Н		Н	- -	Н	\vdash	+	Н	H	+		ᅱ	+	Н
	I]]									-		H	1	_	\exists	1	口
-	╀	1	Щ		Н	_	_	\vdash	H		1		Н	\pm	j	∃	İ	Н
-	╁	1	-	H	Н	Н		Η	H		-	F	Н	4	7	\exists	Ŧ	П
	T	1 1						7		_	ŀ	L	⇈	1		╛	\pm	Н
L	L]	Щ	Ц	Н	Н	Ц		Н	-	÷	\vdash	Н	7	4		+	Н
H	╄	1	Н	Н	Н	Н	-	_	H	[]				1	1		土	Н
L	t	1 1								-		Н	Н	╁	┥	H	+-	Н
F	L]	П		Щ			_			1			#	7		I	目
\vdash	╀	1	Н	H	Н	-	\dashv	_	\vdash	H	÷	┢	Н	+	┨	Н	+	Н
-	t		\Box	Ħ	H	Н	H	_	7		-	Г	П	7	7		T	口
		1	T			٠			コ		<u> </u>	Н	Н	+	\exists	Н	+	H
L	1	1	0	Н		QS	Н	L	4		-		\dashv	7	7		丰	口
\vdash	┝	1	M		Н	M	Н	-	\dashv	Н	+	Н	H	+		H	╁	Н
	L	1	ľ			1	1	1	ゴ	F	-	\Box	H	1	8	\Box	F	П
	L	I	L		\Box	Ĺ	101		7		-	H		+	5	Н	╁╌	Н
┝	╀	 	۱ (۵	Н	-	ιo	0	7	-		-	\Box	\Box	3	7		\Box	\Box
\vdash	┢	1	3	Н	3	.	E	3	ᅥ			H		=		Н		H
		1	Ŧ		L	•	1	1			-		\Box	7	<u> </u>	F	-	\Box
L			۸۷	\sqcup	> V	>	۸٧	۱۸	4			H	H	7	3	Н	$\dot{\cdot}$	H
\vdash	┝	}	×	Н	N	X	N	'n	\dashv	F	-	N	V Z	<u> </u>	₹			\Box
		†	×		¥	И	Ж	K	╛		×	×	¥	2		6		
		[ΚX	Δ	Y	¥	٨	A	\Box	\vdash	×	Κ	×	<u> </u>				\Box
\vdash	┡		O	×	DK	D	×	D K				ō	0	9		Ē		
H	┢		3	=	-	7	10	-	¥	\vdash		님	1	4		밁		\Box
		İ	w	w	W	E	3	3	囯		0	OE	30	X X X X X X X X X X X X X X X X X X X	I KI O E I LI DI KI Y I KI N A I VI T I E	KENKUNOTOA		
L	L		o ×	O	Ω	α	σ	٥	르	Н	×	Ī	¥1	<u>*</u>	Ĭ	벌	\dashv	\mathbf{H}
\vdash	Н		=	=	=	Ė	=	H	13		1	Ξ	3	4	3	13		
			11	3	-	1	11	三	W	H	¥ ^	ž	치	Š	Ĭ	2		Н
Д		[ı K	×	, K) K) K	×	日		×	Ξ	¥	4	4	9		
\vdash	\vdash		×	> ×	> ×	× ×	KVKL	DAKVKI	SVITTIELSNIKEN		4010	TOAKVK	XAXVO	O T D A K V K	GITIDIAIKIVIKIL	1 6 1	\dashv	H
		t	₹	₹	<	٧	٧	4	>	F	=	<u> </u>	-	1		E		日
		[ō	٥	٥	٥	٥	_		E	12	7	×	ZI:	27	>		Н
H	Н	ļ	-0	6	10	H	0 1	믕	밁		5	ī	2	X	ENKU	[0]		A
\vdash	Н	ŀ	Ĭ	Z	Z	Н	ž	Z	3	E	ΪΞ	Z	Ì	2	3	Ē		
			<u>ं</u>	ပ	ပ		ŭ	0	o	>	×	2	KE	<u> </u>	X	ě		H
H	Н		¥	×	¥	<u> </u>	L	×	1	A H	<u> </u>				1	Ĕ		口
H	Н		ž	W	Z W	\vdash	┝		듬	=	2	- 2 0	Z	=	\dashv	1	_	H
	H		×	×	Ē			¥	<u> </u>	Ξ	<u> </u>	-		#	1	1		口
П	П		Ε	Ε	匚				•	100	-	=	9	+	\dashv	1	-	Н
Н	Н		8	2	1-	⊢	-	2	놁	0	Ŀ	Ε	于	#	ゴ	Ε		口
Н	Н	}	둗	=	t	Н	\vdash	H	뉱	IRKSOE	∐ ₹	-	딍	+	\dashv	5	_	Н
			=	w		L		口	0	Ξ		7 8 V	9	7	\exists	6		口
Н	ş		二	1=	\vdash	_	-	Н	심	4	-	1	H	\pm	7	1	1	Н
RSV	Peptide #		1-22	1-23	T-24	1-25	1-28	T-27	T-68 IV SKOY SALRTOWYT	T-334 A F	1.37	1372	1.373	7	55	T-575 A V 9 K 0 V L 9 A L R T 0 W Y T 8 V		

FIF. 278

7872-020 (SHEET 30 OF 63)

7		Т	Т	Т	Π	П	П	Т	Т	Τ	Γ	Γ.	Γ	Г	П	П	Ì				Г	П	П		
				.].	l.				ا.			١.	١.	ļ.					•		‡	;	ŧ		
		ľ	٦	l	١			1		l			l						ľ				l		
	H	B	†	t	t		Н	1	t	t	T	T	t	t	T	T	Ī	Π	Γ	ز	Ī	Ī	П		
Fusion Assery	7	E4 X 77	2	3	╪	92	3	뒥	#	٥	ŧ	ŀ	-	1	ŧ	187	B	9	66	F	É	2	204	ļ	
2	2	2	Т	7	Ŧ	F	۲	Н	†	t	t	t	t	†	T	T	t	f	r	t.	t	1	T		
۴		Ш	₹	1	<u>'</u>	*	•		1	1	<u>'</u>		ľ	1	ľ	ľ	ľ	Ľ	ľ	ľ	ľ	ľ	ľ		
_	Γ	_	=	_			2	1.418	7.170							1	1	3	ŀ					١	
ı		RSV	11111	1.5			Ž	Ξ	71					Ì		ľ	ľ	ľ	ľ	ľ	ľ	ľ	Ľ		
_	E	E	1	Ħ	7	Ŧ	Ŧ	F	H	+	‡	1	1	#	1	1	1	Ŧ	Ī	Ŧ	1	1	ŀ	4	
Ė	E	Ė	Σ	Н	3	Ŧ	Ŧ	E		1	7	7	1	1	1	1	1	1	1	1	1	zŀ.	2 2	4	
ш	E	F	-	Н	#	‡	‡	‡	H	4	‡	4	#	#	#	‡	†	‡	J		4		4	₹.	
F	‡	‡	Ě	H	\exists	‡	‡	‡	H	Ħ	7	7	7	7	7	7	1	1		2	ŧΙ	ž	2		
F	‡	‡	6		H	7	7	Ŧ	E	\exists	7			٥	급	台	4	J,	7	1	ð	a			
E	\mp	Ξ	7	E	\exists	1	1	I	H	Н		۸	X	S			Ş	Ź	1		Š	킼	Š	\$	
Ŀ	‡	‡	Ě	Ė	Ħ	#	#	‡	Ŀ	•	ě	8 K				-			Ì			-			
þ	‡	‡	Ę	ŧ	H	4	‡	,	\F	7	1	7	11/	I II A	V L	-	-	,	4	7	٧	7	7	3	
F	‡	‡	<u> </u>		Ħ	Ţ	<u> </u>	,	9	-) I	1010	8 7	Á	A IS	8 /	3	-	2	8	8 6	3	9		
þ	‡	‡	Q N	I	5	0	9	9		0	9 %	NO	0 1	0	ON	ON		9	<u> </u>	0	N O	N O		Ş	
F	‡	‡	-	-	-	1	9		2	-		• 1	=	=	8	(1)	1	=	L 18	1. 18	B 7	1 6	9	=	
E	\mp	1	,	•	>	VIS	2	2		>	>	Ž	≥	E	2	ž	N IS	2	٠ د	8 A	S A	Σ	Ž	ž	
-	+	1	ľ			<u>></u>	2	3	<u> </u>	₹	3	3	×	Š	₹	Ž	λV	AMX	AΜX	KIVIN	××	È	KAV	XX	
ŀ	#	#	‡		. Z	Ĕ	¥	Ξ	2	1 ×	×	Ē			Ē	Ξ	Ē	Ī	I PK J		Ξ	Ξ	=		
ŀ	7	╡	Ï	-		-	8		-		-	т	Ē	E	-	-	E		8	2		2	•	9	
Ė	\exists		-	7	1	Z	7	1	4	-			ŀ		-	4	4	3	ž	Y	K	ź	É	Н	
	_		_	2	4	ŧ	×	¥	Ξ,	+	ŧ					-	×	×	×		F	‡	þ	Ħ	l
ł	╛			-	1	. 2	₽	2	2	<u> </u>		1	1	1		ŀ		≥	۴	ļ	ŧ	Ŧ	Ŧ	H	
	\dashv		П	히	0 0	_	0	0	Б	٠,		1	1	3	3			Ŧ	Ē	Ī	I	1	F	E	
1	\exists	Ξ		를	:	4].	1	1		를	4			1	1	+	1	t	t	t	‡	‡	‡	t	l
	\exists		Н	Ħ	Ź	\$	ŧ		Ž		#	\$	#	‡	‡	‡	‡	‡	ļ	ŧ	‡	‡	Ŧ	ŀ	l
			F	Ŕ	ş	Ŧ			9	1	1	1	1	1	1	1	Ŧ	Ŧ	-	1	1	1	Ŧ	ŀ	١
	Ē	Е	E	VA	S	3					1	1	1	1	#	‡	‡	‡	‡	‡	‡	‡	‡	ţ	l
	E		t	VADBY	7 0 8 V	2	‡	‡	t	Ħ	4		╡	#	#	#	‡	‡	‡	†	7	7	+	+	1
	100	r	t	Ì	Ì	1	1	T	T	П	П		•			٦	1	T	Ī	٦			Ī	T	1
	FRE	L			Ц		1		L	Ц	Ц			Ц	Ц		_	1	4	1			1	1	1
	Ę		2	:	1.170		اءِ			1.13	1-117	111	41.1	2	1:431	1-132	178	3	3	2	1433	1711	233	ş :	
	RSV DP-107-LIKE REGION (F1)	L	ľ		۴	1111		٠	֓֜֞֜֜֜֜֜֓֓֓֓֜֜֜֜֡֓֜֜֜֜֡֡	ľ	۲	Ľ	۲	۲	Ľ		۲		•	۲				1	1
	200				۱		I	1			•	١				۱						H		١	
	قا	4	+	+	╀	Н	Н	+	+	╀	\vdash	H	\vdash	┞	-	H	Н	Н		H	H	H	Н	\dashv	+
		-	-						1	1										L	L		l		
	•	•	-	_	_	_	_	_	_	_	_	_	_	_				_		_	_				

F16, 27 C

7872-020 (SHEET 3) OF 63)

Pepide#
T X X Y V V S L S N Q V S V L D L X N V
VI H L M O M V K K S A L L S T N K A V (S L S Z O L
1-28 A B O V A V B K V L H L E O E V N K I K B A L L S T N K A V V S I A N O V
V L H L E G E V N K I K S A L L S T N K A V V S L S N G V S V L T S K
69-1 V V V V V V V V V V V V V V V V V V V
MINISTER SIMINISTER OF THE OFFICE STATES
T-2/6 STIBINITE TVITE FFOOD KINNRILLE TITRE FISIVINA DIVITED VB

FIF. 27 D

7872-020 (SHEET 32 OF 63)

Fullon Asiang Fullon Ful
O O O O O O O O O O O O O O O O O O O
の の い の の の の の の の の の の の の の の の の の
8
T-67-4h9
<u>Ĭ</u>
178-LI 1-47 1-104 1-104 1-104 1-110
RSV DP-178-LIKE REGION (F1) RSV T-67 T-104 T-106 T-106 T-106 T-106 T-106 T-113 T-114 T-116 T-116 T-117 T-117 T-117 T-117 T-117 T-117
EIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

F1G. 284

7872-020 (SHEET 33 OF 63)

AVG. ICEO	138	NOT TESTED	×100	*100	× 8	×180		NOT TESTED		×100		NOT TESTED	7	4	•	8	8	×100		60	9	14	¥180	\$	8		NOT TESTED
E	H						⇉	Ì																	コ	⇉	Ī
1-1-1	Н	H	H	Н	4	-	┥	4	Н	Н	\dashv	Н	Ч	Н	Н	H	Н	Н	-	Н	Н	Н	-	Н	4	┥	\dashv
							コ	コ							Π	П							╛		耳	7	コ
	П	H		Н	-	-	\dashv	4	4	Н	-	Щ	Н	Н		Н	Н	Н	Н	Н	Н	Н	\dashv	Н	\dashv	┥	-
┡╃┩	Н	H					コ	╛														П	⇉				コ
 - 	H	H 1	Н	Н	┥	4	┥	┥	Н	Н	Н	Н	Н	-	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	+	┥	-
		H :		Ħ	コ		コ						Π							П		П				コ	コ
	H	H	Н	Н	\dashv	\dashv	\dashv	-	Н	Н	Н	Н	Н	Н	H	H	Н	Н	Н	Н	Н	Н		Н	H	┥	\dashv
┝┼┤	H			П								П									\Box	П	\Box			4	コ
	\Box	H	\vdash	Н	-	Н	4	-	Н	Н	Η	Н	Н		H	Н	Н	Н	Н	Н	Н	Н	\dashv	Н	Н	┥	\dashv
	\Box			П	1						П	П						П		П							7
	Н	 	Н	Н	۲	Н	Н	\dashv	-	Н	Η	Н	Н	H	┝	H	Н	Н	Н	Н	Н	Н	Н	Н	۲	┥	\dashv
	H		I	П										П				П	П			П				7	コ
		H	╁	Н	Н	Н	Н	\dashv	Н	Н	Н	Н	Н	Н	┝	┝	Н	Н	Н	Н	Н	Н	Н	Н	Н	┥	\dashv
Ш	H	日	F	口			\square			П	Е	П	I		F	Г	Г	Д	П	П	П	П		П	耳	コ	\exists
H	H	Н	\vdash	Н	Н	۲	Н	Н	H	H	H	Η	H	-	Ι-	۲	H	Н	Н	Н	Н	Н	H	Н	Н	\exists	\exists
H	\Box		L		Д						Ш		П	П				П		П	П					7	コ
	\Box	Н	╁	Н	H	Н	Н		H	H	H	H	Н	H	H	-	H	Н	Н	Н	Н	Н	Н	Н		┨	\dashv
H	2		L	П							Ц			I		F		П	П	П						\Box	7
HH	日	Н	⊦	Н	Н	H	Н			H	H	H	Н	H	H	┝	-	Н	Н	-	Н	Н	Н	Н		\dashv	1
		H	F			Ц			_						Г				П		П		\Box	П		Ц	7
田	N Q S L AF	Н	H	Н	H	H	Н	H	-	┝	H	┝	H	┝	├	+	┝	Н	Н	H	Н		\exists	Н	\exists		1
HH	븳	\Box	F		П	Е							F	F	F	F	L]		П		7
H	ō	Н	H	H		L	Н	-	H	\vdash		-	۲	H	-	H	1			Н	Н		Н	Н	H		<u></u>
	囯	П	F	Г	Г	F	\Box	F	F	F	Г		Ē	F	F	F	F		F	Ē	П	Ē	ı 🗀	1	1		6
	×	H	E	t				L	-		L	\vdash	ō	L	t	t	t		H		8	9	8	8 ×	K S		ᇹ
H		\Box	F	F	F	L			Ε	L	L	L	× ×	4	F	L	F	L	L	×	S S	×	0 K	OK	×		딁
	Z	≥	t	t				L		L		t	>	>	>	t	t			4	3	1	٧	•	V		ヨ
Ш	E F D A S 1 S Q V N E	FITRKEDELLLHNIV	F	┞	H	F	_	H		F	-	-	3	2 2 3	> Z	Ę	Ł	H	L	7	7	X	NVN	NAN	LHHVVNA	Н	I RK DDELLHNVNA OK
1-1-1	틝		L	L		L			<u>-</u> -	t	Ì	L	5	Ξ	-	-		t		Z	2	Ž			Ξ		彐
 	17		F	╀	H	F	L	H	!	F	ŀ	H	=	1	1	1		┞	H	3	Ξ	Ξ	ΗЭ	Ξ	3	Н	=
Ш	9	6	E	Ŀ	E	E			Ė	L	t	İ			o	0	0	ō		2	Ξ	7	1	2	ļ		画
144	됣		15	12	8	- ×	Ͱ	┝	-	┝	┞	Ŀ	8	8 X	8	*	ŀ	<u>∞</u>	Г	30	0	8	0	30	10	Н	4
 	튑	◪	Alolalal	A C K	A O K 8 7	A O K 8 T	L	L	L	Ŀ	L	Ē	I R K B D	œ	8 X	O S X	A X S O E	2				X B O E	K 6 D E	X 0 D E	KSDEL	П	
田		딊	1	<u> </u>				=	╀	E	1	ᇉ	-	-	-	-	-	Ξ	┝	×	E	Ę	Œ	E	Ē	Н	=
H	19	I	2	12	2	Š		4	Γ	₹	I	3	3	3	1	4	3	3	L	Ε	Ξ	E	Ξ	Ξ	Ξ	П	3
 		님	ŀ	Ī	Ī	Z	┝	-	+	>	+	4 1 8	-	=	-	1=	1=	6	╁	4	-	-	_		•	H	a
		•	E	1=	Ξ	1	I	8 0 2	F	3	Γ	2	9	0	C	9	0	0	F	F	L	L	_	_	_	F	回
Ш	区	끍	1	1=	=	=	1	乬	H	X	+	╬	=	1=	=	ť	+	 -	1	6		0	0	0	0		Ħ
1	爿		1	P	c	9	F			1-	4	Ŀ	1	2	2	1	1	¥	Γ	Z		Z	Ξ	Ξ	Ξ	F	Ĭ
 	1		+	X X X X X X X X X X	=	B K A D E L L	+	N E X	1	0	╁	7 5 7	Ė	Ė	ŀ	1	- W - W - W - W - W - W - W - W - W - W	ŧ	H	Ī	Į	Į	ķ	÷	t	Ė	B
Ш	区	国	F	T	9	•	F	b	1.		Ţ		•	2	1	₽	, <u>,</u>	2	-		-	N N E	N E K	F	F	F	
Ш			+	\dagger	t	-	-	9	+	×	+	9	۔ ا،	۔ ا	al a	;;	#	10	1	3	ţ	5	Ť	t	t		ğ
H	픰	耳	F	Į.	F	4	-	Ŀ	1	Ē	F	ŀ	F	ŀ	F	F	I	F	F	Īc	0	9	F	F	F	F	님
	目	F	t	t	t	t	t	٥	+	t	1	ť.	:	ŀ	#:	;	ť	ť		ľ		1	t	t	t	L	I
口到		[2]	F	Ŧ	F	F	F	9	1	4	1	F	1	٩	1	3	ļ	10	F			F	F	F	F	F	삅
RSV Peptide #	T-71 PIIINFYDPLVFPSD	T384 RINKIOLLEIDKIVIETELLILIBKILLAT	5	1	=	1	1	Ē	T	5		Ē	į	18	į	1	į	į	t	Ė	2	Ę	1	38	2	Γ	T-730 F D A B I S Q V NE K I I N O S L A
القاط	Ŀ		4.643	1	ŀ	7.616	1	7.617	1	7,662	1	ļ		1	1	1	15	1.670 F O A S	1	15	. 2	1	E	Ŀ	1	L	Ë

FIF. 28 B

7872-020 (SHEET 34 OF 63)

				F	F	E	E	F	É		-	F		_	_	_	=	_	_	_	_	_	_	_			=	=	_	_	=	_					
KPIV	PIVS OP 107-LIKE REGION IT	REGION	3	7	#	1	1	‡	‡	ŧ	ţ	ŧ	Ŧ	ŀ	‡	ŀ	ŧ	t	ŧ	F	F	F	F	þ	F		Ш	Ш	Н	Ш	Ш	Ш					
			1	7	#	1	7	‡	‡	Ŧ	ŧ	ŧ	Ŧ	ŀ	‡	E	Ŧ	ŧ	F	E	F	F	t	F	F	Е	Ш	Н	Ė		Е	ш		H	973		
			1	ı	Ϊ	1	}	Ŧ		ŀ	i e	É	i	Ġ	ř	Ľ	M	Ē	MAG	Š	Δ	ΔA	9 5 0	_	HMIO	ial il	XIIV	8	Al olo	MAL	INIM	dalt	KPW3 187	W AV			60
	19131101		=	4		-1	1	+	ŀ	1	'n			4		1	Ē	9	Т	L		F	F	t	þ	Е	H	Ш	Ħ	Н	Е	Н	496	•	15	•	•
	(1)]	1	2	7		₽	d	#	1	ľ	ľ	K	-	F	ŀ			E	F	F	Þ	t	þ	Е	Ш	ш	Ш	E	Н	Н	1113		111		•
	=		3	4	₹ 		3	7	ľ	41.	1	£	ł	7	Ŧ	Ŧ	1 1	9	Z	E	F	F	ŧ	t	E	E	H	Е	H	H	Н	H	111		107	•	٠
	483		1	4	2	#	Š,	₽	œ	t			ŧ	9	4		1 16	1	F	×	E	F	F	t	E	Е	F	Ш	Н	Н	Н	П	996		.316	•	٠
	91				ž	3		+	#	#		71.	į.				ı	Ė	L		E	F	þ	þ	F	Ŀ	H	ш	F	H	Ш	H	121		190	•	•
	=		-	Ξ	3	=	왕	=	3	1	1	3.	त	1	9	1	þ	1	Ŀ	k	ļ	F	ŧ	t	ŧ	E	F		F	E	E	H	1		Н	•	•
	=		H		4		2	1	∢ŀ	ąį.	•	2 K		1	Τ		Ţ.	ŧ	ŀ	¥	0	F	ŧ	t	þ	E	F	E	F	F	E	Ш	111		121	•	٠
	=				4	=	2	=	< -	ł	4	œ	1		Ţ,	+			ŀ	¥	٨	ļ	ŧ	t	t	E	F	E	F	þ	E	E	111		1	1.067	1
					4	Ⅎ	왕	•	7	ď	+	d	ď	ł	Ŧ	ı,		ŀ	ŀ	¥	Ь	A	ŧ	t	F	E	F	E	F	E	E	E	111	Ŀ	•	130	•
	=			3	1	\$	2		1	1	ł	ch	t		4		ŀ	-	Ļ	¥	2	Þ	b	r	þ	E	F	ш	Н	П		Ш	111		340	•	
	١			3	1	\$	1	Ŧ	त	1		٤ħ	ŧ		ŀ	Į,	ŀ	Ē	F	Ş	7	E	100	F	þ	E	F	ш	H	ш	Ш	Ш	494	•	2150		
			H	3	+	\$	1	Í	*	1	1	ή	ŧ	1	ł	d	į	•	L	k	0	4	80	Ė	F	E	F	Н	F	Ë	E		971		680	•	
	=			3	4	1	1	7		4	+	ď	d	Ī	÷	1.	4	ŀ	ŀ	ķ	9	E	110	Ļ	þ	E	F	E	L	Ł	E	E	111		51.1		ŀ
	٤		E		H	4	1	1	킼	1	H	ш	ł	ŧ		4.	÷	ł	Ţ	ŧ	9	E	ŀ	į	E	E	F	E	Þ	Ļ	E	E	Ē	ŀ	ŀ	.95	
	-		Н	H	H	4	1	7	7	₫	ŧ	313	#	ł	ł		Τ	Ī	2	4	Þ	Ė	ŀ	Ļ	N N	E	ŧ	ŀ	F	ŀ	E	Ł	Ē	ŀ	433		
	Ē		F	E	Ħ		_	7	‡		i	1		1	+	1	ł	ł	Ŧ	Ь	ķ	E	Ε	L		ŀ	ŧ	E	t	ŧ	E	ŧ	Ē	ľ	Ľ	:	ŀ
	-		F	E	Ħ	4	1	7	#	7	i	¥#	4		#	4	ŀ		Ŧ	ŀ	ķ	P	Į	Ļ	Ь	Ŀ	ŧ	E	F	ŧ	E	ŧ	=	1	Ļ	ė	١.
	١		H	E	H		1]	‡	‡	į	ХĽ		ľ	Ť	4		ŧ	Ţ		Þ	₽	E	Ļ		2	ŧ	E	F	t	E	t	Ē	ł	L		
	٤		Е	Ħ		4	1	3	‡	1	1	1	ď	Ì	+	d,	4		ŀ	ŀ	Þ	Þ	ŀ	Į,	×	È	ļ	E	F	t	E	Ė		ŀ	<u> </u>		1
	١		H			#	1	1	‡	1	I	ŧ		ŀ	ł	4	Τ	9	Т	Ŀ	2	Þ	ь	L	×	2	k	E	F	ŧ	E	E	Ē	:		<u>ا</u>	
L	160			3	1	#	1	1	‡	‡	Ŧ	f		ł	ł	Ţ	Ţ	9	F	¥	₽	Þ	E	Ĕ		È	XIIX	E	Ė	F	E	Ė	141	Ľ	•	\$	1
	Ē		H	\exists	1	#	\$	-	‡	‡	ł	‡	ł	ŀ	1	1	Ţ	Ĭ	Ţ	ŀ	8	P	6	Ĕ	Ξ	L,	X	Ŀ	F	þ	E	E	Ē	Ŀ	F	ė	ŀ
L	161			3		‡	‡	7	‡	1	Ŧ	ŧ		9	ŀ	Ŀ	H		Ε	¥	9	2	Ю	Ĕ	NIO O	ΑU	ķ	VI SIX	F	F	Н	Ь	161	:		1 .0	•
L	915		4	1	‡	‡	\$	Ξ	‡	ŧ	Ŧ	ŧ	+	12	Ė	¥	Į	•	200	×	8	٥	9 6	Ě	SIMIC	ΛI	XIV	ΛIS	Lie	F	Ш	ш	411	•	Н	2950	
	189		#	1	1	‡	‡	1	‡	ŧ	Ŧ	Ì	ŧ		Ė	1	Ī		ŀ	×	9	6	9	Ĕ		2	ABK	Δs	9	F	E	E	3		113.	•	
L	=		4	1	1	‡	#	I	‡	f	Ŧ	İ	ŧ	£	Ė	L	2		Z O	ž	910	3 (É			XIII		190	H	Н	Н	100	_	626		
	=		#	1	‡	‡	‡	ł	ŧ	f	£	Ė	ŧ	E	É	2	2	Ě	Ε	Y	Iolai	М	Help	111	HMIO	μV	XIIIY	Alsi	0	Jaka	Ш	Ш	10	·	107		•
	111		#	1	1	‡	‡	I	ŧ	‡	f	Ė	ŧ	E	F	ž	K A	×	101	Ě	2	ΛIS	lislo	É	SIMIC	Ш	xlılx	Mel	lalel	MAIN	ш	Ш	504	•	17	218.50*	1
	133		#	1	#	‡	‡	Ŧ	†	‡	£	Ŧ	ŧ	E	F	Ŀ	1	0.4	L	×	⊵	2	6	É	DINIC	NΙ	Ě	Δ	9	MALA	×	E	3	•	(7)	1	**
	=		#	1	1	‡	‡	Ŧ	‡	‡	F	F	ŧ	E	E	ř		3	ㄷ	×	Σ	2	8	Ĕ	MMO		¥	Λe	9	MALA	¥		Ē	Ŀ			
			‡	1	1	‡	‡	Ŧ	Ŧ	‡	F	F	ŧ	E	E	t	Ε	Š	E		0	Ž	8	É	N N	2	XIV	A S	Ю	MAA	X	Ę	100	ŀ	19		
	=		#	1	1	‡	‡	Ŧ	Ŧ	‡	f	Ŧ	ŧ	I	E	ŧ	E	5	Ŀ	¥	<u>0</u>	Ž	6	Ē		-	Ě		la	⊵	×	≧	Ē	ľ	F	•25	
	395		‡	#	‡	‡	‡	Ŧ	Ŧ	ŧ	£	Ŧ	ŧ	E	E	ŧ	E		E		9 2	2	6	Ē) NO	2	XIV	8	0	A V M	×	Ē	Ē	Ŀ	699		
	948		‡	‡	‡	‡	‡	‡	Ŧ	‡	ŧ	E	ŧ	ŧ	E	ŧ	E		L			E	F	F	Ħ		E	Е	F	F	Е	Ė	L				
			4	4	1	1	1	1	1	1	1	1	1											l	l		l	l	l	l							

F1G. 29A

7872-020 (SHEET 35 OF 63)

$\overline{}$	7	_		-	_	7	_	_	_	_	_	-	ТТ
	AVG. 1535	١		Ę	è	Į	1	F	Ę	1	į		Ę
	5	١		843.000 ugmr	855,000 ug/mf*	720.000 upme	700.000 upher	54.714 upml	228.140 up/mt	488,000 up/m²	M8.000 up/m²		137.654 LOTHE
	₹			2	3	휥	8	5	28.1	3	릛		12
口	1	_	_				$\tilde{\Box}$	Ϊ		Ì		•	
H	4	4	-	Н	Н	\dashv	_	\vdash	Н	Н	2		H
口	1		_								◛		口
H	4	4	_	H	Н	4	-	Н	Н	\dashv	Y V N K E		H
世	1	╛				╛					Ź		口
\Box	4	4	_	H	Н		4		Н	٨	늿		Н
世	╛			Ħ						90	9		Ħ
Н	4	4	-		Н		Н	Н	Н	2	긤		닒
H	1	۲	_		Τ			П		×	¥		国
口	\Box				L		П			Ī	Ξ		目
H	┪	۲	-	\vdash	H	Н	Н	Á	۸,	Ź	뒭		討
口			-					ш	Ш	Ш	Ξ		日
H	4	4	H	1	Н	Н	Н	1	1	=	븢		딀
世]					П		0	0	10	0		LK EALIRIOTHWKAVIOS VIOSSION LIVALIKE
H	4	Ц	-	F	F		Ĺ	L	=	چا			
H	_	-	-	L		8	8	•	8	•	9 9 0		9
П				F		0	0	0	0	0	0		힏
H	┥	۲	-	┝	Н	ì	-	-	-	6	9		듬
Ħ						0	ō	σ	o	◙	0	İ	回
Н	_	_	-	⊢	1=	?	2	~	~	~	۸		긝
世			Ė		¥	×	¥	¥	¥	×	Ì		国
\Box			F	F	Ξ	3	Ξ	Ξ	Ξ	2	П		Ξ
H	-	Н	-	⊦	6	6	5	6	-	6	Н		-
\Box					Ξ	=	E	Ξ	E	Ξ			፪
H	_	-	-	F	듷	 	두	Ę	 =	⊨	H	ŀ	1
口		L		三	_	2	_	=	w	匚			ভ
H	_	H	-	E	Ľ	×	Ľ	본	Ľ	┝	H		Ĭ
		Ш	t	E	¥	×	×	¥	¥	L			
Н	_		F	=	=	۳	=	=	=	┞	L		Н
Н	_	H	+	10	6	10	٥	ā	┝	╁	┢		Н
		L			60	9	80	R 8 D	L				Я
Н	-	┝	┝	1	뜮	F	ŧ		╀	╀	┝		Н
口			<u> </u>	ē	o	o	o	K O X	L	L		1	
Н	_	┝	╁	¥	ŧ	¥	¥	ŧ	╀	╀	╀	ł	Н
日			t	Ē			Ĺ	Ė	t	L		1	
Н	1	L	-	1	2	<u>}</u>	+	╀	╀	╀	⊢	ł	\vdash
Н		L	İ	1	<	1	t	t	İ	t	L	1	
Н		F	F	12	^	VAV	Ŧ	Ļ	L	╀	L	ļ	-
Н	-	┢	t	1		₹	+	t	t	t	t	1	
		L	Ī	E	Τ	L	Į	Ţ	L	I	F	1	
Н	┝	┝	+	[0	+	╁	t	+	t	╁	╁	ł	
	L	T	I	3	1	Ţ	I	Τ	T	I	L	1	\vdash
H	⊦	╀	+	1	+	╀	╀	╀	╀	╁	╀	ł	-
Ħ	T	t	İ	Ė	1	İ	1	İ	İ	1	T	1	
F	ě	F	F	F	F	F	Ŧ	Ŧ	Ŧ	+	╀	1	<u> </u>
H	5	t	t	t	1	t	t	1	İ	\pm	$^{\perp}$	1	T.
F	Ħ	F	Ţ	F	F	F	Ţ	Ŧ	Ŧ	F	F	1	Ę
H	9	۲	†	+	+	t	\dagger	†	\pm	†	t	1	j
F	HPIN-3 DP 107-Like Walks	F	Ŧ	F	Ŧ	Ŧ	Ţ	Ŧ	Ŧ	Ţ	F	1	T-582 warring 184
	<u> </u> ≥	1		9	3	7		1		ř	3		3
	Œ	L	<u> </u>	12	11	ŀ	. μ	۱۲.	ш	h	1	Ŀ	

8 (2)

7872-020 (SHEET 36 OF 63)

Ī	٦	٦	_	Ī	T	١	7	7	7	1	1	I	1	1	1	1	1	٦			1	T	1	T	Ī	I	I	1	T	1	
1		H	-	ļ	1	1	-	-	-	+	+	+	+	+	+	+	+	-	H	$\frac{1}{2}$	-	+	+	+	ł	+	+	+	†	1	
			L	L							_	1				_						1	1	1	1	1	4		4	4	
				ļ	,			•		·	·	;	·		·		2	•			•		-	-	ŀ	\cdot	·		١	١	
4	_	L	ŀ	1	+	-	Ц		Н	H		1	-			H	_	۲	H	Н			+	+	1	1	1	Н	1	1	
1			ľ	1		./78	175.	. 219	- 61	-525	•19	49	-	. 15	325	, ,	•0.1	1.2240		390	0.211	174	2.0.	3		. O.	2.0			۱	
			ŀ			8	ιι -	9	59	25	7			u = 1	10.1			0	L	ė	٥	0.							Ц		
1			Ī	Ţ			•	•	ŀ		•	٠	***	•	•	ı	1	i	i	1	i	•	ŧ	:	:	1	:				
4	L	┝	ł	┨	4	_	H	┞	ŀ	H	H	Н		H	-	H	ŀ	-	H	H	ŀ	H	Н	Н	-			H	Н	d	
			l	Ì	2	3	3	Ē	Ē	₽	Ī	į	¥	ì	Ē	Ē	ž	ž	Ē	Ē	ž	ž	Ī	ž	Z	ı	2.5				
_	L	-	1	-	2		L	L	L	-	L	L	L	L	L	Ŀ	L	Ł	Ł	L	Ł	L	E	Н		Н	L	F	H	Н	
Ξ	E	I	1			H	E	ŧ	ŀ	ŧ	E	Ė	E	ŧ	E	ŧ	ŧ	ŧ	ŧ	ŧ	ŧ	E	F	Ħ		E	E	ŧ	F	E	
		ŧ	†	1		E	t	ŧ	ŧ	Ė	E	Ė	Ė	Ė	İ	E	Ė	İ	ŧ	Ì	İ	E	E	E	H	E	E	ŀ	E	E	•
	E	Ī	1		F	ŀ	Ī	ļ	Ŧ	+		ļ	ŧ	+	ŧ	+	ŧ	t	‡	‡	ŧ	ŧ	t	F		E	E	ŧ	Ė	E	
Ė	Ė	1			Е	ŀ	ŧ	Ì	ŧ	1	ŀ	F	ŧ	ļ	Ŧ	Ŧ	Ŧ	Ŧ	Ŧ	Ī	Ŧ	F	F	F	F	ŀ	H	F	-		•
E	ŧ	#		18	-	ŧ	ŧ	‡	‡	‡	ŧ	ŧ	ŧ	‡	‡	ŧ	ŧ	ŧ	‡	‡	ŧ	ŧ	ŧ	ŧ	F	ŀ	ŀ	Ī	Ŧ	F	
E	‡	+	_				‡	1			1	ŧ	ŧ	‡	ŧ	+	1	1	7	1	1	Ŧ	ļ	50	9	ŀ	ŀ	-	Ŧ	F	
ŀ	+	+	_	1111	2	Į	‡	#	†	†	‡	‡	‡	╪	‡	†	‡	#	‡	†	+	†		Ξ	1	Ŀ	ŀ	1	Ī	Ī	
t	\pm	4	_	-	į	ij	1	1	1	1		1	1	1	1	1	1	1	1	-									+	‡	
ŀ	1		_				1	4	+	+	‡	‡	‡	‡	+	+					_	-			-				+	‡	:
t	1		L	ŀ		4				3	7	1	1					<u>ا</u>	¥				×	v.			1	計	+	†	j
	+		F	ļ	1						-	-	-	=	-	=	=	8	-	3	Ξ	3	3				1	=	7	-]
Ì	\exists	_	I	ŀ	₫.	10.15	Н	Н		ı u	N N	5	5	8	ř v	-	E E		1	1 3	N N I				-			3		‡	1
	H	_	İ	1		<u>₹</u>		M	74	W 3	(IM	E W	*	ı	ľ	W 3	*	X C W	KIW	K I W	M E W		Ę		-	7		A D H	+	†	‡
	H	=	ł	1	=	*	×	3 X	×	1) ()	3 8 B	3 6 B	M S B	•) 6 B	N 6 3	3	9	8	8		(1 5		9	16 3		8 3 3		-	7
		Ξ	Ī	-	13			100	-		110	1	3 710	10	2		10	•		110	2	1 1 0) 1 O	110	9	0 K (0	110	1		3	3
į	Ħ		İ		•	9 8 8		Ŀ	Ī	Ŀ		e	-	5	9		-			8	-	1		K	A K 8	A K IS	AKIS			H	_
	E	Ш	1	_	3 4 6	YIXIE					¥		×		X	È	ŀ		×	ž	ŀ	×	Ë	¥	×	×	¥	¥	H		7
	E	E			6 8 1 1 2 9		E	ŀ	1	1	Ŀ	1			E		4:	4	1	ŀ	F	-	1=	=	111111	Ĕ	Ė	E	Ė	Ë	
	E	E			\$	ŀ	ŀ	ł		ť		Œ	Ŀ	Ŧ	F	ť	ľ	ľ	1	ľ	1	Ŀ	L	Œ	Ē	Ė	E	ŧ	İ	E	Ë
	Ė	Ė		E	2	ŀ	Į	1	ł	1	Ŧ	ł	}	Ŧ		ŀ	1	ŀ		Ŧ				Ŧ	F	ŀ	+	+	‡	t	
	F	ŀ	_	F	Ė	Ţ	4	7	4	3	+	4	4		Ι.	1	1	1	4		1	1	ŧ	1	ļ	Ī	Ŧ	ļ	Ŧ	Ŧ	Ħ
	E	ŀ	_	E	ŀ	ŀ	1	1	2	4	1	•	1	_	-1	=		4	‡	‡	1	Ì	1	İ	İ	1	1	1	‡	Ŧ	\exists
	Ė	1	=	ŀ	ŀ	1	3	=	=	3	3	1		3		=	-	7	1	+	-	+	+	‡	ŧ	1	1	1	1	‡	Ħ
	F	‡		ŧ	ļ	•	=	0 1.	_		_]					1				7	=	7	7	1	Ŧ	1	1	-	7	‡	\sharp
	ļ	1	£	1	1	•		W d L			Ĭ	1	-		H			H		7			1	#	‡				#	‡	Ħ
	Ì	7	Ž			Ξ	14.11	F	É	F	H	Ħ		F	F	H		F	H	H		H	H	H	1			H	H	1	\dagger
	١		Cao				L	L	L				L	L			L	L	Ц	L	L	Ľ	Ц	Ц		Ц	Ц	Ц	H	Н	H
			1716	Š		١	5	١.	١,	1	2	E	Į	3	1	è	E	5	E	Ē	Ē	£	I	ž	E	È	Ē	E	ž		$\ \ $
			1000	PINA DIPTION LINE NEGICE		L	5		ľ	ľ	ľ	Ĺ	Ĺ	Ĺ	L	ļ	ļ	ļ	1	1	Ļ	L	L	Ц	L	L	L	1	ļ	Ц	\mathbb{H}
		ſ		2	ſ	۱	I					1	١		١	1		1			l	١									
						•	-																								

7872-020 (SHEET 37 OF 63)

PMQU 005 (55)	1308.568 ngm	133.783 vg/m² 197.177 vg/m²
T-268 bruncated 201	T-626 [205 mutant	1.500 x x x x x x x x x x x x x x x x x x

7872-020 (SHEET 38 OF 63)

LLDVVKROOELLRLTVWGTKNLOTRVTAIEKYLKDOAOL ↑NAWG ▼ CAF

VALLMOTI5 →*LVS Predicted Coiled -Coil

RQVCHTTVPWPNASLTPDW *NND **VTWQEWERKVDFLEENITALLEEAQIQQ**

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWP WQIEYIHF

7872-020 (SHEET 39 OF 63)

MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSFPFRVCELSSHGDLFRFSSD

4107x178x4**4**

IQCPSFGTRENHTEGLLMVFKDNIIPYSF *KYRSYTKIYTNILIYNGWYADSVTNRHE*
EKFSVDSY ETDQMDTIYQ CYNAVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR
YASQTELYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN
KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW
QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD
RYTKGQEAIT YFITSGGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG
STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA
RAWCLEQKRQ NMVLRELTKI NPTTVMSSIY GKAVAAKRLG DVISVSQCVP VNQATVTLRK
SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

<u>↑107x178x4</u>↑ EIHVYNDYHH FKTIELDGIA TLQTFISLNT <u>↑SLIENIDFASLELYSRDEQRASNVFD</u> *LE↑

LVS Predicted Coiled Coil TM Potential
GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

÷P12LZIPC÷

TM Potential

LVSTVGGLFSSLVSGFISF FK N *PFGGMLILVLVAGVVILVISL* TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQKR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

7872-020 (SHEET 40 OF 63)

MMDPNSTSED VKFTPDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQGQ

*
LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@ <u>\$107x178x4</u> +Dimerization+
@KRY KNRVASRKCRAK <u>\$FK@Q</u> +<u>LLOHYREVAAAKSSENDRLRLLLKO</u>

MCPSLDVD+ SI IPRTPDVLHE DLLNF

7872-020 (SHEET 41 OF 63)

Fusion

Peptide ♥ALLMOTI5♥

LVS Coiled-Coil

FAG

♥VVLAGAALGVATAAQITAGIALHQSML*NSQAIDNLRASLETTN

QAIEAIRQAGQEMI*LAVQGVQDYINN ▼ ELIPSMNQLSCDLIGQKLGLKLLRYYT

P23LZIPC

*****P6,12LZIPC*****

★107x178x4★

▼ALLMOTI5▼

EILSLFGPSLRD +PISA +VEISIQALSYALGGDINKV+ LEKLGYSGGDL+

÷P1,12LZIPC÷

LGILES ↑ RGIKARI ▼ THVDTESYFIVLSIAY +PTLSEIKGVIVHRLEGV+ SY

NIGSQEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

P23LZIPC

→P12LZIPC →

♥ALLMOTI5 **♥**

LVS Coiled-Coil

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP ♣P ♥IS*LERLDVGTNLGN

◆ Transmembrane Region ◆

AIAKLEDAKELL + ESSDOI + L + RSMK +GLSSTSIVYILI ▼ AVCLGGLIGIP

<u>ALICCC</u> ◆ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL

7872-020 (SHEET 42 OF 63)

Pre S1 and Pre S2
MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRIGDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

♣P12 & 23LZIPC♣

MENITSG FLG +PLL VLQAGFFLLTRILTI+ PQSLDSWWTSLNFLGGTTVCLG

P12 & 23LZIPC
QNSQSPTSNHSPTSCPPTC *PGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQGML*
PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKF

◆ <u>Transmembrane Region</u> ◆
LWEWASARFSWLS ◆ <u>LLVPFVOWFVGLSPTVWLSVI</u> ◆ WMMWYWGPSL

- ♦ Transmembrane Region ♦
- +YSILSPFLPLLPIFFCLWVYI+

7872-020 (SHEET 43 OF 63)

Fusion ▼ALLMOTI5▼ <u>↑107x178x4</u>↑

Peptide *LVS Coiled Coil

AIQLIPLFVG LGI ▼TTAVSTGAAGLGVS ↑IT *QYTKLSHQLISDY

QAISSTIQDLQDQVDSLAEVVLQ* NRRGLDLLTAE A QGGI ♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region
RLEQEDSGGSYLTLT......?????????????????????......

FIG 36

7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

- **4107x178x44**
- **♥ALLMOTI5♥**
- **↑** ¥YODYTARTOVTRAVSEVSALKTAAESAILEGKEIVSSA ↑ T¥

PK DTQYDIGFT

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **♠♥ESTLLDGSGKSQIQVTDNQDGTVELVATLGKSSGS**♠AIKGAVITVSR♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

- 4107x178x44
- **♥ALLMOTI5♥**
- **★▼KDNTSAGVASSSSIKGKYVKEVKYENGVYTAT**

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **♦♥SWKNVDKENNFTLKNEQTTADYATNVNI**

QLMESNGTKAISVVGKETE

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

7872-020 (SHEET 47 OF 63)

MNKKLLMNFF IVSPLLLATT ATDFTPVP

- **4107x178x44**
- **♥ALLMOTI5♥**
- **↑** VLSSNQIIKTAKASTNDNIKDLLDWYSSGSDTFTNS ↑ V

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

- **↑107x178x4↑**
- **♦DLNTKRTKKSOHTSEGTYIHFOISGYT♦**

N TEKLPTPIEL PLKVKVHGKD SPLKYG

- · *P12LZIPC ÷
 - *PKFDKKQLAISTLDFEIRHQLTQI*

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

F19. 40

7872-020 (SHEET 48 OF 63)

♥ALLMOTI5♥

MKKTAFILLL FIALTLTTSP L ♥VNG

↑107x178x4↑

- *LVS Predicted Coiled-Coil*
- *S & EKSEEINEKDLRKKSELORNALSNLROIY* YYNEKAITENKESDD &

OFLENTLL♥ FKG FFTGHPW

- **4107x178x4 4**
- **♦YNDLLVDLGSKDATNKYKGKKVDLYGAY**

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEEKKVP INLWIDGKQTTV

- +P12LZIPC+
- *PIDKVKTSKKEVTVQELDL* QARHYLHGK FGLYNSDSFGGKVQ

♣P12LZIPC♣

RGLIVF HSSEGSTVSY DLFDAQGQY +P DTLLRIYRDN KTINSENLHI+

DLYLYTT

7872-020 (SHEET 4 OF 63)

♥ALLMOTI5♥

MKKTAFTLLL FIALTLTTSP L

▼VNGS

4107x178x44

♦EKSEEINEKDLRKKSELOGTALGNLKQIYYYNEKAKTENKESHD ♦ Q**▼**

FLQHTILFKG FFTDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKKVPINLWLDGKQNTV

<u> 107x178x4</u> ♦

♥ALLMOTI5**♥**

P12LZIPC

♣P ♥L ♠ETVKTNKKNVTVQELDLQARRYL♣ QEKYNLYN♠

SDVFDGKVQR♥ GLIVF HTSTE

P23LZIPC

PSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHI DIYLYTS

F1G. 42

7872-020 (SHEET 50 OF 63)

MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

- **♥ALLMOTI5♥**
- **▼OMNINLYDHARGTQTGFVRYDDGYV**
- 4107x178x44
- **♦STSLSLRSAHLAGOYILSGYSLTIYIVI ♦** ANMFNVNDVISVY **♥**

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

- **♥ALLMOTI5♥**
- **▼ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL ▼**

7872-020 (SHEET 51 OF 63)

MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM
GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLVQPA
LVSSVAPSQT RAPHPFGVPA PSAGAYSRAG VVKTMTGGRA

LVS Predicted Coiled-Coil
QSIGRRGKVE QLSPEEEEKR RIRRE *RNKMA AAK

★107x178x4◆

- **♥ALLMOTI5♥**
- ◆CRNRRREL <u>*TDTLQAETDQLEDEKSALQTEIANLLKEKEKL</u> ◆

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

7872-020 (SHEET 52 OF 63)

SGWESYYKTEGDEEAEEQEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCIQSVYISKIISSDRDLLAVVFYGTEKDKNS
VNFKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR
TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

↑107x178x4↑

♥ALLMOTI5♥

LVS Predicted Coiled-Coil

♥LRVH *FEE &SSKLEDLLRKVRAKETRKRALSRLKLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTKTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS DSFENPVLQQHFRNLEALALDLME

P12LZIPC

PEQAVDLTLPKVEAMNKRL GSLVDEFKELVYPPDYNPEGKVTKR
KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG
LKKQELLEALTKHFQD

7872-020 (SHEET 53 OF 63)

GGGALSPOHSAVTQGSIIKNKEGMDAKS

- **4107x178x44**
- ♥ALLMOTI5♥
- ▼▲LTAWSRTLVTFKDVFVDFTREEWKLLDT▲ AQQIVYRNV

 MLENYKNLVSLGYQLT♥ KPDVILRLEKGEEPWLVEREIHQETHPD

 SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR

 DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT

 HTGEEPYECKECGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH

 SSRLIRHQRTHTGHKPYECPECGKSFRQSTHLILHQRTHVRVRPYECN

 ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSRSSHLYSHQRTH

 TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN

 DLIKHQRIHVGAETYKCNQCGIIFSQNS
- +P23LZIPC+
- *PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI * RENAY

7872-020 (SHEET 54 OF 63)

			Ë	1.5	É	9	1	ř		9119	2	<u>=</u>	9	¥ 2	Ŀ	<u>۲</u> ۲	ׅׅׅׅׅׅׅׅ֓֟֝֟֝֟֟֝֟֟֟֟֟֟֟֝֟֟	¥	X E IL		8 8	100	ן ה	RB	7	400		
Residue 438	F O A V T L M A		1	-1	1	1	+	#	т	Ŧ	1	I	Т	t	t	E	E	F	F	F	F	F	F	-	_			
	4	4	1	4	7	7	#	‡	‡	+	‡	$\frac{1}{2}$	$\frac{1}{1}$	\pm	‡	t	Ŧ	F	F	F	F	F	F	F	F	E		
	Measica Ed. 178-like walk	E 12		į	7	7	+	‡	‡	‡	#	1	\mathbf{f}	\pm	‡	\dagger	Ŧ	F	$oxed{F}$	F	F	F	F	F	F	L	Average	8
	7	#	#	‡	7	7	+	‡	‡	‡	\pm	#	+	\pm	‡	†	F	F	F	F	F	F	F	F	F	L	9324	
	ļ	-	╣.	1	-	9		-	-	2	2	=	1	Z	<u> </u>	×	<u> </u>	F	E	F	F	E	E		Ħ	Н		٠
T-282AO			4	т	1	1	;		т	4	1	12	C	5	-	×		[F	F	F	F	F	F			•	•
T-253A0	0	<u>></u> >	<u> </u>	<u>~</u>	0	9		2	-	2	-1	<u> </u>	2	=]	_	-	7	$\frac{1}{1}$	Ŧ	Ŧ	†	ţ	ļ	t	l		
4.96440		>	=	ď	10	0 1		3	w	<u>و</u>	<u>0</u>	z F	1 6	×	<u>۷</u>	×	8	Y X	-	7	-	+	7	1	†	‡		
	+		1-	•	c	0	8	3 1	<u> </u>	110	2	E F	0 1	¥ N	<u>۷</u>	×	E	×	E	_	\exists		#	1	7	1	·	\cdot
0.000 P	‡	<u>;</u>	4	7	•	•	0	-		-	2	1	0	¥	<u>۲</u>	KIL	1 3	Y K	1 3					7	7		•	•
T-256A0	+	+	4	т	7	1	1	ļ	+	Ţ	1		-	5	-	-	-	¥	<u>ا</u> الا		E						1.35 up/m	•
T-25761,C1			_	=		9		-+	-	4	4			-	Į.	-	Ţ	ŀ	-	•	F	İ	F	F	F	F	343 notm	
T-25681			<u>=</u>	= «	9	0		3	2	2	Σ		4	1	1	-+	7	-1	1	1	\prod_{i}	1	‡	Ţ	ŧ	ļ	1	
T.259B1		F	F	R	0	0 7		8	<u></u>	RILD	٥ >	Z -	1 6	≤	<u> </u>	×	_	¥	1	3		1	‡	1	‡	‡		
	+	+	t	F	3	9	ŀ			9118	VG	T	0	⋖	<u> </u>	X L		×	<u>u</u>	<u> </u>	80			_	7		.188 ug/ml	
1-26051	1	1	#	+	1	1	1	-	т	4	Ŀ	ŀ	Ι.	ŀ	١.	-	ŀ	1	-	-	8	٥	F	L	F	-	•	•
T-261A0		_	_		٥	L O	l l	2	-		1	=	4	=	1	-	Ţ	7	1		+		‡	F	ŧ	ţ	Ample Con	
7.24281		F	F	F	Ē	0 7	14 4	8	LE	A LO	N 0	<u>=</u> =	의	<u> </u>	-	-+	<u></u>	_		יי נ	-	_	‡	7	†	‡		
1000		t		F	F	0		18	1 1	RLO	>	z -	10	∢	۷.	٦ ۲	1	AK	1	1	2	-	7	7	†	‡	1-15 (CDM)	
	1	+	‡	F	F	F	9	5	3	R 1.0	2	N.	0 1	V N	<u>≺</u>	X	<u> </u>	×	בונ	LE	5 3	0	4			1	1,01 upmr	
1.28481	1	‡	‡	+	Ŧ	F		•	-	9	7	Ē	9	×	=	¥	w	¥	61	3 7	8 8	00	1	N.		- -	.072 ug/mt	•
7.28581	1	+	‡	7	Ŧ	$\frac{1}{2}$	Ŧ	1		4	1	ŀ	1-	2	-	-	-	×	-	<u>.</u>	8	0	=	8	F	F		•
T-266A6		+	#	7	7	$\frac{1}{1}$	-		1	4	Į	ŀ	١.	-		-		•	-	<u> </u>	8	-	Ē	8	-	L	÷	
T-267A0		4	7	-	7	$\frac{1}{2}$	7	9	_	4	1	-]	٠.	:	J		Ţ	7	ŀ	-	_	-	ŀ	ŀ	1	ļ		
T-261AD				7	7	\exists	3	7	1	N P	2		리			4		<u>د</u> د			-1	-	4]	٦.	1		

F1G. 47

7872-020 (SHEET 55 OF 63)

				I	١	ŀ	ŀ	F		L	L	_	_		_	-	_	_	_	_		_	_	_	_			1	1			1			
Sinter	Emme	Straten Immunodeficiency Virus MM251	5 45	S MM2		-		1	1	J	1	1	†	‡	1	ļ	F	+	t	t	t	F	H	F	F	F	F	L				_	_	_	
E	E	F	[E	F	L	F	F	_	_	_	_	_	_	_	_	_		_		1	-	-		1	1	Ŧ			1	I	t	ļ	ŀ	ŀ
-	-		J	Ŧ	ł	t	ţ	T	-	ŀ	t	t	t	ļ	F	F	F	L	L		_		_	_	_	_				_		_	_	Antivira	2
DP178-Dt	•		\exists	$\frac{1}{2}$	\pm	1	1	#	-	\pm	1	‡	‡	‡	‡	Ŧ	F	+	t	ļ	t	F	-	L	t	Þ	F	E		Н	H	┝	L	Activity	_
						1	1	7	7	$\frac{1}{2}$	╁	1	1	#	+	7	-	<u> </u> ;	ľ	T	4	ŀ	_	3	5	Š	3		1	1	Preldue	F	L	3	
Reelchie	F	177	17 W O	3	a M	×	<u> </u>	M.	ר פ	Z	<u>-</u>	V	<u> </u>	2		9	=	2	=	1	1	1	1		#	1	-	-			-	+	t	-	Ι
E	Į		E	L	L	E	F	L	F		_				_	7	7	\exists	1	#	7	7	$\frac{1}{1}$	1	‡	‡	Ŧ	$\frac{1}{1}$		1	Ŧ	† :	1	$^{\downarrow}$	1
	-		13		3	È	2	-	-	Z	=	1 V	3	Ě	101	ō	9	z	<u>></u>	-	0		-	1	1	1	7	1		7	7	1		\downarrow	į
R :	1	2		1			1	ŀ	т	-	ŀ	-	-		c	Ö	0	×	A PR	ובור	0	K				_	_		201			35	Ē		:
1.3	-	2	2			4	1	Ţ	_	2	ľ	#	4 -	, .	—	_	•	+-	+	<u>.</u>	_	Ī	F	L	þ	Ė	F	E	282			38	T392	_	•••
T- 392	7	2	-	9	2	4	1	1	т	-	<u></u>	#	#	ŀ	т	_	1	•	_	-	-	-	2		t	F	F	E	283	_	F	38	1313	-	:
1. 393		248		w	<u>ت</u> ک	ž	₹	4	7	_	1	1	4	٠,٠	_	-	-	-	+	+	-		. 2	t	t	F	F	E	72	F	F	35	35	Ė	:
7. 384		249		$\frac{1}{2}$	<u> </u>	×	2	-	<u>.</u>			₹.	<u>"</u>	4	-	-	-	_	-	_	+		—	13	t	F	F	E	53.5	F	-	2	200	Ē	:
7. 388		250		$\frac{1}{2}$	븨	┪	2	_	الد	-]	₫:	4	1	5	2 0) u	_		1 =	-	4	_	-	‡	F	+	£	982	F	E	2	Ē	L	:
1. 394		285		$\frac{1}{2}$	\pm	×	1	_	<u> </u>	<u> </u>	#	₹.	"	1	3	_		1	#	-	4-		2	_	₺	F	1	£	282	F	E	Ę	Ē	Ė	:
T. 397	_	252		$\frac{1}{2}$	1	1	2	-	-		<u></u>	4	4		4	-	_	: !	1		•		2	•	2	ļ	F	E	Ę	F	-	38	238	Ŀ	:
7. 380	_	233		$\frac{1}{2}$	-		킬	4	1	2		1	4	7	-	-	-	4	<u> </u>	+	-	Ţ.		+	ļ	ļ.	F	t	2	F	-	35	138	Ė	:
-	E	150						_	<u> </u>	-+		4		4	0	-	+	<u>ا</u> د :	1	#	-	4.	9 • E 2	•	‡	-	ļ,	£	:	F		1	148	ŀ	
1.		288			\exists	1	1	4	<u>.</u>			\$	4	4	7	7	3	7	‡	#	7	4	+	-	1	+	+	£		F	-		L	t	
E	E	Н		\exists		\exists	\exists	7		Ⅎ	1	1	4	7	7	7	-	1	1	1	7	-	1	1	1	1	1	1		7	}	1	1]

48

F S

7872-020 (SHEET 56 OF 63)

		Ī				2 Mary 2 Mary 2											I					T	1						Ī	1												000	22		1											1000	90091	9							9 1800e	90084 4	+ 14008				3
	1				Г	Г	F	Т	į		227		124				-	2	•	à	İ		•	•	~		ļ			ĝ	220	2	\$1	_		L	1	ı				֚֚֓֞֜֜֜֟֜֜֝֟֜֜֜֟֜֜֜֟֜֜֟֜֜֟֜֜֟	•												9.0	-	•	۽]	L	l			10100	L	e 18008			L	Ji	
I	Į	I	I	L	L	L	ļ	į				į	7467	200				7813	7063	i		5		티	ē	2	1			Ē	Ţ	ž	tres.	1981	3	3	ļ	l				횔	Ē	4	4	4	4	4	4		H	Ц		L	*	2	Ē	1	1	1			3	1633	1631	1636	116200	1636	È	‡	$\frac{1}{2}$
世	Í	-	†	ľ	t	t	l	l	t	ţ	1	╛		L	t	t	1		t	ŀ	ţ	‡	1	1	_	L	t	ţ	1	1			L	L	F	t	ļ	‡	‡	‡	1	1	7	1	‡	1	#	1	1	Π	H	H	L	þ	F	ļ	t	t	t	ţ	‡		_	1 1	L	L	F	Γ	ļ	‡	1
出	1		Ŧ	ŀ	Г	ŧ	ŀ	ŧ	ł	1	‡	╡		F	ŧ	‡	1	_	F	ŧ		1	‡		_	H	ŧ	ŧ	1	4			H	F	F	ŧ	ŧ	‡	+	‡				4	‡	#	1	4	4	Η	ш	Ш	Ш	F	þ	þ	t	t	ŧ	‡	†	4		Η	H	F	F	F	ŧ	‡	‡
出	1	-	ŀ	b	L	ļ	t	t	t	‡	1	╛	_	E	t	‡	1		t	t	1	1	╡			þ	ļ	‡	‡			Н	þ	þ	þ	ŀ	•	ļ	‡	1			, M	1	#	4	4	4	7	Η	Н	Ш	F	þ	þ	ļ	t	t	ļ	‡	‡	7		П	L	L	F	F	ļ	‡	1
世			ŀ	Ŀ	I	ŧ	ł	ŧ	ŧ	1	#	4	_	Ŀ	ŧ	‡	╡		F	t	Ť	1	#			þ	ŧ	‡	#	7		H	Į		Ė	t	t		#	1	•	AB	•	4	#	4	4	4			Ш	Ш	þ	F	t	t	t	t	ŧ	ŧ	‡	1	=	Н	F	F	F	F	ŧ	ŧ	1
世	1			Ŀ	Ι	t	ţ	t	ţ	1	1			t	t	1	1		t	ţ	7	ī	1			Ė	ţ	1	1			W W	E	Ŀ		t		1	1	1		K W	K W		1	7	4	7	=	•	Ē	L	F	F	F	ļ	ļ	ļ	ļ	1	1	7			F	F	F	F	ļ	ļ	1
\vdash	1		•		Ī	ł	ł	ł	ł	ł	1		_	L	t	t			ł	t	ŀ		1		L	E	ŀ	1				10	┡-	١.	١.	+	-	-	1	1	۰		•		1	1			•	4	-	Ξ	t	L	t	t	t	t	t	ţ	1	1		L	L	L	L	t	Ŀ	ŧ	1
H	4	•	•	ŀ	1	Ŧ	Ŧ	Ŧ	Ŧ	1	4		_	H	ł	+	-	-	ŀ	ł	-	4	-	1	Ш	-		4	=	Ц	10	111	Ė	Ė	Ė	+	1	4	-	_	1	1	1	Н	+	-	-			• •	-	È	H	╁	ł	t	ł	ł	ł	\dagger	1	-	_	L	Ł	H	E	E	-	ł	1
H	1	1		ļ	1	ļ	ļ	‡	ţ	7	1		F	ļ	ļ	1	4	F	F	ļ	4	3	3	_	1111	Ē	+	7	3		0 0	_	↓-	-	ŀ	Ī	7	7	3	3	7	1111	1111	П	H	4				-	٤		F	F	F	F	F	F	Ŧ	Ŧ	1	4		F	E	=	-	-	F	Ŧ	7
世	1	-	-	ŀ	-	t	ţ	t	1	1				t	t	1		H		ŀ	1	3	=	-	2	Ŀ	t	=		3	Ŀ	Ξ	Ē	ŀ	ŀ	ļ		1	-	-	-	1	8	Ц	H		H		•	10	=	-	<u>.</u>	t	t	t	ţ	ţ	#	‡	1		-	=	E	2	-	_	-	‡	1
H	4	-	-	+	+	Ŧ	ł	1	4	4	Н	H	ŀ	+	+	4	1	0		†	2	9	•	0 1	•	•	1	<u></u>	•	•	٥	•		Ė	ľ	!	4	-	-	9	•	0 1	0 1	Н	Н		Н		•	•	ŀ	=	Ĺ	t	ł	t	\dagger	\dagger	\dagger	1	-	1	M 1	3	3	•	-	Ė	+	+	1
耳		9	=	Ì	1	1	1	1	1			F	Ļ	ŀ	_	=	*	1	-	-	-	3	×	K	2	-	-	=	K	×	¥	3	1	ŀ	ŀ			=	×	X X	2	R H	KIN	Н	Н	Η	Н	Н	•	•	-	3	F	F	ŀ	F	ļ	ł	ļ			KW	M H	H	3	W II	*	1	ŀ	-	4
世		9	∄		1	t	1	1	1			E	Ē	ŀ	1	-	-	Ξ	ŀ	İ	=	_	-	Ξ	Ŀ	ŀ	İ	=	•	IJ	Ŀ	Ŀ	Ŀ	ŀ	ŀ	ŀ	=	=	=	=		•	1	П	Ц			Ц		Ē	-	Ŀ	ļ	t	ļ	ļ	Į	ŀ	ļ	1	3	-	1	E	E	E	=	E	ŀ	‡	1
H	4		•			╁	┨	┨	4	0	6 6	-	_	1	4	9	0	9	+	4	_	9	0	0 0	-	-	-	-	0	0 0	-	-	-	٠		٠.	-	_	0	0	0 0	0	•	Η	Н	Η	Н		• •	-	•	-	t	t	t	ŀ	į	ŀ				=		=	•		Ē	Ē	ŀ	1	t
H		•	3		1	1	1	-	-		1 10	Ξ			-	0	200	Ξ	4	_	_	N 0	N 0				-		×	-		_	-	٠.	ľ	-	_	=	0		2	20	_	Н	Н		ш		9 10	-	-	2	-	ļ	ŀ	٠.	+	4	•	-			1 M	2 3	1	_	_	-		-	$^{ m H}$
世		•	-	•	•	1	1	1	=	•)	·	Ŀ	-	=	•	•	Ŀ	ŀ			•	111	•	-		1	•	•		-	ŀ	ŀ	ŀ	ŀ	1	-		•	•	•	-	•		Ц				Ŀ	Ē	•	Ē	l	ļ	ŀ	Ŀ	ŀ	_	1	1	3	=	l III	=		_	_	•	1	1	1
H		•		-	-	+	┨	1	=		-	-	١	!	4			-	+	=	•		-	Ë	ŀ	1	1		-	-	-	ŀ		+	t	1	=	-	-	_	11	-	-	H	Н				•	-	•	3	-	t			+	1		-	-	3	M 1	3	-	ŀ	Ė	Ė	ľ	Ì	t
H		Ξ	Н	=	=	1	4	4	=	1	E	E	ŀ			-	Ш	E	-	1	-	-	1	-	ŀ	ŀ	-			E	-	ŀ	ŀ	ŀ	I	-	=			1	1	-	-	L	Н	Н	F	Н	•	-	-	•	٠.	ł	ŀ			-	+	•	٧	•	• •	+-	-	-	-	1		╣	┨
廿	_	Ē			=	1			_	101	-	Ŀ	ŀ	_		•	•	-	1	•	•	•	•	-	4	ŀ	3	•		Ŀ	•	-	ŀ	+	-		_	•	•	•	-	٠-	•		Ħ	L	Þ	Ľ	•	-	-	ŀ	t	1	ļ	t	4	_	4	_	×	*	* 1	-	1	3	-	-		1	7
H	_	•	•	16	=	+	-	_	=		=	-	ľ	1	=		Ē		-	=	_	M	=	=			-	-	# ! !	=	-	ľ	<u>'</u>	Ì	1	-	-	-		ë	-	-	-	L	Н	L	E	L	•	L.	ŀ		-	t	Ŀ	t	-	1	-	-	0	•	•	₽-	-	-	٠.	•	Ġ	•	1
H	_	-	Ξ	1	1	-) (-	-		-	-	1	1	2	ŀ	4	3	-	1110	=	-	ŀ	1	-	2	7	•	ŀ	1	1	1	1	-	1	8 L	110	1		-	-	\vdash	Н	F	H	H	•		-	-	+	ł	_	:	1	1	1	4	-	1	-	F	-	=	F	=	-	1	┨
日	_	Ē	Ē		ı		_		L	Ŀ	ŀ	ŀ	-	-	-	L	Ŀ	•	4	=	-	E	٤	Ŀ	ŀ	1	Ξ	ı	E	ŀ	ŀ	ŀ	ŀ	1		Ξ	1	-	111	1	-	-	ŀ	Ļ	П	ļ	F	-	•		•	-	1	1	ŀ	1	1	1	1	=	1	1	=	-	E	E	E		_	7	7
H	_	•	-	_	A 80	Н		\perp	A	•	ľ		1	-	•	<u>\</u>	Ė	-			AH	2	-	ŀ	+			A M	2	ŀ					-	-	H		*	2	Ŀ	ŀ	ľ	L	Н	t	ŀ	L	Ė	ŀ	ŀ	ŀ	1	t	_		-			=	=		Ē	Ē	ŀ	Ŀ	Ė	-	ŀ	-	╛
H	_	E	E	111					# 1	ŀ	ŀ	ŀ	ľ	-		=	ŀ	ľ		1.4	=	=	-			-			-		ľ	Ţ	1	-	-	-			-	=	ŀ	+	ł	╀	H	┞	┞	┞	-	ŀ	-	ŀ	_	+	_	<u>'</u>		-	-	=	-	0	-	-	•		•			<u>•</u>	\exists
Ħ		Þ	E	•	_	Е		L	•		ŀ	-	1	1	_	-	ŀ	•	-1	2			_	ļ		-	ı	1 1	1	ŀ	1	İ	-		1	3		F	F	F	ļ	ļ	ļ	F	F	F	ļ	F	ŀ	ļ	•	1	_	Ŧ	_	4		4	-		=	10 10	-	-	-		F	-		=	7
H			E				Ш	L		t	ŀ	t		_	_	•		t		-			•	ŀ	ł	1	•	•		ŀ		ŧ	•	=	1	1		L	t	t	t	t	t	t	t	t	t	t	ŀ	t	t	Ŀ	1	‡	ŀ	1	1		-	Ξ	-		Ŀ	ŀ	Ŀ	Ŀ	Ŀ	Ŀ	ŀ	=	1
H	_		-				H	F		-		1		_	_	*	٠.		=	_	_												+	┨	+	4	_	ŀ	┞	┞	ł	ł	ł	╁	╀	ł	ŀ	ŀ	-		ł	ľ		\dagger										1	1	1	, 0	9	9	न	Ⅎ
H		Ė		-	•	-	ļ	ļ	Ē	ŀ	ī	ı	7	7	•	•	ŀ	١	=	ī		1	ī	ī	ī	=		•	ļ	ļ	1	1	7	1	7		F	F	I	-	ŀ	Ŧ	Ŧ	F	F	F	F	F	ŀ	ľ		Ţ		Ŧ			0														\dashv
	-	ŀ	ŀ	ŀ	F	Г	L	t	Ŀ	ŀ	ŀ	-	-	•	l ě	١	ŀ	-	•	•	E	ŀ	Ŀ		1	1	_	L	t	t	1	†	1	1	1		L	t	t	t	t	ţ	ţ	t	ţ	ļ	ţ	ļ	ľ	ľ	T	Ŧ	Ī	#	1	•	=	╛	⋽	•	-					ŀ	1	1	1	7	7
H	H	ŧ		-	=	╀	┝	╀	ŀ													Ė	+	ł	+	4	_	┞	ł	ł	+	+	┨	┨		Н	H	┝	l	ł	ł	t	t	t	t	t	t	t		Ť	İ		•	t						1		-	ŀ	ŀ	ŀ		1	‡	1	╛	
	F	Τ.		F	E	Г	I	Į	ŀ	T		=	=			1	ı	=1	=		F	Ī	Ţ	Ţ	7	4		I	Į	Ŧ	7	4	4				F	F	F	F	Ŧ	Ŧ	Ŧ	ŀ	ł	ł	I	Ŧ			1		1	+	+	1	1	-	-	-	-	-	-	_	╁	+	+	t	+	4	H
DP178	L	ŀ	٠	ŀ	F	Ī	t	t	ŀ	ŀ	1	1	-	•	Ŀ	ŀ	Ì	1			t	t	t	1	1		L	t	t	1	1	1	1			Ī	t	t	ţ	Ì	Ì	‡	‡	t	Ţ	ļ	Ì	ļ	ľ	1	Ť	1	•	1	1	•	•	•	•	•	•	Ŀ		1	1	1	Ŧ	7	7	Д	П
. 0	-	ŀ		F	ŀ	ī	ł	ł			!					+	1	4		L	ŀ	H	+	+	4	4	L	H	ł	+	+	+	+		_	H	H	H	\dagger	+	t	\dagger	\dagger	\dagger	1	t	t	t	ľ	1	1	1		\dagger	1	-	-	•	-	=	Ĕ	t	t	1	†	1	‡	‡	1	ď	d
100	F	ŀ		ŀ	E	1	ļ	ļ	Ŀ	1	1	=		Г	F	ļ	1	1		F	ļ	ļ	ļ	1	1		F	F	Ŧ	1	1	7	1	_	_	F	F	F	Į	Ŧ	Ŧ	Ŧ	Ŧ	Ŧ	Ŧ	Ŧ	Ŧ	Ŧ					3	7		1	1		1	F	Ľ	ŀ	+	Ŧ	+	+	+	+	4	Н	H
	L	1		ŧ	ŧ	t	t	ţ	ŀ	1	1	1		Н	t	t	1	1		E	t	t	t	1	1		t	t.	‡	1		1				t	t	t	ţ	ţ	‡	‡	‡	‡	ļ	‡	ţ	‡	ľ	1	ণ		7	1	1	_	Ξ		H	F	F	Ť	Ŧ	7	7	7	7	7	7	F	F
ĮΞ	۲	ť	!	Т	ľ	+	t		ľ	+	+	\dashv	4	Н	H	ł	+	4	H	H	ł	t	+	+	+	_	H	ł	t	+	+	ğ	H		_	H	H	H	t	t	t	\dagger	†	t	t	-	1	t	f	7	-	+	1	1	Į		٦	H	۲	r	t	t	t	†	1	1	†	†	7	۲	H
됳	H	+	1	+	+	+	ł	ľ	1	1	4	4	4	L	ŀ	Ŧ	4	4	L	H	ļ	+	1	4	4	_	H	1	+	4	4	ð	Н		_	\vdash	H	ł	+	+	Ŧ	+	+	+	+	-	ŀ	+	+	+	+	+	1			H	\dashv	Н	H	H	H	1	+	+	+	+	\dagger	\dagger	+	۲	۲
15	Ŀ		t	t	1		1												L	L							Ŀ	1	1						L	L		l		L	1							ŀ	4	-	1	1		4	i		Ц		L	L	L	1	ļ	1	_	_	1	1		Ĺ	L
18	ſ	Ţ	I	I	ſ	ſ		l	Į	-	-	-	-	•	ŀ	Ī	-	1	•	ŀ	ŀ		ļ	-	•	ì	ŀ		-	-	l	Ì			•		ŀ	ŀ			I	-	-	I								I			1		=	•	•	Ŀ				1	-	1	•	4	•	-	
HIV-1 BRU Walks N-Terminal to	r	1	1	t	t	Ť	Ť	t	Ì		2	3	3	150	ļ	1	2	į	2	į	t	İ		2	2	ě	ļ,	ļ	į	į	ä	Ę	200	192	1	2	1	1				Ž	2	į	Ť			Ţ	1	1	1	٦		٦		96.	328	2	î	2	1				2	ē	2	2	9	į	\lceil

FIE. 49A

7872-020 (SHEET 57 OF 63)

Τ	Γ							Γ	Ţ	Ι	Ι	1			Ι	Ι	Ι	Ι	Ι	I	I	Į	1				Γ	L		L			П		П	I	Ţ	1	1	Į	I	I	L	L		L		Ĺ	I	I	I	L	Ī	Ē	1
Γ	T							MAY (Alls)	1				100000	9	9	2	2	2 2	!	į	2		3	400 0	2000	8	000 <u>1</u>	2 00 00 00 00 00 00 00 00 00 00 00 00 00	00000	807	10000	90000	180000	6316	10000	14500	9009	8	8	20000	1	1	100000	10000	10000	10000	1000	10000	883	80	7300	100001	100001	\$160000	١
+	╁	\vdash	┞	۲	Н	H	H	f	ľ	ı						+	+	+	t	1	7	-	-		Г	Г	Г	Г	Г	Г	Г	Г	Г	Т	П	П	П	┪	Ē	T		Т	É	Т	Т	Г	Г	Г	Т	133				è	
	ľ	١	ŀ	-	4			l		ŀ	1	Ē	E	Ē		Š	ŀ					٦	1617102	Ē	14	Ē	7	2	Ē	1111	1578	Ē	7	Ē	Ц	180	Ш		┙	1	ľ	ľ	F	ľ	ľ	٢	٤	Ē	f	٦	1	Ê	ľ	٢	1
1	#	ļ	ļ	•		Ľ	Ľ	ļ	ļ	1	1			E	Į	Į	Į	I	Į	4]	2			F		L	F	L	L	L		L	F	2		7	٥	의	١,	+	ł	F		ŀ	Ļ	L	ļ	ļ	Ļ	ļ	ŧ	╁	t	ŀ
╀	╀	╀	E	È	-	3	┞	ł	ł	+	1	Н	H	-		1	-				3	*	3	_ *	3	F	3	3		3	_		×	3		3	3	3		4			9	Ø	•	1		•	ŧ	į	1	•	•	_	
İ	1	t	E	Ē	ŀ	Ξ	Ĺ	ļ	1	1			L	Ξ	+	1	-	4		-4	4		M	×	Ξ	٠.	٠.	-	-	-	-			3	•	Z 3	Ξ	Į.		탉		ļ		3	_	1		٠,	-	-	+	+		-	
╀	+	╀	E			3	ŀ	ł	ł	┨	4	Н	┞	2		1				•	3	3	M 3	M .	3	3	3	1	*	**	9	ľ	È	Ē	F	F	-	-			-	4	ŧ	1	·		•	Ť	4	1	1	·	Ē	1	1
t	1	t	ŀ	F	E	Ė	İ	1	İ	1		Ш	L	ŀ	ŀ	-	1	=	3	•	•	•	=	-	٠	E	+	ŀ	F	+	-	F	F	F	┿	-	•	•		•	-	-	•	ŀ	ŀ	ŀ	+		+		+	+		-	:
Ŧ	+	ł	Ė	-	-	∀	•	+	+	4	_	Ľ	┞	4	4	1		\$	-	<u>۷</u>	W	M	<u> </u>	Š	٠.		+		-	-	+-	-	-	+	+-	٠.	×	Y M	Y M	_	-	*	1		-	-	_	-		-	4	4		_	H
t	+	t	F		•	+-		1	†				t	ŀ	1	=		-	-	×	×	×	₽-	-	ŀ	Ŀ	+	-	ŀ	ŀ	Þ	٠.	-	ŀ	×	E	E	Ξ	Ξ	-	-	_	-	_	1			-	_	_	-	-	1	Į]
Į	\downarrow	Į	F	-	-	e	٠	1	1			L	ŀ	K	1	박	4			0	داه	٩	Ê	0		+	ŧ	+	k	_		ŀ	-		1	0	1	-	١	9	<u>ا</u>	<u> </u>	+	*	¥	-		•	1	+	4	1	\dagger	+	┨
+	+	+	f		F	Ė	٠	+	+	+	۲	+	t	F	1		-			-	F	E	E	ŧ		+		-		+	+	+	4.		Ė	Ē	E	E	E		-	=	4	•	•	1	-	٠,	4	4	1	#	#	1	1
ţ	1	1	ŀ	ŀ	ŀ	Ŀ	ŀ	1	1		F	Į	Į	ŀ	4	-	3	11	1	2	E	E	F	F	1	+	+	+	+	4	4	1	1	-	-	-	0				4	4	‡	‡	‡	4	‡	4	4	+	+	+	+	+	4
+	+	╀	ł	!		-	+	+	-	_	-	H	ŧ	+		=	1	1		L	-	E		+	-	+	+	†	-	-	;	+	1	-	-	f		f	F	H		d	1	1	1	1	1	1	1	1	1	1	1	İ	1
İ	\exists	1	Ŀ	ŀ	ŧ	ŀ	-	1				Ĺ	ķ	-	9	0	σ	9	0	0	۰	6	ŀ	Ī	4	1	1	1	-	4	+	+	1	-	Ţ	Į	Ţ	Į	L	П		Ц	4	4	4	4	4	4	4	4	4	4	4	4	4
1	4	4	ŧ	ļ	ľ		:	4		L	2	ŀ			- X	a l M	H	H	1	Ξ	Ę	-		4	╬	┪	+	┨	-	:	+	;		-	╬	- 1	╟		\vdash	eyelltrod.	Н	Н	1	+	1	1	†	1	+	1	1	1	†	†	-
t	1	+	-			+	1	1		\vdash	2	-	-	-	×	×	.	¥	M	-	-	T	T	Ì	1	1	1			1	1	-	Ė	-	1	ľ	1	ľ		٤	Ц	П	1	1	1	1	1	1		4		4	4	ceil	_
1	\Box	1	1	•	•	+				L			1	4	i (-	3 1	-	Ŀ	-	+		-	1	1	4	4	4	_	-	4	-	+	-	╬	+	+	+	╀	H	L	Н	-	4	+	-	-	\dashv		4	Н	┨	┨	+	\exists
+	\dashv	+	-	:	+	-	7		Н	┞	0	-	-	_	0	0	0	0	0	٠-	-	t	t	†	1	+	1	٦	-	-+	•	+	+	-	1	1	1	İ	Ì	Ì		Ц											1	I	_
1				•	1	+	-		L	İ	Ī	+			z	Ξ	Ξ		Ξ	-	1	Ī	1	1]				1	=		=	-	_	1	4	Ŧ	Ŧ	ļ	L	L	Ц			4	4	4	Ц	Ц	Ц	Н	4	4	\dashv	-
4	\dashv	Н	Н	<u>:</u>	4	-	•	L	L	ł	K) (• •		9	0 8	6	0	-	0	+	+	+	+	+	+	-	-	۲	\dashv	7	-	3	_	-	4	+	\dagger	\dagger	t	t	┝	Н		Н	Н		H					d			
		Н	Н	-	=	-				t		1	-	•	1	F	+-	+	Ŀ	t	1	İ	1	1						◂	×	Ξ	=	3	3	1	1	Ţ	Ţ	Į	L	L	П						\perp		П		Ц	Ц	L
				•	-	=	<u>.</u>	L	ļ	Į	ŀ	ľ	=		2		-	-	1	ļ	+	4	4	4	4	Н	Ш		Ц	Y	2	_	_	_	<u>₹</u>	┨	╁	╁	+	╁	╁	┝	Н	Н	Н	Н	Н	۲	Н	Н	H	Н	Н	Н	۲
	┝	H	H	-	•	•	_	┞	╁	ł	Ť.	7	7]	2	-	-	-	+	t	1	1	+					H	Ш				•	-	3	1	1	1	1	1	t	t						L	L				П	П	Ĺ
		L		•	•	•		Į	Ţ	Į	ŀ	-	•	•	-	ŀ	+	+	Į	Į	1	1	4			L	L	Ļ		_		Н	1	H	H	4	+	+	+	+	╀	╀	L	L	H	L	H	\vdash	┞	ŀ	┞	H	Н	Н	ŀ
F	┝	┞	┞	-	•	-	2	┞	╀	+	ł	-	=		=	-	ŀ	+	t	+	+	┨	1	٦	H	H	-	┝	┝	H	۲	H			Н			Ì	†	1	t	t				t		L	L						L
L	L	İ	İ	Ē	•	•	2	Ĺ	1	İ	-	3	_	11	Ŀ	ŀ	Ė	1	Ţ	1	1	1			Ľ	L	L			L			2		Ц	П	Д	4	4	4	ļ	I	Ļ	L	L	L	L	L	┞	L	┞	Ļ	H	H	ŀ
L	L	ļ	┞	Ŀ	•	•	₹ 14	1	ļ	4	ł	-	Ē	-	ŀ	+	╀	+	+	+	4	4	Н	_!	┝	┞	╀	┞	┞	╀	┞	H	3	┝	Н	H	Н	+	+	+	t	t	t	t	t	H	H	t	t	t	t		L	t	t
┝	2	t	t	F	_	-	-	t	t	1	1	٨	A	-	t	†	1	†	t	1	1				t	t	İ	İ	İ	t	L	t		L			П		1	1	1	ļ	I	L	I		L	I	Ţ	L	I	L	F	F	Į
Ļ	15		Į	1	•	Γ	Γ	Į	Į	1	1			L	Į	Į	Į	Į	1	1	\Box		\perp	L	L	L	ļ	ļ	╀	ļ	╀	╀	╀	ŀ	L	H	Н	Н	4	┩	╁	t	╀	ł	ł	ł	╀	ł	ł	╁	╁	┞	t	t	t
┞	Toncato	ŀ	╁	۴	-	F	ŀ	ł	t	+	4	Pe AC	┝	H	ł	+	+	+	┨	4	H		۲	H	ł	t	t	t	t	t	t	t	t	t		L				1	1	1	t	t	İ	İ	İ	İ	İ	Ţ	Ţ	I	Į	Į	Ţ
t			Ŀ	E	E		İ	1	1			Ш	L	İ	1	1	1	1	1				L		I	I	Į	Į	Ţ	Ţ	Į	Į	Į	L	L	L	Ц	Ц	Н	4	1	1	1	Ŧ	Ŧ	ŀ	Ł	ł	Ŧ	ł	Ŧ	Ŧ	₽	ł	ł
Ė	٤		‡	ŧ	ŧ	ŧ	ŧ	‡	†			Ē	F	ŧ	‡	#	=	1			Η	Ш	E	E	Ė	ŧ	1	ŧ	ŧ	Ŧ	Ŧ	Ŧ	Ŧ	ŧ	E	E	E	E	H		1	1	+	1	‡	+	+	‡	‡	‡	‡	‡	ŧ	‡	‡
	Mina		Ī				I		Ī	Acres	Actes	×											×							ŀ	•	-	•	-	-	-	×	*	ř	-	×											1			
I	T E E		1	†	t	T	1			4	PACE A		I	T	1	1																						ř	×	×	×	×	1		4	1	ŀ	1				1	1		
	178 5	3	1	1	T		1			AMERICA	82		†	1		×	×	×	×	×	-	ŀ		ļ	1		•					•	ŀ	ļ		•	-	×	×	×	×	×	×	×	4	•	•	-	×		×				×
	Uny 1 Br. 178 Constructs Midations	710 I - AIL	+	1	\dagger	\dagger				F			+	+	8	1941	TEATH	1114	114	1	2		*						ŝ	Ē		3	E I		+				9	Ē	1811	1270	1,61	Ē	Ê	2	2	ŝ	Ē		1	E	1807.238		2

FIF. 49B

7872-020 (SHEET 58 OF 63)

But 149 Constitution			T		Ī					9	(June		,						,	1																		اً					8	1
## 179 Constructs, Mutations March										Š	£ 50	111	8	2	9	9	81	9	9	re :	CP .	1	7	2	3	9		~	٦	-											•	2		
## 179 Constructs, Mutations March	T				•	Ţ	Ī	Ī				565	1/2	8	173	И	O	8	101	2	8	×	37	8	8	8	22	2	214	215	92	S i	3		2/2	5	ă	3	2	8	8	3	2	S
Hunted Mutations	+	-	+		ł	t	1	1	1			Ē	Ē	Ĕ	Ë	Щ	Ě		4		Щ	Ē		1	W	1		Ц	4	4	I	J	Į	1	Į	1	1	1	1	1	\Box	\Box		-
Here 1.12 Constructes - Wilson State	Ŧ	L	+	+	+	+	-+	4	4		Ц	┺	_	-	┡-	┡	-	٠.		_	ᆫ	_	-		_				_	_	_		-	_	_	4	4	-	-	-	_	-	3	ŀ
### A CONSTINCTS - MAINTAINCES	+	┝	+	+	+	4	4	+	1	-	┝	⊢	₽	₩.	┝	┝	-	٠.	-	•	,	Ľ	Н	_	₩.	Н	_	_	Н	-	-	٠,	-	-	٠,	-	-	-	-	3	=	3	٠	ŀ
But 176 Constructed, Mutations	1	t	Ţ	ŀ	-	1	1	1				E	3	3	3	3	3	E	3	3	*	₹	3	┡	⊢	┢	Н	Н	3	3	-1	4	4	-{	-	4	┥	4	-	_	ч	Н	Н	١
But 170 Constructed with the construction of t	1	L	-	4	4	4	-{	4	4	L	L	╄	╄	₽	╄	=	Ę	+	₽	┿	₽	₽	Ļ	┡	L	Ŀ	Н	_	Н	1	4	_	4	-1	-	4	-4	-	-1	٥	Н	j	j	ŀ
Hunting Constructs, Mutations Material Constructs, Mutations Mutations	+	╀	-+	+	+	4	4	┪	_	۲	┞	+	+-	+-	├ -	┝	₽	₽	ŧ-	╄	₽	+	٠.	₩	╄	⊢	Н	Н	Н	Н	Н	-	-	4	4	3	3	₹	4	∢	٧	•	4	l
But 178 Constructs, Mutations Main 178 Constructs, Mutations Mutations	\pm	t	1	-	-		3				L	1	1	3	3	3	3	1	Ŀ	3	3	╄	+-	₩.	٠.	-	-	Н	Н	_	ч	н	-	-4	→	-	-	-	٥	Н	Н	Н	Н	ł
But 178 Constructs, Mutations Mathematical Constructs	I	Į	-	4	4	-1	-			L	L	+	+	+	+	₽-	┿	+-	╄	╄	╄	┿	+-	╄	٠.		1-	┖	Н	I	Н	Н	4	-	-4	-	-	-	Н	-	н	Н	⊢	ł
Martin M	+	╀	-	4	4	-	Н	Н	Ц	┝	╀	┿	+	╄	╄	╌	┿	┿	╄	┿	╄	╄	╀	╄	┿	₽	┿	-	Н	Н	Н	Н	-	4	-	_	Н	_	н	_	Н	Н	┝	ł
Note Note	+	t	-1	4	→	-	Н	Н	Ħ	t	t	+	+	┿	┿	┿	ŀ	1	ŀ	ŀ	Ŀ	ŀ	Ŀ	ė	ŀ	E	=	E	E	Ε	0		•	•	-		•	•	Ξ	•	Ε	1	μ.	ł
But 178 Constitutes, Mutations Note	コ	Ţ		-	-	_	Н	П			Ţ	╀	+	+	+	┿	╇	ŀ	+	+	+	+-	+-	+	+-	╄	۲	╄	₽	Ľ	۲	Н	Н	-	_	Н	7	Н	Н	Н	Н	₩	0	j
But 178 Constitutes, Mutations Market Marke	+	╀	4	4	-	-	_	H	ŀ	╀	╀	+	+	┿	+	╀	╄	1	+	+	+	+	٠.	٠,	+	┿	٠	₽	₽-	Н	L	Н	_		Н	Н	Н	_	Н	Η	Н	┡	-	I
But 178 Constructs, Mutaulons Maintage	+	t	┨	-4	_	_	⊢	H	┝	t	t	+	+	+	+	+	+	,	4	4-	4	+		١.	+	4-	4-	ŀ	•	₽-	_	0	0	0	0	0	0	0	0	•	•	E	E	
But 178 Constructs, Mutations Name		1		•	•	8	-			Ī	l	ŀ	+	+	+	+-	+	+	4	+	+	+	+	+		٠.	+-	₽	-	-		Ļ	Н	Н	_	-	_	⊢	-	⊢-	╌	⊢	₽	-
## Constructs, Mutations Authorse	4	4	4	-	Н	_	⊢	⊢	L	Į.	+	+	+	+	+	+	+	+	+	+	+	+	4	+	4	+	+-	╄	+	₽	1_	1_	Н	Н	Н	⊢	_	┝-	-	┝	₽	╄┈	╄	-
### Particles, Mutations Maintail	+	+	4	_	_	-	⊢	H	┞	t	+	+	+	4	+	+	+	+	+	4	+	+	+	+	+	+	┿	╄	+-	₽		_	⊢	Н	Н	-	⊢	-	⊢	-	-	-	ŀ	,
Multiplications Multiplica	7	1		•	•	•	•		İ	İ	İ	Ţ	•	•••	•	1	•	•	•	9	•	ď	9	1	-	4	9	+-	+	+	+-	+	₩	┡-	⊢	-	┞-	┺	╌	₽-	+	₩	┿	
Multiple Multiple	\Box	Ţ		H	Н	H	₽	╄	L	1	1	4	4	+	+	+	+	+	+	-	-+-	+	4	+	-	+	_	٠.	+-	+-	+	╄	₽-	⊢	₩		┡	+-	₩	╄	╄	╄	╀	-
Multiplications Multiplica		+	_	⊢	⊢	⊢	₽	٠	╀	╁	┨	4	+	4	+	+	+	+	4	-	-	+	+	+	-	4		Ļ	4	+	+-	╄	₽	١-	⊢	₩	١-	₽-	⊢	╄	+	+	+	-
Bru 178 Constructs, Mufations Bru 178 Constructs, Mufations Bru 178 Constructs, Mufations Bru 178 Constructs Bru 178 Construc	\dashv	1	_	⊢	⊦	⊢	╄	╄	t	1	1	1	-	-	•	1	-	-	-	-	1	•	•	·	-	•	ŀ	Ŀ	Ŀ	Ŀ	٠.	۰	•	-	╄	₽	•	Ŀ	╄	Ļ-	┿	┿	+	-
Bru 178 Constructs, Mufations		4		⊢	 -	₽	╀	┿	Į	1	1	+	+	+	+	+	+	+	4	+	4	-+	+	+		+	+	+	-	٠.		_	┿	╀	┿-	+-	╄	╄	┿	╄	+-	֓֡֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֜֡֡֡֡֡֡֡֡֡֡֡֡֡֡֡֡֡֡	┿	
### Removed Mufations Mufations Mufations Mufations Mufations Mufations Mufations Mufaming M	Н	+	_	۱	₽	⊦	┿	+	ł	+	+	+	_			_	-	-	-	-	-	+	-	-	-	-	1	1	1	1	Ī	-	-	-	┿	╄	1-	╄	╆	╀	+	†	+	_
Bru 178 Constructs, Mutations	Н			₩	₽	٠	┿	†	t	1	†	1	4	4	-	7	7	-	=	-	-	-	-1	7	-	4	1	1	1	Ė	Ŀ	ŀ	Ŀ	E	E	E	Ŀ	ŀ	ŀ	E	ŀ	ŀ	Ŀ	-
Bru 178 Constructs, Mutations				₽	ł-	₽	+	┿	Į	1	1	4	4	-+	4	4	4	4	-+	-	4	4	+	7	-	-	_	4	+	+	┿	+	+-	٠.	_ر	+-	+-	+	┿	+-	+	+	+	-
### Buckenticks, Mutations No. 178 Constructs, Mutations No. 178 No.	Н	Н	L	₽	٠	+	٠	+	╁	+	4	-	-	-+	1	-	+	+	4	-	╣	-	+	=	╗	7	1	-	+	+	┿	╋	-	ľ		-	t.	+	-	+	-	+	+	
Bru 178 Constructs, Mutations	H	H	H	٠	٠	+	+	+	t	+	1	1	_	-	ᅴ	4	4	킈	4	ᅴ	4	킈	4	4	4	4	1	4	4	1	1	1	Ŀ	ŀ	Ė	ŀ	Ė	ŀ	ŀ	1	4	1	1	
Bru 178 Constructs, Mutations				Ŀ	Ē	ŀ	ŀ	•	1]			-	-	=	3	-	-	=	=	-	-	-	-	-	-+	-	+	+	+	+	+	ŀ	+	+-	+	+	+	+	+	+	+	+	-
Bru 178 Constructs, Mutations	L	L	L	┿	4	+	.1		4	4	_	Ц	_	Н	-	_	-	-	-	-	-	_	-	-	-	-	-	4	-	-	4	+	+	+	+	+	+	+	4	-	_		+	_
Bru 178 Constructs, Mutation Pi	┝	Н	 	ľ	+	+	+	7	1	4	Н	Н	I	H	П		Н	Н						1			+	1	1	†	†	†	t	t	İ	t	İ	1	İ	İ	†	1	1	
Bru 178 Constructs, Mutation Pi		L		ŀ	ŀ	ŀ	•	3	Ì				0	8	투	to Ac	ė	Hottn	ò	Ö							_	I	I	1	Ţ	1	Į	Ţ	Į	Ţ	1	1	1	1	4	1	4	_
Bru 178 Constructs Municipal Municipal Constructs	18	L	Ļ	ļ	+	+	1	1	-			L	٥	3H27			\vdash		CH2)	7 5	Н	Ц	Н	Ц	Н	Н	4	4	4	+	+	+	╀	+	╀	+	+	+	╁	+	+	+	+	-
Bru 178 Constructs Municipal Constructs	喜	1	13	4	+	7	7	+	4	Ц	H	H	H	٤	Ē	Η	\vdash	H	Ŧ	Ī	H	Н	Н	Н	Н	Н	H	+	+	+	+	+	t	t	†	†	†	+	†	†	†	†	†	-
Bru 178 Constructs Municipal Constructs		۲	t	t	†	1	1	†	1	H	H	H	T	H		t			Blot	캶	Ħ		Ц	Ħ				1		1	1	1	1	1	1	1	1	1	1	1	1	I]	
	ğ			Į	1	1		1				L				L		Г		L	L	L	Д	Д	L	Ц	Ц	Ц	4	4	4	4	4	7	+	+	4	+	+	4	4	4	4	-
	psro									emoned	Added		×	×	×	×	×	×	×	×																							١	ĺ
	78 C	1	+	+	+	+	-	H		Г	t	╄	\dagger	\dagger	H	+	\dagger	t	1	\dagger	f	-				t	t	H			1			┧	,				, 		Ţ		×	,
	5		L	ļ			Ц	Ц	Ц	Ľ	į		L	L	L	L	L	L	L	L	L	ľ	Ľ	ľ	Ĺ	ſ			μ					1	1			1		4	H		Ц	l
			ł										1385	1574	o	'n			ļ		2	2	8	ē		2		2	2	3	_	9	اچ	إو	5	اء	اج	g	8	8	8	8	8	١

DEL 49C

PCT/US95/16733

7872-020 (SHEET 59 OF 63)

	П			Γ	Γ	į	Į	•	,				,			•	•		,			*	
	Ц		L	L	L	ľ	ð				Ĺ		•			•				ı	ľ	2	
	ŀ	•	Ŀ	ŀ	Ł	t	Н	20.0	4	•4	Ē	E		i i i	884	u L	Ė	#	L	Ė	-	-1	
	H		F	*	F	F	F	Н	F	F	H	F	H	Н		H	H	Н	Н	H	Н		
	Ħ	I	Ļ	ŀ	t	t	F	L	ļ	Ė	ļ	E	Þ	Ľ	Ε	L	Г	П	П	ŀ	Г	9	
	Н	ш	ŀ	É	ł	t	t		E	L	L	L	t	E	E	L		H	L	L	L	3	
L	H	F	F	•	F	F	F	F	F	F	ŀ	H	H	Ļ			H	H	H	ŀ	ŀ	•	
Г	t	Þ	ļ	Ė	İ	t	L	Ļ	Ļ	L	Į	L	F	=	=	-	F	F	Ц	•	•	•	
Ш	t	L	Ł	ŀ	ł	t	t	L	ł	ŀ	t	L	L	Ē	Ē	Ē	t	t	t	Ē	Ē	Ħ	
F	F	F	F	ŀ	1	╀	ł	ŀ	-	H	┞	╀	┞	Ë	-	å	╀	┞	ŀ	ŀ	ŀ	Ė	
E	ļ	ļ	ļ	ŀ	ļ	t	ţ.	ļ	ļ	F	ļ	F	ļ	Ę	-	-	F	Ļ	F	Ę	ļ	Ŗ	
E	t	t	t	ľ	ł	t	t	t	t	t	t	t	t	Ė	Ē	1	t	•	Ŀ	ľ.	Š	Ī	
F	Ŧ	ŀ	ł	ŀ	1	+	ł	ł	ł	+	ł	╀	ł	F	F	ŀ	╁	F	-	ŀ	ŀ	=	
L	1	Ì	ţ	ļ	1	1	‡	ļ	ļ	Ţ	ļ	Ţ	ļ	E	ŀ	ŀ	Ţ	ŀ	ŀ	ŀ		Ė	l
L	t	t	t	ĺ	1	1	t	t	t	t	t	t	l	Ŀ	Ŀ	ŀ	t	Ė	ŀ	•	ł	ŀ	Ì
F	Ŧ	Ŧ	1	Į	1	7	Ŧ	Ŧ	+	ł	ł	ŀ	1	1	:	ŀ	1	ŀ	ŀ	1	ł	÷	ı
Þ	‡	ţ	1	-	1	‡	1	ļ	‡	ţ	‡	ŀ	ŧ	ŀ	t	ŀ	1	ŀ	ŀ	İ	ŧ	ŀ	
H	t	ł	ł	ł	=	1	t	t	1	t	t	t	Ī	ŀ	ŀ	ŀ	ŀ	ŀ	ŀ	ŀ	ŀ	•	1
F	Ŧ	Ŧ	7	-	3	4	Ŧ	Ŧ	Ŧ	Ŧ	7	Ţ		1		-	ŀ	1	-	-	-		ı
L	‡	ţ	1	1	1	1	1	1	1	1	1	ŀ	ŧ	ŧ	ŀ	‡	ŀ	ŀ	ŀ	ŀ	1	1	1
H	+	ł	1	+	•	1	1	t	t	1	•	1	1	1	1	1	ŀ	•		1	1	1	1
F	7	Ŧ	1	7	3	7	4	Ŧ	4	-	3	3	1	1	1	1	Ţ	7	1	1	-	7	1
t	1	1	1		•		1	1	1	1	-	=		1	1	1	1	1	-	1	ŀ	1	1
H	+	┨	1	4		Н	+	╁	↲	┪	•	7	:	-	#	:	+	+	1	•	7	1	ł
F	7	1	7		1714	Н	4	7	3	3	3	3	3	-	-4	1	7	1	1	<u>্</u>	7	Ŧ	7
t	1	1			1	Н		1	Ξ	Ξ	Ξ	Ĭ	Ξ	=	=	=	1	=	1	-	1	1	1
ŀ	4	4	Н	_	٠	Н	Н	4	4	-	-	-	-	-	-	:	┨	7	4	1	┪	+	\mathbf{I}
þ	4			F	-		П		3	3	3	Ξ	3	3	3	3	7	3	7	4	4	7	7
t			H	L	Ŀ	L	Н		•	•	•	•	•	_	•	•		3	╛	1	#	1	1
ł	-		H	┞	:	╁	Н	Н		•	• [•	-		•	•	-		•	+	Н	Н	1	ł
ļ		Η	F	F	ŀ	ļ	F		1010				•	•	4	í					Н	4	7
t	_		L	t	Ŀ	t		Н	141	IAI	۸	M	Å	•		•					Ħ	1	1
ł	4	H	ŀ	ŀ	ŀ	╁	H	H		ŀ	•	ŀ	Н	Н	Н		Н	8	-	Н	Н	1	1
ţ	_	F	F	F	ŀ	Ţ	F	F	F	Ē	E	Ē	F	H	A	Д	Н	H	H	H	A	4	1
t		L	t	t	ŧ	ŧ	t	t	Ē	-	-	Ė	H	Ħ	H	Н	Ħ	Ц	H	Ħ	Ħ	H	1
ł	_	┞	ł	ł	ŀ	+	╀	H	۴	•	•	÷	H	Н	Н	H	Н	Н	Н	H	Н	Н	1
I	_	L	ļ	ļ	ŀ		F	F	Ė	t	t.		F	Р	Г	F	L	Р	L	F	P	Н	4
1		t	t	t	ľ		t	t	•	•	ľ	t	t	t	E	t	t	Ľ	t	L	t	Ħ	I
	-	ł	ł	ł	ŀ	╪	╀	┞	ŀ	ŀ	+	╁	╀	╀	┝	┞	H	┞	┞	┞	╀	Н	Н
	_	ļ	ļ	Į	ŀ	1	Į	F		•	Į	Ŧ	F	F	F	F	F	F	F	F	F	P	Н
		t	t	1	1	1	t	t	ť	t	t	t	t	t	t	t	t	t	t	t	t	t	Ħ
	9	F	7	+	1	+	t	ł	ŧ	+	ł	t	Ļ	+	H	ł	t	Ļ	ķ	+	Ļ	۲	Н
	90	1			Į	١	١	ŀ			1		100		١	ķ		H			United and		H
	HIV-1 BRU DP-107 peolides	1	ł	1	┨	+	t	f.	۴	+	ł		f	+	t		+	f	f	Ŧ	f	t	Н
ļ	ģ	i			1		1			I	١	١	l	1		l	h	r	ŀ	t	4	١	
	38		+	1	1	+	†	ť	1	1	1	1	t	ılı	ļ	1	t	t	t	t	╁	ļ,	,
1	5	:	1	إ		4	1	Į	Ų	1	•	¥	¥	#			l	ļ	ļ	ļ	ľ		Ě
	Ē	1	1				1	1	F	ij	4	٩	\$	f	F	ŀ	ŀ	ŧ	•	ì	ľ	Ŧ	Ê

7872-020 (SHEET ⋈ OF 63)

7	J	<u>e</u> i	φį	36	2	80	36	9	200	32	36	18	32	12	1	Т	Τ	Т	13	ı	न	T	R	2	9	3	8		1 4	F	19	×	1	ī	Т	Т	Т	ר
4	7	2	• 36	_	-	-	٢	£	 "	ļ-	۲	1	-	1	4	╀	4	4	-	4	4	4	7	-	7	_	-	7	Ŧ	F	F	F	#	4	+	╂	╀	ŀ
\dashv	4	딯	٠	4		_	Н	┝	┞	┝	╁	╁	╁	╁	╁	╀	┨	+	┪	<u>;</u> }	╁	┥	+	┪	-†	4	: -	┧.	╁.	t	t.	١,	+	+	+	-	+	ł
H	7	듹	-	٠	-	٠.	Ė	ŀ	ŀ	ŀ	t	t	ť	ť	+	t	╁	┨	+	+	┪	4	ᅥ	\dashv	+	┧	Ť	Ŧ	t	ť	ť	ť	t	t	†	†	1	1
H	5	┪	308		210	211	212	5	214	218	2	12	318		†	t	†	†	T	1	3	1	ន្ត	딞	ন্ন	ន	, i	र्गः	318	į	18	Į	i	⇟	†	T	Ť	1
Ц	1		R	200	7	7	~	~	2	<u> `</u>	Ľ	12	1	1	4	1	4	4	4	4	4	4	7	7	7	7	7	1	1	r	Ţ	#	#	4	+	+	+	4
H	4	-	Н	-	Ц	Ļ	L	1	┞	╀	╀	╄	╀	╀	+	╀	+	+	╁	+	4	4	-	Н	\dashv	+	+	+	-}-	╀	╀	╀	╀	╁	+	+	+	┨
H	4	-	Н	_	Н	H	╁	┝	╀	ł٠	╁╌	╁	╁	۴	+	╁	╁	+	╁	+	1	┪	┥	-	\dashv	+	+	+	+	+	t	t	t	+	+	+	┪-	┨
H	4	ᅥ	Н	_	Н	┝	┢	┝	┢	t	t	七	Ħ.	Ŧ	#	t	†	†	╅	+	3	7	┪	H	┪	1	7	†	\dagger	t	t	, i	1	†	†	†	†	1
H.	-		H		Н	r	t	T	T	t	t	. a	:		:	t	1	1	†	٠.	5	7	٦	П			7	1	T	1	,	+	7	-	Ť	Ī	Ī	1
Π.	3					Ш				L	Ţ	Ŀ	Ŀ	Ŀ	1		1	Ι	T	Ţ	9							I	1	1	s le	k	1	1	I	I	I]
Ĭ				Ц	П	Ц		L	Œ	ď	<u> </u>	<u> </u>	a	: -	4	1	1	1	1	ŀ	╛			Ц	Ц	Ц	4	4	4	4-	4	4	4	4	4	4	4	4
_	익	Ц	Ц		Ц	Ļ	L	9	+-	+	+-	+	+	+	-	+	4	4	4	4	쁴	4	_	Н		Н	4	약	뱍	4	¥	4	+	+	+	+	+	-
H	3		Н	L	Ц	L	₽	₽	+-	+	+	+	+-	+-	-	+	4	4	4	-	4	4	Н	Н	Н	Ц	4	4	-1	4	+	*	1	-	+	╀	+	4
1	-	Н	H	┝	Н	3	=	۳	-	╁═	+	+	+	+	+	+	+	┪	+	-	نا ع	┥	-	Н	¥		_	_	2 K	2 (S	-	_	-	1	+	+	╁	┨
_	9	Н	H		-	9	-	8	+	+-	+-	٠,		+	+	+	+	┪	+	_	킑	┥	Н	o	ı	_	_	_	3	+	+	-	5 -	-	†	†	+	1
	×	Н	L	Z	7	Ž	1	Ž	+-	1	+	┰	_	_	+	†	†	7	7	-1	7	┪	¥	×	K	7	┪	┪	-	1	1,	+	-+	×	†	†	†	1
$\overline{}$	7	П	7	A	~	₹	1	+-	+-	_	_	-	+-	+	1	†	_	7	7	1	7	٦	_					1	J.	1.	j.	Ţ.	1	1	Ţ	J	Ī	1
H	<		<	<	<	۲-	-	1-	+-	+-	+	+	4	-	4	1	_	╛]	ار		_		1			4	٦.	J.	J.	J.	4	1	I	I	m I]
	<		<	<	<	4	4	4	4	4	4	4	<	4	⋖	Ţ		\Box		\mathbb{I}	_		_	_	1	9	_	_	4	4	4	4.	4	4	1	-[.[.	_
Ш	٧	Ĺ	2	≥	≥	≥	ŀ	Þ	•	•	<u>.</u>	•	Ŀ	Ŀ	1	1	\perp	_	_	\rfloor	R		R	Я	R	R	R	Œ	E C	s (5	sļ	ij	4	4	4	4	┙
Ц	w	L	=	<u> </u>	-	4	-	-	1	4	4	뽀	4	4	4	4	4	4	4	_	=	Ц	=	=	1	닏	늬	4	4	4	4	4	4	4	4	4	4	4
\vdash	<u>«</u>	L	ᄩ	Œ	Œ	٩	1	4	+	┿	+	嵉	뱍	_	ጜ	4	-4	4	4	-1	۳	Н	R	-	۳	٤	_	7	_	-	SI.	-	7	=	+	+	+	4
Н	<u>~</u>	┝	Ě	^	>	È	ť	봗	÷	+	-	_	÷	-	井	+	4	4	4	4	<u>-</u>	Н	٥	10	2	읩	Н	-1	_	-	2 C	-1	-+	밁	+	+	+	┨
_	I	┝	5	0	Z	+	+	+	+	+	+	= 2 	-	-	뒤	┥	┥	-	\dashv	┥	Z	Н	Ξ	1	Z	Ξ	2	_	7	2	┱		┪	_	╅	+	+	ᅥ
H	-	H	۲	ľ	۲	۲	19	#	#	#	羋	#	#	#	#	+	1	٦	\dashv	┪	8 E	H	8	8	9	5	5	-	_	-	+	7	-+	=	7	†	+	┪
H	_	┪	Ē		Ē	Ť	Ť	Ť	1	#	#	#	1	Ï	#	7	7	T	┪	┪	9	Г	8	+-			9	-	_	-	-	-+	-	•	7	7	7	٦
Н	0	٢	6	a	a	•	-	,	, (3	3 0	9	3	7	a	7	┪		П		K	Г	×	1	1	1	X	_	7	7	7	2	7	┙	1	I	Ī	
	X	Γ	Ŀ	-	-	ŀ		ı,	4,	4	₹,	₹,	₫,	-	\leq						٧		٧	4	<	V	٧	⋖	⋖!	∢.	₹.	∢.	⋖	⋖	\Box	ightharpoons	I	
Ã	Ы	L	-						J	Ţ	٠,		J	_	_			I			٧		۷	⋖	<	۷	٧	⋖	⋖	≤	⋖!	악	-	≤	_	4	4	_
2E1	X		×	+-	Ŀ	ŀ	4	4	4	4	<u> </u>	4	4	-	뇍	4	_		Ц		۷	L	⋖	+	ַ	+	≤	_	-+	-+	_	-	-1	4	4	4	4	4
8	≤	Т	₽	+	4	+	4	-	+	+	약	4	+	_	왹	4	_		Н		^	L	₽	+	₽	≥	2	4	7	7	-	7	7	긕	+	┥	+	ᅱ
E81	=		=	+-	+	+	= 9	-	+	+	-+	-	-	-	=	4	_	-	Н	Н	3 1	┝	1	+-	1	•	<u> </u>	-	7	-1	-*	-	7	쀤	┥	╅	+	ᅥ
E	K		100	+	10	٠	<u></u>	4	+	┱	<u> </u>		약	-1	의	┪	Н	-	Н	Н	ЫY	┝	7	₩	\ <u>\</u>	1	7		5		3	-	-+	7	\dashv	+	7	┪
5	9		t	۰		+	. 4	-+	+	¥ ;		2		-	2	┪	Н		H	H	Ē	H	Ę	+	1	1-	Ī	H	Ξ		Ξĺ	→	ᇽ	Ξ	T	1	┪	٦
1	ē	т	t	ļ	t	+		_		, 	7	7	7	→	=	┪	П		П	П	0	T	6	+-	-	_	-	ō	-	o	ø	ð	_	0		╛		
ē	•		ŀ	ŀ	ŀ	d	7	+	4	4	₹	₹.	₹	4	₹						_	Γ	L		L	_	_	1	7	_	4	4	L	_		\square	\square	_
M	5	Ī	7	ŀ	þ	ŀ	1	<u> </u>	2	\geq	\geq	\geq	>	≥	>		I				2	L	[L	1	1	ب	4	_	_	4	_	_	닏	Ц	Ц	Ц	_
IBACTIVATOR PROTEIN EBT OR ZEBRA	•	Ļ	ŀ	-	-		_	-	-	_	-	_	_	=				Ĺ		L	ø	•	þ	-					의		-	_	٥	Ц	Ц	Ц	Н	_
		+	Þ	4	2	₽	뱍	-+	-	-+	≅∤	롹	≥	4	Ц	Ц	Ш	L	L	L	¥	1	ŀ	-	_	<u>'</u>						뇍		Н	Н	Н	Н	_
E	1	4	ŀ	-	4	7	_	4	4	×	_	半	4	4	Н	Н	L	┝	H	\vdash	۳	+	ŀ	_			-	×	KIF	*	-	4	Н	Н	Н	Н	Н	_
15	2	+	P	-	_	-	_			_	뉙	+	┥	4	Н	Н	┝	┝	┡	┝	×	_		_	-	+-	7	_	AK	×	Н	۲	Н	Н	Н	Н	Н	-
Z	2	+	ť	٩	┱	Т	┰		┪	띡	┪	+	┨	ᅥ	Н	Н	┝	┝	┝	┝	1	1	1	7	+-	-			H	Н	Н	٦	H	Н	H	H	Н	Г
3	f		ť	ť	+	4		_	肖	+	+	+	4	\dashv	Н	H	1	†=	+	t	0	_		_	_			f	Н	H	H	П	Н	Г	Г	Н	Н	Г
	=	†	Ţ.	J.			J	7	+	7	7	7	┪	H	Γ	Г	H	T	۲	t	Ĭ	1	į,	4 2	4	_	_	T	Г					Γ				E
13	ļ.	1	Ţ.	Ĵ.	1	1	1	1	┪	7	7	T	7		Г		Γ	Γ		Γ	Ē	+	le	_	: 4	-	Γ											Ĺ
E	-	J	Ţ	ŀ	1	Ţ	1	1]]]					Γ	Γ	Γ	•	т	ŀ		۰	I	I			Ц	Ц		Ĺ	Ĺ	Ĺ	Ц	Ц	L
2	•	1		•	I	Ţ	I	_	\exists	_		\Box			Ĺ	L	L	L	L	Ĺ	I	4	ŀ	4	1	1	ļ.	L	L	Ц	Ц	L	L	L	L	L	Ц	Ŀ
Ž	L	1	1	1		1		Į		لِ			إ		Ļ	L	L	L	L	Ļ	1	1	Ļ	1	ļ	1	Ļ	Ļ	Ļ	F	H	Ļ	L	6	1	μ	\vdash	H
18	:	3	į		1	3	2	2	178	2	180	181	182	183	ī		ŀ	l	l	1	i i		į			2		3	Ē	102	193	101	198	3	1			l
Ž	Ť	t	†	†	†	+	+	+	+	┪	H	一	\dashv	Н	H	t	t	t	t	t	ť	†	t	+	t	t	†	t	T	T		Γ	Γ	Γ	T	Ti	1	Ì.
EPSTEIN-BARR VIRUS STRAIN 895-6 BZLF1 TRAN	ŀ,	,†	†	†	†	1	-†	7	7	1	П	Γİ	٦	H	T	T	t	T	T	t	t.	,†	†	Ť	1	†	T	Ι	Γ	Γ	Γ		Γ	Γ	Γ	Γ	Γ	
243	ŀ]	Ş		ş	1420	T-427	Ŗ	1-429	홁	157-1	त	5	37.1		Ι	Γ	I	Γ	1		J	1	?	2 8	97	3	3	3	3	3	3	14.0	L	Ľ	Γ	Ĺ
	ŀ		•	1	_	1	1	1	17	Ţ	ĭ	3	Ξ	Ξ	[L	-	L	L	L]];	٠,	١,	1			-	2	E	7	7	E	L	Ŀ	L	L

FIE. 51A

PCT/US95/16733

7872-020 (SHEET 61 OF 63)

	<u></u>		101	10		l to	lio.	140	100	Tue	فداد	صا	صا	100	_		-	7	-1	~[_	8	9	20	_	-	_	_	_	_	т	т	Т	Т	Т	Τ	1
Ц	46		36	36	3	36	38	36	1		'n	F	36	6	L	i	-	4	4	7	_	-	_	-	_	-	╀	L	╀	╀	╀	+	+	╀	╀	╀	┨
Н	Н	Н	Н	Н	H	┝	╀	┞	╁	╀	╁	╀	╁	┝	H		Н	┨	Realdue	\exists	-	Ⅎ	ㅓ	H	┝	-	╁	H	t	╁	t	\dagger	†	†	t	t	1
		H		_	Г	r	T		t	t	1	T	L		t		⇈	╛	ě							-	İ	L	İ	İ	1	1	1	I	I	I	1
	242		232	22	72	22	22	22	Ę	Š	12	241	242	253	Γ		П			246		244	248	240			T		Ī	ı	Ţ	1	١	١		۱	
-	12	Н	H	-	H	F	F	H	Ť	T	+		+	H	t		H	1	Ⅎ	H		Н	H	H	H	-	t	t	t	t	t	t	†	†	十	t	1
Н	Η	Η	Π	Τ	r	T	t	t	T	t	t	İ	t	_	t		╚							Ш		•	İ	İ	I	Ī	I	I	I	I	I	I]
	0				L	L	I	L	L	I	I	I	٥	٥	I		П		[Ш	L	_	1	Ļ	Ļ	ļ	4	4	4	4	1	1	4
L	3	L	L	L	L	Ļ	ļ.	╀	╀	╀	+	100	+	1	+		Н	_	Ц	Н	Ц	Н	Н	H	┝	-	+	╀	╀	╀	╀	+	+	+	+	╁	┨
┝	H 1	┝	\vdash	Ė	┝	╁	╀	╁	╁	╁	F	7	F	E	+		Η	-	Н	H	۲	Н	H	┝	┝	-	†	t	t	t	t	†	†	†	+	+	1
۲	5	H	۲	H	t	t	t	t	5	, 5	, 	,	5	+=		•	H	_	Н		Г		L	Г	T	· •	I	İ	İ	İ	İ	1	Ī	1	1	İ	1
Ш	٥					I	I	٥	c	k	3	2	\o	٥	I		\Box							L	L		1	ļ	1	ļ	1	1	1	4	4	Į	1
L	-	L	L	L	L	1	1	ه.	+	ŀ	4	•	<u> </u>	-	╀		4	_	Ļ	L	┡	┞	L	Ļ	┞		+	+	╀	╀	╁	+	+	+	+	+	-
┝	E	┝	┝	┞	Ł	۴	Ë	ľ	Ť	+	+	: 0	+	÷	+	•	\dashv		┝		┝	┝	┝	Ŀ	╁	-	+	t	t	t	+	\dagger	\dagger	+	十	+	┨
۲	٣	t	H		5	-	+	. a		:	5 0		+		+	-	٦			Z	T	T	z	Z	T	•	T	t	T	İ	1	1	1	1	İ	İ	1
Г	Ē		L	L	Ī	Ţ	Ţ	Ţ	Ţ.	Į.]	Ţ	I	.[_	I	-			L	_		_	=	т	Т		I	Ţ	I	Ţ	Ţ	Ţ	Ţ	Į	Į	I	1
Ĺ	-		F	Ē	E	F	-	-	-		=		-	-	1	_	٦		Ĺ	-	L	1-	F	H	4		4	+	+	+	4	4	4	4	+	+	4
H	100	+	2	-	15	-	-	+	-	-	1	-	-	+-	+	-	4	\vdash	ŀ	9	\vdash	은	1	+	+		+	+	+	+	╁	+	+	+	+	+	+
H	2	+	13	+	+-	+	+	+	+	-) > >	_	_	+	+	-	-	H	┢	포	H	분	1	•	1		+	t	t	t	†	†	7	†	†	†	1
۲	6	1	6	+-	+	_	_	_	7	┱	٥	7	_	+	+	_		L				_	1	_	т	•	1	1	Ī	Ī	I]		I	I	I]
	L	I	L	L	Ţ	I	1	4	4	4	4	4	4-	4-	1	_			L	≥	L	>	2	≥	L		4	1	1	4	4	4	4	4	4	4	4
L	4	4	Þ	+	٠	+	9	+	_	-	9	+	약	+	+	_	_	L	Ļ	10	┡	卢	+-	7	1	-	4	+	+	+	+	4	ᆛ	4	+	+	4
ŀ	6	+	0	+	+	-	-) (-	-		-	<u>ا د</u>	-	+	-	_	┝	╁	-	╁	-	-		+	•	+	+	t	†	†	┪	+	+	+	+	1
H	Ė	+	Ę	-		-	-	#	-	-	-+	-	<u> </u>	-	+	-	-	H	t	Ę	1	Ę	+-	۰	+	-	†	1	1	1	1	1	_	1	I	1	1
t	c	+	c	+	-	-	-	3	-	-	-	-	9 0	3	3	_	_		L	٩	I	<u> </u>		٥.	I		I	I	I	I	Į	\Box	Ц	\Box	ユ	1	7
		4	ŀ	ŀ	4	4	4	4	4	×	¥	4	₹.	4	4	_	_	L	╀	╞	╀	╞	╞	₽	╀	-	4	4	+	4	4	4	Н	\dashv	+	+	4
ŀ	╪	4	╪	+	7	4	4	4	4	4	4	4	4	4	4	-	_	┞	╁	=	+	╏	-	:	╁	•	+	┪	╁	+	┪	\dashv	Н	\dashv	+	+	\dashv
ŀ	ŧ	#	╁	#	#	†	 	#	1	_	#	#	#	1	1	_	-	t	t	6	-	+	٦	+	+	•	7	1	†	†	7	П	П	┪	7	†	1
t	ļ		Ī	2	Ξ (2	æ i	2	=	æ	æ	=	æ	2	=	_	_	Ι	Ī	5	Ī	>	•	•	1	-	I	1	I	Į				П	コ	1	
	ļ	4	Ţ	4	4	4	4	4	4	4	4	-1	4	4	4	_	_	Ļ	ļ	٥	4	ļ	عإد	뱍	4	-	4	4	4	4	4	Н	Н	Н	4	4	4
ŀ	+	1	_	-	7	_	_	7	_	_	-	-	_	+	듹	_	-	╀	╁	ŧ	+	+	:	1	+	-	\dashv	┨	╅	┨	┨	Н	Н	Н	+	+	┨
ł	+	2	-	-	7	-	-+	_	-1		-		_	-+	밁		-	t	t	ť.	+	Ť.	+		╈	-	┪	1	1	7	T	П	П	П	☐	1	1
t	+	-	j.	7	┪	7	7	7	_	3	_	_	_	-+		_	-	İ	İ	k	+	ķ	-	,	-	-	\exists		I		Ц			Д	Д	\beth]
Ţ	I	•	-	-	-	_	_	0	_	8	•	•	•	9	•	_	_	I	Ţ	P	+	1	-		-	_	4	4	4	4	Ц	μ	H	Н	Н	4	4
ŀ	7	4	7	7	막	~1	7	┪	_			_	_	-1	쀠	_	-	+	+	ľ	+	_	쏫	7	┱	-	\dashv	4	+	4	Н	H	H	Н	H	\dashv	\dashv
ł	-1	4	_		4						¥	_	_	┪	+	_	-	†	†	_	1	ť	Т	#	╬	-	\exists	_	1	_	H	Γ		Г		╛	
t		₹					₹	4	<	٧	/ V	ď		I	1		-	1	1		4	Ţ.	+	4	1	<u>-</u>						L	Ľ	\Box	Д	Д	
ſ	_	⋖	Ţ	_	⋖	۷	٧	⋖	A	A	٧		\Box	4		_	-	1	\downarrow	-	4	_	4	4	4	_	4	_	4	4	\vdash	Ł	ŀ	H	Н	Н	Н
ļ	_	쇡	_	╛	_			J		≥	Н	Н	Н	4	4		-	+	+	_	=	7	т	┪	"	-	-	-	Н	Н	H	\vdash	H	H	Н	Н	Н
ŀ		<u>۳</u>	-1	╗		RE		N.		\vdash	Н	Н	Н	+	4	\vdash	-	+	+	_			#		#	-	_	۲	Н		H	t	t	t	H	H	H
ł	_	5						H	۲	H	H	H	H	1			-	†	†		5				ā	_						I	Γ	Γ	П	口	口
1	_	Ξ			F	Ξ					Г	П	П					1	Ţ	1	=	į	z	_	3	_	_	Ĺ	Ц	Ĺ	Ĺ	Ĺ	Ļ	Ļ	\vdash	Н	Н
1	4	9		σ		Ц	Ц	Ц	L	L	L	\vdash	Ц	Ц	4	<u>_</u>	-	4	4	-	4	_	_	삑	4	_	_	L	Н	┝	⊦	╀	╁	╁	H	Н	Н
	4	4	4	4	Н	Н	Н	Н	L	\vdash	┞	┝	Н	Н	-	\vdash	-	╁	+	+	믝	+	읙	+	┥	-	_	H	Н	┝	H	t	t	t	H	H	Н
	1	딋	Η	107	88	100	8	16	22	2	ă	208	902	207	208	1	•	†	1	+	ᆰ	1	8	250	딁	-	-	۳		r	t	T	t	t	T	Γ	П
Į	Ц	1107	Ц	Ξ	Ξ	تّ	×	7	12	ř	A	ř	ñ	~	8	\vdash	-	4	4	4	R	4	7	7	~	_	_	H	L	H	╀	+	+	+	╀	H	Н
	Н	Н	Н	Н	Н	H	۲	H	┞	╀	+	┞	Н	Н	\vdash	\vdash	-	+	4	+	1	+	+	4	4	-	-	-	۲	┝	t	+	t	+	+	t	H
	Н	Residue	Н	(3	81	3	H	듈	뎚	2	3	20	2	87	88	1	•	+	1	\dashv	Perde	7	밁	힑	ş	_	-	T	T	T	T	t	†	T	İ	T	Г
j		Res	d	1	877-1	1	•	Ī	7	1	1	Ī	7-456	7	1-468	Ľ	ٺ	1			흳	╛	1	2	7	_	ī	L	Γ		Ι	I	I	Ι	I		
	_	=	_	ټ.	_	_	_	_	4	_	-	-	_	_	-	ب	_	_	_	_	-	_	_	_	_	_	_	_		-	_	_	_		_		_

7872-020 (SHEET 62 OF 63)

Domain I: 174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

FIF. 52 A

L-I-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I-P-G-8-8-T-8-T-G-P-C-R-T-C-M-T-T-I-P-G-8-8-T-6-T-G-R-T-C-M-T-T

7872-020 (SHEET 63 OF 63)

C-L-1-7-2-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-1-P-Q-9-8-T-8-T-G-P-C-X-T-C-M L-C-L-I-P-L-L-V-L-L-D-Y-Q-Q-M-L-P-V-C-P-L-I-P-G-8-3-T-8-T-G-P-C-R-T-L-L-C-L-I-Y-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G-8-8-T-8-T-0-P-C-R-T L_L_L-C-L-1.P-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-1-P-G-8-9-T-5-T-G-P-C-R F-I-1-1-1-C-C-1-F-L-L-V-L-L-D-Y-Q-Q-H-L-P-V-C-P-L-I-P-G-8-9-T-8-7-G-P L-P-1-L-L-L-C-L-1-P-L-L-V-L-L-D-Y-Q-G-N-L-P-V-C-P-L-1-P-G-8-8-T-9-T-0 ₽•L•₽•I-L•L•L•C•L-I•F•L•L•V•L•L•D•Y•Q•G•M•L•P•V•C•P•L•I•P•Q•8•₽•T•8•T I-F-1-F-I-L-L-L-L-C-L-I-P-L-L-V-L-L-D-Y-Q-O-H-L-P-V-C-P-L-I-P-G-8-8-8-F-I-I-F-L-F-L-L-L-L-L-C-L-I-P-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P+L-I-P-Q-S-S-T R-F-I-I-F-L-F-I-L-L-L-L-L-L-I-F-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G R-R-F-I-I-F-L-F-L-L-L-L-C-L-I-F-L-L-L-L-D-Y-Q-G-H-L-F-V-C-P-L-I-P-O L-R-R-P-I-I-9-L-P-I-L-L-L-L-L-I-P-L-L-V-L-L-D-Y-Q-G-H-L-P-Y-C-P-L-I-P C-L-R-R-P-I-1-F-L-P-I-D-L-C-L-I-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-I M-C-L-R-R-F-I-I-I-F-L-F-I-L-L-C-L-I-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-E R.W-M-C-L-R-R-R-T-I-T-F-L-P-1-L-L-L-L-I-P-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C T-R-H-M-C-L-R-R-B-1-1-F-L-F-I-L-L-C-L-I-F-L-L-V-L-L-D-Y-Q-Q-M-L-P-V G-X-R-W-C-L-R-R-P-I-I-P-I-L-L-L-L-C-L-I-P-L-L-V-L-L-D-Y-Q-G-W-L-P

FIF. 52B

Domain II:

INTERNATIONAL SEARCH REPORT

International application No. PCT/US95/16733

LPC(6) :	SSIFICATION OF SUBJECT MATTER CO7K 7/04,14/025, 14/16; C12N 9/94, 9/96, 9/98, 9/ 530/324; 424/184.1 o International Patent Classification (IPC) or to both n		
	DS SEARCHED		
	ocumentation searched (classification system followed	by classification symbols)	
	530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1,		
Documentat	ion searched other than minimum documentation to the	extent that such documents are included	in the fields searched
	ata base consulted during the international search (name, AIDSLINE, APS	ne of data base and, where practicable,	, scarch terms used)
c. Doc	UMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where app	ropriste, of the relevant passages	Relevant to claim No.
×	PROCEEDINGS OF THE NATIONAL		1-3, 9, and 10
	OF THE UNITED STATES OF AMER 21, issued November 1992, Wild e	ICA, Volume 89, Number	4-8 and 11-15
Y	21, issued November 1992, Wild e Inhibitor of Human Immunodefic	iency Virus Replication:	4-0 and 11-13
	Correlation Between Solution Struct		
	pages 10537-41, see entire docum	nent.	
		•	
	·		
		•	
X Furt	her documents are listed in the continuation of Box C		
	pocial categories of cited documents: ocument defining the general state of the est which is not considered	" " " " " " " " " " " " "	pation but cited to understand the
•	be of particular relevance	*Y* downers of particular relevance: If	he claimed invention cannot be
	artier document published on or after the interactional filing date ocument which may throw doubts on priority chim(s) or which is	considered novel or cannot be considered when the document is taken alone	ICEOR TO MINOTING OUR MINORITY OR ORD
c =	ited to establish the publication date of earther citation or other pecial reason (se specified)	"Y" document of perticular relavance; to considered to involve an inventive	a stap when the document is
	ocument referring to an orei disclosure, use, exhibition or other	combined with one or more other ma being obvious to a person skilled in	ch documents, such combination the art
'P' d	comment published prior to the international filing date but later than he priority date claimed	*&* document member of the same point	
	e actual completion of the international search	Date of mailing of the international se	earch report
28 MAR	CH 1996	09 APR 1996	
Commiss	mailing address of the ISA/US ioner of Petents and Trademarks	Authorized officer	h Frus 10
	on, D.C. 20231	JEFFREY STUCKER Telephone No. (703) 308-0196	•
Facsimile	No. (703) 305-3230	1 1 etchtorie 140. (140) 300-0190	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/16733

Category®	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
<u> </u>	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency	1-3, 9 and 10 4-8 and 11-15
(Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex*, pages 12676-80, see entire document. PROCEEDINGS OF THE NATIONAL ACADEMY OF	1 and 4
·	SCIENCES OF THE UNITED STATES OF AMERICA, Volume 81, Number 24, issued December 1984, Collins et al, "Nucleotide Sequence of the Gene Encoding the Fusion (F) Glycoprotein of Human Respiratory Syncytial Virus", pages 7683-87, see pages 7683 and 7685.	9 and 11
ζ Υ	VIROLOGY, Volume 204, Number 2, issued 01 November 1994, Bousse et al, "Regions on the Hemagglutinin-Neuraminidase Proteins of Human Parainfluenza Virus Type-1 and Sendai Virus	1 and 5 9 and 12
	Important for Membrane Fusion", pages 506-514, see pages 506 and 510-513.	1 and 6
х Y	JOURNAL OF VIROLOGY, Volume 67, Number 9, issued September 1993, Wang et al, "Ion Channel Activity of Influenza A Virus M2 Protein: Characterization of the Amantidine Block", pages 5585-94, see pages 5585-86.	9 and 13
X Y	JOURNAL OF VIROLOGY, Volume 67, Number 5, issued May 1993, Lazinski et al, "Relating Structure to Function in the Hepatitis Delta Virus Antigen", pages 2672-80, see pages 2672-73 and 2678.	1 and 7 9 and 14
P, Y	JOURNAL OF EXPERIMENTAL MEDICINE, Volume 182, Number 2, issued August 1995, Suzuki et al, "Viral Interleukin 10 (IL-10), the Human Herpes Virus 4 Cellular IL-10 Homologue, Induces Local Anergy to Allogenic and Syngeneic Tumors", pages 477-486, see entire document.	1, 8, 9, and 15